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(54) Title: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF LUNG CANCER

(57) Abstract: Compositions and methods for the therapy and diagnosis of cancer, such as lung cancer, are disclosed. Compositions may comprise one or more lung tumor proteins, immunogenic portions thereof, or polynucleotides that encode such portions. Alternatively, a therapeutic composition may comprise an antigen presenting cell that expresses a lung tumor protein, or a T cell that is specific for cells expressing such a protein. Such compositions may be used, for example, for the prevention and treatment of diseases such as lung cancer. Diagnostic methods based on detecting a lung tumor protein, or mRNA encoding such a protein, in a sample are also provided.

COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF LUNG CANCER

TECHNICAL FIELD OF THE INVENTION

The present invention relates generally to therapy and diagnosis of cancer, such as lung cancer. The invention is more specifically related to polypeptides comprising at least a portion of a lung tumor protein, and to polynucleotides encoding such polypeptides. Such polypeptides and polynucleotides may be used in compositions for prevention and treatment of lung cancer, and for the diagnosis and monitoring of such cancers.

10 BACKGROUND OF THE INVENTION

Cancer is a significant health problem throughout the world. Although advances have been made in detection and therapy of cancer, no vaccine or other universally successful method for prevention or treatment is currently available. Current therapies, which are generally based on a combination of chemotherapy or surgery and radiation, continue to prove inadequate in many patients.

Lung cancer is the primary cause of cancer death among both men and women in the U.S., with an estimated 172,000 new cases being reported in 1994. The five-year survival rate among all lung cancer patients, regardless of the stage of disease at diagnosis, is only 13%. This contrasts with a five-year survival rate of 46% among cases detected while the disease is still localized. However, only 16% of lung cancers are discovered before the disease has spread.

Early detection is difficult since clinical symptoms are often not seen until the disease has reached an advanced stage. Currently, diagnosis is aided by the use of chest x-rays, analysis of the type of cells contained in sputum and fiberoptic examination of the bronchial passages. Treatment regimens are determined by the type and stage of the cancer, and include surgery, radiation therapy and/or chemotherapy.

In spite of considerable research into therapies for this and other cancers, lung cancer remains difficult to diagnose and treat effectively. Accordingly, there is a

need in the art for improved methods for detecting and treating such cancers. The present invention fulfills these needs and further provides other related advantages.

SUMMARY OF THE INVENTION

Briefly stated, the present invention provides compositions and methods
5 for the diagnosis and therapy of cancer, such as lung cancer. In one aspect, the present invention provides polypeptides comprising at least a portion of a lung tumor protein, or a variant thereof. Certain portions and other variants are immunogenic, such that the ability of the variant to react with antigen-specific antisera is not substantially diminished. Within certain embodiments, the polypeptide comprises a sequence that is
10 encoded by a polynucleotide sequence selected from the group consisting of: (a) sequences recited in SEQ ID NO: 1, 11-13, 15, 20, 23-27, 29, 30, 33, 34, 39, 41, 43-46, 51, 52, 57, 58, 60, 62, 65-67, 69-71, 74, 76, 79, 80, 84, 86, 89-92, 95, 97, 98, 101, 110, 111, 113-119, 121-128, 130-134, 136, 138, 139, 141, 143, 146-151, 153, 154, 157-160, 162-164, 167-178, 180, 181, 183, 186-190, 192, 193, 195-220, 224, 226-231, 234, 236,
15 237, 240, 241, 244-246, 248, 254, 255, 261, 262, 266, 270, 275, 280, 282, 283, 288, 289, 290, 292, 295, 301, 303, 304, 309, 311, 341-782, 784, 785, 790, 792, 794, 796, 800-804, 807, 808 and 810-826; (b) variants of a sequence recited in SEQ ID NO: 1, 11-13, 15, 20, 23-27, 29, 30, 33, 34, 39, 41, 43-46, 51, 52, 57, 58, 60, 62, 65-67, 69-71, 74, 76, 79, 80, 84, 86, 89-92, 95, 97, 98, 101, 110, 111, 113-119, 121-128, 130-134,
20 136, 138, 139, 141, 143, 146-151, 153, 154, 157-160, 162-164, 167-178, 180, 181, 183, 186-190, 192, 193, 195-220, 224, 226-231, 234, 236, 237, 240, 241, 244-246, 248, 254, 255, 261, 262, 266, 270, 275, 280, 282, 283, 288, 289, 290, 292, 295, 301, 303, 304, 309, 311, 341-782, 784, 785, 790, 792, 794, 796, 800-804, 807, 808 and 810-826; and (c) complements of a sequence of (a) or (b). In specific embodiments, the polypeptides
25 of the present invention comprise at least a portion of a tumor protein that includes an amino acid sequence selected from the group consisting of sequences recited in SEQ ID NO: 786, 787, 791, 793, 795, 797-799, 806, 809 and 827, and variants thereof.

The present invention further provides polynucleotides that encode a polypeptide as described above, or a portion thereof (such as a portion encoding at least

15 amino acid residues of a lung tumor protein), expression vectors comprising such polynucleotides and host cells transformed or transfected with such expression vectors.

Within other aspects, the present invention provides pharmaceutical compositions comprising a polypeptide or polynucleotide as described above and a
5 physiologically acceptable carrier.

Within a related aspect of the present invention, vaccines, or immunogenic compositions, for prophylactic or therapeutic use are provided. Such vaccines comprise a polypeptide or polynucleotide as described above and an immunostimulant.

10 The present invention further provides pharmaceutical compositions that comprise: (a) an antibody or antigen-binding fragment thereof that specifically binds to a lung tumor protein; and (b) a physiologically acceptable carrier.

Within further aspects, the present invention provides pharmaceutical compositions comprising: (a) an antigen presenting cell that expresses a polypeptide as
15 described above and (b) a pharmaceutically acceptable carrier or excipient. Antigen presenting cells include dendritic cells, macrophages, monocytes, fibroblasts and B cells.

Within related aspects, vaccines, or immunogenic compositions, are provided that comprise: (a) an antigen presenting cell that expresses a polypeptide as
20 described above and (b) an immunostimulant.

The present invention further provides, in other aspects, fusion proteins that comprise at least one polypeptide as described above, as well as polynucleotides encoding such fusion proteins.

Within related aspects, pharmaceutical compositions comprising a fusion
25 protein, or a polynucleotide encoding a fusion protein, in combination with a physiologically acceptable carrier are provided.

Vaccines, or immunogenic compositions, are further provided, within other aspects, that comprise a fusion protein, or a polynucleotide encoding a fusion protein, in combination with an immunostimulant.

30 Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a

patient a pharmaceutical composition or immunogenic composition as recited above. The patient may be afflicted with lung cancer, in which case the methods provide treatment for the disease, or patient considered at risk for such a disease may be treated prophylactically.

5 The present invention further provides, within other aspects, methods for removing tumor cells from a biological sample, comprising contacting a biological sample with T cells that specifically react with a lung tumor protein, wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the protein from the sample.

10 Within related aspects, methods are provided for inhibiting the development of a cancer in a patient, comprising administering to a patient a biological sample treated as described above.

 Methods are further provided, within other aspects, for stimulating and/or expanding T cells specific for a lung tumor protein, comprising contacting T
15 cells with one or more of: (i) a polypeptide as described above; (ii) a polynucleotide encoding such a polypeptide; and/or (iii) an antigen presenting cell that expresses such a polypeptide; under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells. Isolated T cell populations comprising T cells prepared as described above are also provided.

20 Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a T cell population as described above.

 The present invention further provides methods for inhibiting the development of a cancer in a patient, comprising the steps of: (a) incubating CD4⁺
25 and/or CD8⁺ T cells isolated from a patient with one or more of: (i) a polypeptide comprising at least an immunogenic portion of a lung tumor protein; (ii) a polynucleotide encoding such a polypeptide; and (iii) an antigen-presenting cell that expressed such a polypeptide; and (b) administering to the patient an effective amount of the proliferated T cells, and thereby inhibiting the development of a cancer in the
30 patient. Proliferated cells may, but need not, be cloned prior to administration to the patient.

Within further aspects, the present invention provides methods for determining the presence or absence of a cancer in a patient, comprising: (a) contacting a biological sample obtained from a patient with a binding agent that binds to a polypeptide as recited above; (b) detecting in the sample an amount of polypeptide that
5 binds to the binding agent; and (c) comparing the amount of polypeptide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within preferred embodiments, the binding agent is an antibody, more preferably a monoclonal antibody. The cancer may be lung cancer.

The present invention also provides, within other aspects, methods for
10 monitoring the progression of a cancer in a patient. Such methods comprise the steps of: (a) contacting a biological sample obtained from a patient at a first point in time with a binding agent that binds to a polypeptide as recited above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in
15 time; and (d) comparing the amount of polypeptide detected in step (c) with the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

The present invention further provides, within other aspects, methods for determining the presence or absence of a cancer in a patient, comprising the steps of: (a)
20 contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a lung tumor protein; (b) detecting in the sample a level of a polynucleotide, preferably mRNA, that hybridizes to the oligonucleotide; and (c) comparing the level of polynucleotide that hybridizes to the oligonucleotide with a predetermined cut-off value, and therefrom determining the
25 presence or absence of a cancer in the patient. Within certain embodiments, the amount of mRNA is detected via polymerase chain reaction using, for example, at least one oligonucleotide primer that hybridizes to a polynucleotide encoding a polypeptide as recited above, or a complement of such a polynucleotide. Within other embodiments, the amount of mRNA is detected using a hybridization technique, employing an
30 oligonucleotide probe that hybridizes to a polynucleotide that encodes a polypeptide as recited above, or a complement of such a polynucleotide.

In related aspects, methods are provided for monitoring the progression of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a lung tumor protein; (b) detecting in the sample an amount of a polynucleotide
5 that hybridizes to the oligonucleotide; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polynucleotide detected in step (c) with the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

Within further aspects, the present invention provides antibodies, such as
10 monoclonal antibodies, that bind to a polypeptide as described above, as well as diagnostic kits comprising such antibodies. Diagnostic kits comprising one or more oligonucleotide probes or primers as described above are also provided.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All
15 references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

SEQUENCE IDENTIFIERS

SEQ ID NO: 1 is the determined cDNA sequence for clone #19038, also referred to as L845P.

20 SEQ ID NO: 2 is the determined cDNA sequence for clone #19036.

SEQ ID NO: 3 is the determined cDNA sequence for clone #19034.

SEQ ID NO: 4 is the determined cDNA sequence for clone #19033.

SEQ ID NO: 5 is the determined cDNA sequence for clone #19032.

25 SEQ ID NO: 6 is the determined cDNA sequence for clone #19030, also referred to as L559S.

SEQ ID NO: 7 is the determined cDNA sequence for clone #19029.

SEQ ID NO: 8 is the determined cDNA sequence for clone #19025.

SEQ ID NO: 9 is the determined cDNA sequence for clone #19023.

SEQ ID NO: 10 is the determined cDNA sequence for clone #18929.

30 SEQ ID NO: 11 is the determined cDNA sequence for clone #19010.

SEQ ID NO: 12 is the determined cDNA sequence for clone #19009.

SEQ ID NO: 13 is the determined cDNA sequence for clones #19005, 19007, 19016 and 19017.

SEQ ID NO: 14 is the determined cDNA sequence for clone #19004.

5 SEQ ID NO: 15 is the determined cDNA sequence for clones #19002 and 18965.

SEQ ID NO: 16 is the determined cDNA sequence for clone #18998.

SEQ ID NO: 17 is the determined cDNA sequence for clone #18997.

SEQ ID NO: 18 is the determined cDNA sequence for clone #18996.

10 SEQ ID NO: 19 is the determined cDNA sequence for clone #18995.

SEQ ID NO: 20 is the determined cDNA sequence for clone #18994, also known as L846P.

SEQ ID NO: 21 is the determined cDNA sequence for clone #18992.

SEQ ID NO: 22 is the determined cDNA sequence for clone #18991.

15 SEQ ID NO: 23 is the determined cDNA sequence for clone #18990, also referred to as clone #20111.

SEQ ID NO: 24 is the determined cDNA sequence for clone #18987.

SEQ ID NO: 25 is the determined cDNA sequence for clone #18985, also referred to as L839P.

20 SEQ ID NO: 26 is the determined cDNA sequence for clone #18984, also referred to as L847P.

SEQ ID NO: 27 is the determined cDNA sequence for clone #18983.

SEQ ID NO: 28 is the determined cDNA sequence for clones #18976 and 18980.

25 SEQ ID NO: 29 is the determined cDNA sequence for clone #18975.

SEQ ID NO: 30 is the determined cDNA sequence for clone #18974.

SEQ ID NO: 31 is the determined cDNA sequence for clone #18973.

SEQ ID NO: 32 is the determined cDNA sequence for clone #18972.

30 SEQ ID NO: 33 is the determined cDNA sequence for clone #18971, also referred to as L801P.

SEQ ID NO: 34 is the determined cDNA sequence for clone #18970.

SEQ ID NO: 35 is the determined cDNA sequence for clone #18966.

SEQ ID NO: 36 is the determined cDNA sequence for clones #18964,
18968 and 19039.

SEQ ID NO: 37 is the determined cDNA sequence for clone #18960.

5 SEQ ID NO: 38 is the determined cDNA sequence for clone #18959.

SEQ ID NO: 39 is the determined cDNA sequence for clones #18958
and 18982.

SEQ ID NO: 40 is the determined cDNA sequence for clones #18956
and 19015.

10 SEQ ID NO: 41 is the determined cDNA sequence for clone #18954,
also referred to L848P.

SEQ ID NO: 42 is the determined cDNA sequence for clone #18951.

SEQ ID NO: 43 is the determined cDNA sequence for clone #18950.

15 SEQ ID NO: 44 is the determined cDNA sequence for clones #18949
and 19024, also referred to as L844P.

SEQ ID NO: 45 is the determined cDNA sequence for clone #18948.

SEQ ID NO: 46 is the determined cDNA sequence for clone #18947,
also referred to as L840P.

20 SEQ ID NO: 47 is the determined cDNA sequence for clones #18946,
18953, 18969 and 19027.

SEQ ID NO: 48 is the determined cDNA sequence for clone #18942.

SEQ ID NO: 49 is the determined cDNA sequence for clone #18940,
18962, 18963, 19006, 19008, 19000, and 19031.

SEQ ID NO: 50 is the determined cDNA sequence for clone #18939.

25 SEQ ID NO: 51 is the determined cDNA sequence for clones #18938
and 18952.

SEQ ID NO: 52 is the determined cDNA sequence for clone #18938.

SEQ ID NO: 53 is the determined cDNA sequence for clone #18937.

30 SEQ ID NO: 54 is the determined cDNA sequence for clones #18934,
18935, 18993 and 19022, also referred to as L548S.

SEQ ID NO: 55 is the determined cDNA sequence for clone #18932.

SEQ ID NO: 56 is the determined cDNA sequence for clones #18931 and 18936.

SEQ ID NO: 57 is the determined cDNA sequence for clone #18930.

5 SEQ ID NO: 58 is the determined cDNA sequence for clone #19014, also referred to as L773P.

SEQ ID NO: 59 is the determined cDNA sequence for clone #19127.

SEQ ID NO: 60 is the determined cDNA sequence for clones #19057 and 19064.

SEQ ID NO: 61 is the determined cDNA sequence for clone #19122.

10 SEQ ID NO: 62 is the determined cDNA sequence for clones #19120 and 18121.

SEQ ID NO: 63 is the determined cDNA sequence for clone #19118.

SEQ ID NO: 64 is the determined cDNA sequence for clone #19117.

SEQ ID NO: 65 is the determined cDNA sequence for clone #19116.

15 SEQ ID NO: 66 is the determined cDNA sequence for clone #19114.

SEQ ID NO: 67 is the determined cDNA sequence for clone #19112, also known as L561S.

SEQ ID NO: 68 is the determined cDNA sequence for clone #19110.

20 SEQ ID NO: 69 is the determined cDNA sequence for clone #19107, also referred to as L552S.

SEQ ID NO: 70 is the determined cDNA sequence for clone #19106, also referred to as L547S.

SEQ ID NO: 71 is the determined cDNA sequence for clones #19105 and 19111.

25 SEQ ID NO: 72 is the determined cDNA sequence for clone #19099.

SEQ ID NO: 73 is the determined cDNA sequence for clones #19095, 19104 and 19125, also referred to as L549S.

SEQ ID NO: 74 is the determined cDNA sequence for clone #19094.

30 SEQ ID NO: 75 is the determined cDNA sequence for clones #19089 and 19101.

SEQ ID NO: 76 is the determined cDNA sequence for clone #19088.

SEQ ID NO: 77 is the determined cDNA sequence for clones #19087, 19092, 19096, 19100 and 19119.

SEQ ID NO: 78 is the determined cDNA sequence for clone #19086.

SEQ ID NO: 79 is the determined cDNA sequence for clone #19085,
5 also referred to as L550S.

SEQ ID NO: 80 is the determined cDNA sequence for clone #19084,
also referred to as clone #19079.

SEQ ID NO: 81 is the determined cDNA sequence for clone #19082.

SEQ ID NO: 82 is the determined cDNA sequence for clone #19080.

10 SEQ ID NO: 83 is the determined cDNA sequence for clone #19077.

SEQ ID NO: 84 is the determined cDNA sequence for clone #19076,
also referred to as L551S.

SEQ ID NO: 85 is the determined cDNA sequence for clone #19074,
also referred to as clone #20102.

15 SEQ ID NO: 86 is the determined cDNA sequence for clone #19073,
also referred to as L560S.

SEQ ID NO: 87 is the determined cDNA sequence for clones #19072
and 19115.

SEQ ID NO: 88 is the determined cDNA sequence for clone #19071.

20 SEQ ID NO: 89 is the determined cDNA sequence for clone #19070.

SEQ ID NO: 90 is the determined cDNA sequence for clone #19069.

SEQ ID NO: 91 is the determined cDNA sequence for clone #19068,
also referred to L563S.

SEQ ID NO: 92 is the determined cDNA sequence for clone #19066.

25 SEQ ID NO: 93 is the determined cDNA sequence for clone #19065.

SEQ ID NO: 94 is the determined cDNA sequence for clone #19063.

SEQ ID NO: 95 is the determined cDNA sequence for clones #19061,
19081, 19108 and 19109.

30 SEQ ID NO: 96 is the determined cDNA sequence for clones #19060,
19067 and 19083, also referred to as L548S.

SEQ ID NO: 97 is the determined cDNA sequence for clones #19059
and 19062.

SEQ ID NO: 98 is the determined cDNA sequence for clone #19058.

SEQ ID NO: 99 is the determined cDNA sequence for clone #19124.

5 SEQ ID NO: 100 is the determined cDNA sequence for clone #18929.

SEQ ID NO: 101 is the determined cDNA sequence for clone #18422.

SEQ ID NO: 102 is the determined cDNA sequence for clone #18425.

SEQ ID NO: 103 is the determined cDNA sequence for clone #18431.

SEQ ID NO: 104 is the determined cDNA sequence for clone #18433.

10 SEQ ID NO: 105 is the determined cDNA sequence for clone #18444.

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SEQ ID NO: 107 is the determined cDNA sequence for clone #18451.

SEQ ID NO: 108 is the determined cDNA sequence for clone #18452.

SEQ ID NO: 109 is the determined cDNA sequence for clone #18455.

15 SEQ ID NO: 110 is the determined cDNA sequence for clone #18457.

SEQ ID NO: 111 is the determined cDNA sequence for clone #18466.

SEQ ID NO: 112 is the determined cDNA sequence for clone #18468.

SEQ ID NO: 113 is the determined cDNA sequence for clone #18471.

SEQ ID NO: 114 is the determined cDNA sequence for clone #18475.

20 SEQ ID NO: 115 is the determined cDNA sequence for clone #18476.

SEQ ID NO: 116 is the determined cDNA sequence for clone #18477.

SEQ ID NO: 117 is the determined cDNA sequence for clone #20631.

SEQ ID NO: 118 is the determined cDNA sequence for clone #20634.

SEQ ID NO: 119 is the determined cDNA sequence for clone #20635.

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SEQ ID NO: 123 is the determined cDNA sequence for clone #20652.

SEQ ID NO: 124 is the determined cDNA sequence for clone #20653.

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SEQ ID NO: 130 is the determined cDNA sequence for clone #20665.
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SEQ ID NO: 132 is the determined cDNA sequence for clone #20671.
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SEQ ID NO: 134 is the determined cDNA sequence for clone #20675.
SEQ ID NO: 135 is the determined cDNA sequence for clone #20679.
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15 SEQ ID NO: 141 is the determined cDNA sequence for clone #20699.
SEQ ID NO: 142 is the determined cDNA sequence for clone #20701.
SEQ ID NO: 143 is the determined cDNA sequence for clone #20702.
SEQ ID NO: 144 is the determined cDNA sequence for clone #20708.
SEQ ID NO: 145 is the determined cDNA sequence for clone #20715.
20 SEQ ID NO: 146 is the determined cDNA sequence for clone #20716.
SEQ ID NO: 147 is the determined cDNA sequence for clone #20719.
SEQ ID NO: 148 is the determined cDNA sequence for clone #19129.
SEQ ID NO: 149 is the determined cDNA sequence for clone #19131.1.
SEQ ID NO: 150 is the determined cDNA sequence for clone #19132.2.
25 SEQ ID NO: 151 is the determined cDNA sequence for clone #19133.
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SEQ ID NO: 154 is the determined cDNA sequence for clone #19137.
SEQ ID NO: 155 is a first determined cDNA sequence for clone
30 #19138.1.

- SEQ ID NO: 156 is a second determined cDNA sequence for clone #19138.2.
- SEQ ID NO: 157 is the determined cDNA sequence for clone #19139.
- SEQ ID NO: 158 is a first determined cDNA sequence for clone #19140.1.
- SEQ ID NO: 159 is a second determined cDNA sequence for clone #19140.2.
- SEQ ID NO: 160 is the determined cDNA sequence for clone #19141.
- SEQ ID NO: 161 is the determined cDNA sequence for clone #19143.
- SEQ ID NO: 162 is the determined cDNA sequence for clone #19144.
- SEQ ID NO: 163 is a first determined cDNA sequence for clone #19145.1.
- SEQ ID NO: 164 is a second determined cDNA sequence for clone #19145.2.
- SEQ ID NO: 165 is the determined cDNA sequence for clone #19146.
- SEQ ID NO: 166 is the determined cDNA sequence for clone #19149.1.
- SEQ ID NO: 167 is the determined cDNA sequence for clone #19152.
- SEQ ID NO: 168 is a first determined cDNA sequence for clone #19153.1.
- SEQ ID NO: 169 is a second determined cDNA sequence for clone #19153.2.
- SEQ ID NO: 170 is the determined cDNA sequence for clone #19155.
- SEQ ID NO: 171 is the determined cDNA sequence for clone #19157.
- SEQ ID NO: 172 is the determined cDNA sequence for clone #19159.
- SEQ ID NO: 173 is the determined cDNA sequence for clone #19160.
- SEQ ID NO: 174 is a first determined cDNA sequence for clone #19161.1.
- SEQ ID NO: 175 is a second determined cDNA sequence for clone #19161.2.
- SEQ ID NO: 176 is the determined cDNA sequence for clone #19162.1.
- SEQ ID NO: 177 is the determined cDNA sequence for clone #19166.

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SEQ ID NO: 180 is a first determined cDNA sequence for clone
#19173.1.
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#19173.2.
SEQ ID NO: 182 is the determined cDNA sequence for clone #19174.1.
SEQ ID NO: 183 is the determined cDNA sequence for clone #19175.
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SEQ ID NO: 189 is a first determined cDNA sequence for clone
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SEQ ID NO: 191 is the determined cDNA sequence for clone #19183.1.
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20 SEQ ID NO: 193 is the determined cDNA sequence for clone #19187.
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SEQ ID NO: 195 is the determined cDNA sequence for clone #19190.
SEQ ID NO: 196 is the determined cDNA sequence for clone #19191.
SEQ ID NO: 197 is the determined cDNA sequence for clone #19192.
25 SEQ ID NO: 198 is the determined cDNA sequence for clone #19193.
SEQ ID NO: 199 is a first determined cDNA sequence for clone
#19194.1.
SEQ ID NO: 200 is a second determined cDNA sequence for clone
#19194.2.
30 SEQ ID NO: 201 is the determined cDNA sequence for clone #19197.

- SEQ ID NO: 202 is a first determined cDNA sequence for clone #19200.1.
- SEQ ID NO: 203 is a second determined cDNA sequence for clone #19200.2.
- 5 SEQ ID NO: 204 is the determined cDNA sequence for clone #19202.
- SEQ ID NO: 205 is a first determined cDNA sequence for clone #19204.1.
- SEQ ID NO: 206 is a second determined cDNA sequence for clone #19204.2.
- 10 SEQ ID NO: 207 is the determined cDNA sequence for clone #19205.
- SEQ ID NO: 208 is a first determined cDNA sequence for clone #19206.1.
- SEQ ID NO: 209 is a second determined cDNA sequence for clone #19206.2.
- 15 SEQ ID NO: 210 is the determined cDNA sequence for clone #19207.
- SEQ ID NO: 211 is the determined cDNA sequence for clone #19208.
- SEQ ID NO: 212 is a first determined cDNA sequence for clone #19211.1.
- SEQ ID NO: 213 is a second determined cDNA sequence for clone #19211.2.
- 20 SEQ ID NO: 214 is a first determined cDNA sequence for clone #19214.1.
- SEQ ID NO: 215 is a second determined cDNA sequence for clone #19214.2.
- 25 SEQ ID NO: 216 is the determined cDNA sequence for clone #19215.
- SEQ ID NO: 217 is a first determined cDNA sequence for clone #19217.2.
- 2.
- SEQ ID NO: 218 is a second determined cDNA sequence for clone #19217.2.
- 30 SEQ ID NO: 219 is a first determined cDNA sequence for clone #19218.1.

SEQ ID NO: 220 is a second determined cDNA sequence for clone #19218.2.

SEQ ID NO: 221 is a first determined cDNA sequence for clone #19220.1.

5 SEQ ID NO: 222 is a second determined cDNA sequence for clone #19220.2.

SEQ ID NO: 223 is the determined cDNA sequence for clone #22015.

SEQ ID NO: 224 is the determined cDNA sequence for clone #22017.

SEQ ID NO: 225 is the determined cDNA sequence for clone #22019.

10 SEQ ID NO: 226 is the determined cDNA sequence for clone #22020.

SEQ ID NO: 227 is the determined cDNA sequence for clone #22023.

SEQ ID NO: 228 is the determined cDNA sequence for clone #22026.

SEQ ID NO: 229 is the determined cDNA sequence for clone #22027.

SEQ ID NO: 230 is the determined cDNA sequence for clone #22028.

15 SEQ ID NO: 231 is the determined cDNA sequence for clone #22032.

SEQ ID NO: 232 is the determined cDNA sequence for clone #22037.

SEQ ID NO: 233 is the determined cDNA sequence for clone #22045.

SEQ ID NO: 234 is the determined cDNA sequence for clone #22048.

SEQ ID NO: 235 is the determined cDNA sequence for clone #22050.

20 SEQ ID NO: 236 is the determined cDNA sequence for clone #22052.

SEQ ID NO: 237 is the determined cDNA sequence for clone #22053.

SEQ ID NO: 238 is the determined cDNA sequence for clone #22057.

SEQ ID NO: 239 is the determined cDNA sequence for clone #22066.

SEQ ID NO: 240 is the determined cDNA sequence for clone #22077.

25 SEQ ID NO: 241 is the determined cDNA sequence for clone #22085.

SEQ ID NO: 242 is the determined cDNA sequence for clone #22105.

SEQ ID NO: 243 is the determined cDNA sequence for clone #22108.

SEQ ID NO: 244 is the determined cDNA sequence for clone #22109.

SEQ ID NO: 245 is the determined cDNA sequence for clone #24842.

30 SEQ ID NO: 246 is the determined cDNA sequence for clone #24843.

SEQ ID NO: 247 is the determined cDNA sequence for clone #24845.

SEQ ID NO: 248 is the determined cDNA sequence for clone #24851.
SEQ ID NO: 249 is the determined cDNA sequence for clone #24852.
SEQ ID NO: 250 is the determined cDNA sequence for clone #24853.
SEQ ID NO: 251 is the determined cDNA sequence for clone #24854.
5 SEQ ID NO: 252 is the determined cDNA sequence for clone #24855.
SEQ ID NO: 253 is the determined cDNA sequence for clone #24860.
SEQ ID NO: 254 is the determined cDNA sequence for clone #24864.
SEQ ID NO: 255 is the determined cDNA sequence for clone #24866.
SEQ ID NO: 256 is the determined cDNA sequence for clone #24867.
10 SEQ ID NO: 257 is the determined cDNA sequence for clone #24868.
SEQ ID NO: 258 is the determined cDNA sequence for clone #24869.
SEQ ID NO: 259 is the determined cDNA sequence for clone #24870.
SEQ ID NO: 260 is the determined cDNA sequence for clone #24872.
SEQ ID NO: 261 is the determined cDNA sequence for clone #24873.
15 SEQ ID NO: 262 is the determined cDNA sequence for clone #24875.
SEQ ID NO: 263 is the determined cDNA sequence for clone #24882.
SEQ ID NO: 264 is the determined cDNA sequence for clone #24885.
SEQ ID NO: 265 is the determined cDNA sequence for clone #24886.
SEQ ID NO: 266 is the determined cDNA sequence for clone #24887.
20 SEQ ID NO: 267 is the determined cDNA sequence for clone #24888.
SEQ ID NO: 268 is the determined cDNA sequence for clone #24890.
SEQ ID NO: 269 is the determined cDNA sequence for clone #24896.
SEQ ID NO: 270 is the determined cDNA sequence for clone #24897.
SEQ ID NO: 271 is the determined cDNA sequence for clone #24899.
25 SEQ ID NO: 272 is the determined cDNA sequence for clone #24901.
SEQ ID NO: 273 is the determined cDNA sequence for clone #24902.
SEQ ID NO: 274 is the determined cDNA sequence for clone #24906.
SEQ ID NO: 275 is the determined cDNA sequence for clone #24912.
SEQ ID NO: 276 is the determined cDNA sequence for clone #24913.
30 SEQ ID NO: 277 is the determined cDNA sequence for clone #24920.
SEQ ID NO: 278 is the determined cDNA sequence for clone #24927.

SEQ ID NO: 279 is the determined cDNA sequence for clone #24930.
SEQ ID NO: 280 is the determined cDNA sequence for clone #26938.
SEQ ID NO: 281 is the determined cDNA sequence for clone #26939.
SEQ ID NO: 282 is the determined cDNA sequence for clone #26943.
5 SEQ ID NO: 283 is the determined cDNA sequence for clone #26948.
SEQ ID NO: 284 is the determined cDNA sequence for clone #26951.
SEQ ID NO: 285 is the determined cDNA sequence for clone #26955.
SEQ ID NO: 286 is the determined cDNA sequence for clone #26956.
SEQ ID NO: 287 is the determined cDNA sequence for clone #26959.
10 SEQ ID NO: 288 is the determined cDNA sequence for clone #26961.
SEQ ID NO: 289 is the determined cDNA sequence for clone #26962.
SEQ ID NO: 290 is the determined cDNA sequence for clone #26964.
SEQ ID NO: 291 is the determined cDNA sequence for clone #26966.
SEQ ID NO: 292 is the determined cDNA sequence for clone #26968.
15 SEQ ID NO: 293 is the determined cDNA sequence for clone #26972.
SEQ ID NO: 294 is the determined cDNA sequence for clone #26973.
SEQ ID NO: 295 is the determined cDNA sequence for clone #26974.
SEQ ID NO: 296 is the determined cDNA sequence for clone #26976.
SEQ ID NO: 297 is the determined cDNA sequence for clone #26977.
20 SEQ ID NO: 298 is the determined cDNA sequence for clone #26979.
SEQ ID NO: 299 is the determined cDNA sequence for clone #26980.
SEQ ID NO: 300 is the determined cDNA sequence for clone #26981.
SEQ ID NO: 301 is the determined cDNA sequence for clone #26984.
SEQ ID NO: 302 is the determined cDNA sequence for clone #26985.
25 SEQ ID NO: 303 is the determined cDNA sequence for clone #26986.
SEQ ID NO: 304 is the determined cDNA sequence for clone #26993.
SEQ ID NO: 305 is the determined cDNA sequence for clone #26994.
SEQ ID NO: 306 is the determined cDNA sequence for clone #26995.
SEQ ID NO: 307 is the determined cDNA sequence for clone #27003.
30 SEQ ID NO: 308 is the determined cDNA sequence for clone #27005.
SEQ ID NO: 309 is the determined cDNA sequence for clone #27010.

SEQ ID NO: 310 is the determined cDNA sequence for clone #27011.
SEQ ID NO: 311 is the determined cDNA sequence for clone #27013.
SEQ ID NO: 312 is the determined cDNA sequence for clone #27016
SEQ ID NO: 313 is the determined cDNA sequence for clone #27017.
5 SEQ ID NO: 314 is the determined cDNA sequence for clone #27019.
SEQ ID NO: 315 is the determined cDNA sequence for clone #27028.
SEQ ID NO: 316 is the full-length cDNA sequence for clone #19060.
SEQ ID NO: 317 is the full-length cDNA sequence for clone #18964.
SEQ ID NO: 318 is the full-length cDNA sequence for clone #18929.
10 SEQ ID NO: 319 is the full-length cDNA sequence for clone #18991.
SEQ ID NO: 320 is the full-length cDNA sequence for clone #18996.
SEQ ID NO: 321 is the full-length cDNA sequence for clone #18966.
SEQ ID NO: 322 is the full-length cDNA sequence for clone #18951.
SEQ ID NO: 323 is the full-length cDNA sequence for clone #18973
15 (also known as L516S).
SEQ ID NO: 324 is the amino acid sequence for clone #19060.
SEQ ID NO: 325 is the amino acid sequence for clone #19063.
SEQ ID NO: 326 is the amino acid sequence for clone #19077.
SEQ ID NO: 327 is the amino acid sequence for clone #19110.
20 SEQ ID NO: 328 is the amino acid sequence for clone #19122.
SEQ ID NO: 329 is the amino acid sequence for clone #19118.
SEQ ID NO: 330 is the amino acid sequence for clone #19080.
SEQ ID NO: 331 is the amino acid sequence for clone #19127.
SEQ ID NO: 332 is the amino acid sequence for clone #19117.
25 SEQ ID NO: 333 is the amino acid sequence for clone #19095, also
referred to L549S.
SEQ ID NO: 334 is the amino acid sequence for clone #18964.
SEQ ID NO: 335 is the amino acid sequence for clone #18929.
SEQ ID NO: 336 is the amino acid sequence for clone #18991.
30 SEQ ID NO: 337 is the amino acid sequence for clone #18996.
SEQ ID NO: 338 is the amino acid sequence for clone #18966.

SEQ ID NO: 339 is the amino acid sequence for clone #18951.
SEQ ID NO: 340 is the amino acid sequence for clone #18973.
SEQ ID NO: 341 is the determined cDNA sequence for clone 26461.
SEQ ID NO: 342 is the determined cDNA sequence for clone 26462.
5 SEQ ID NO: 343 is the determined cDNA sequence for clone 26463.
SEQ ID NO: 344 is the determined cDNA sequence for clone 26464.
SEQ ID NO: 345 is the determined cDNA sequence for clone 26465.
SEQ ID NO: 346 is the determined cDNA sequence for clone 26466.
SEQ ID NO: 347 is the determined cDNA sequence for clone 26467.
10 SEQ ID NO: 348 is the determined cDNA sequence for clone 26468.
SEQ ID NO: 349 is the determined cDNA sequence for clone 26469.
SEQ ID NO: 350 is the determined cDNA sequence for clone 26470.
SEQ ID NO: 351 is the determined cDNA sequence for clone 26471.
SEQ ID NO: 352 is the determined cDNA sequence for clone 26472.
15 SEQ ID NO: 353 is the determined cDNA sequence for clone 26474.
SEQ ID NO: 354 is the determined cDNA sequence for clone 26475.
SEQ ID NO: 355 is the determined cDNA sequence for clone 26476.
SEQ ID NO: 356 is the determined cDNA sequence for clone 26477.
SEQ ID NO: 357 is the determined cDNA sequence for clone 26478.
20 SEQ ID NO: 358 is the determined cDNA sequence for clone 26479.
SEQ ID NO: 359 is the determined cDNA sequence for clone 26480.
SEQ ID NO: 360 is the determined cDNA sequence for clone 26481.
SEQ ID NO: 361 is the determined cDNA sequence for clone 26482.
SEQ ID NO: 362 is the determined cDNA sequence for clone 26483.
25 SEQ ID NO: 363 is the determined cDNA sequence for clone 26484.
SEQ ID NO: 364 is the determined cDNA sequence for clone 26485.
SEQ ID NO: 365 is the determined cDNA sequence for clone 26486.
SEQ ID NO: 366 is the determined cDNA sequence for clone 26487.
SEQ ID NO: 367 is the determined cDNA sequence for clone 26488.
30 SEQ ID NO: 368 is the determined cDNA sequence for clone 26489.
SEQ ID NO: 369 is the determined cDNA sequence for clone 26490.

SEQ ID NO: 370 is the determined cDNA sequence for clone 26491.
SEQ ID NO: 371 is the determined cDNA sequence for clone 26492.
SEQ ID NO: 372 is the determined cDNA sequence for clone 26493.
SEQ ID NO: 373 is the determined cDNA sequence for clone 26494.
5 SEQ ID NO: 374 is the determined cDNA sequence for clone 26495.
SEQ ID NO: 375 is the determined cDNA sequence for clone 26496.
SEQ ID NO: 376 is the determined cDNA sequence for clone 26497.
SEQ ID NO: 377 is the determined cDNA sequence for clone 26498.
SEQ ID NO: 378 is the determined cDNA sequence for clone 26499.
10 SEQ ID NO: 379 is the determined cDNA sequence for clone 26500.
SEQ ID NO: 380 is the determined cDNA sequence for clone 26501.
SEQ ID NO: 381 is the determined cDNA sequence for clone 26502.
SEQ ID NO: 382 is the determined cDNA sequence for clone 26503.
SEQ ID NO: 383 is the determined cDNA sequence for clone 26504.
15 SEQ ID NO: 384 is the determined cDNA sequence for clone 26505.
SEQ ID NO: 385 is the determined cDNA sequence for clone 26506.
SEQ ID NO: 386 is the determined cDNA sequence for clone 26507.
SEQ ID NO: 387 is the determined cDNA sequence for clone 26508.
SEQ ID NO: 388 is the determined cDNA sequence for clone 26509.
20 SEQ ID NO: 389 is the determined cDNA sequence for clone 26511.
SEQ ID NO: 390 is the determined cDNA sequence for clone 26513.
SEQ ID NO: 391 is the determined cDNA sequence for clone 26514.
SEQ ID NO: 392 is the determined cDNA sequence for clone 26515.
SEQ ID NO: 393 is the determined cDNA sequence for clone 26516.
25 SEQ ID NO: 394 is the determined cDNA sequence for clone 26517.
SEQ ID NO: 395 is the determined cDNA sequence for clone 26518.
SEQ ID NO: 396 is the determined cDNA sequence for clone 26519.
SEQ ID NO: 397 is the determined cDNA sequence for clone 26520.
SEQ ID NO: 398 is the determined cDNA sequence for clone 26521.
30 SEQ ID NO: 399 is the determined cDNA sequence for clone 26522.
SEQ ID NO: 400 is the determined cDNA sequence for clone 26523.

SEQ ID NO: 401 is the determined cDNA sequence for clone 26524.
SEQ ID NO: 402 is the determined cDNA sequence for clone 26526.
SEQ ID NO: 403 is the determined cDNA sequence for clone 26527.
SEQ ID NO: 404 is the determined cDNA sequence for clone 26528.
5 SEQ ID NO: 405 is the determined cDNA sequence for clone 26529.
SEQ ID NO: 406 is the determined cDNA sequence for clone 26530.
SEQ ID NO: 407 is the determined cDNA sequence for clone 26532.
SEQ ID NO: 408 is the determined cDNA sequence for clone 26533.
SEQ ID NO: 409 is the determined cDNA sequence for clone 26534.
10 SEQ ID NO: 410 is the determined cDNA sequence for clone 26535.
SEQ ID NO: 411 is the determined cDNA sequence for clone 26536.
SEQ ID NO: 412 is the determined cDNA sequence for clone 26537.
SEQ ID NO: 413 is the determined cDNA sequence for clone 26538.
SEQ ID NO: 414 is the determined cDNA sequence for clone 26540.
15 SEQ ID NO: 415 is the determined cDNA sequence for clone 26541.
SEQ ID NO: 416 is the determined cDNA sequence for clone 26542.
SEQ ID NO: 417 is the determined cDNA sequence for clone 26543.
SEQ ID NO: 418 is the determined cDNA sequence for clone 26544.
SEQ ID NO: 419 is the determined cDNA sequence for clone 26546.
20 SEQ ID NO: 420 is the determined cDNA sequence for clone 26547.
SEQ ID NO: 421 is the determined cDNA sequence for clone 26548.
SEQ ID NO: 422 is the determined cDNA sequence for clone 26549.
SEQ ID NO: 423 is the determined cDNA sequence for clone 26550.
SEQ ID NO: 424 is the determined cDNA sequence for clone 26551.
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SEQ ID NO: 426 is the determined cDNA sequence for clone 26553.
SEQ ID NO: 427 is the determined cDNA sequence for clone 26554.
SEQ ID NO: 428 is the determined cDNA sequence for clone 26556.
SEQ ID NO: 429 is the determined cDNA sequence for clone 26557.
30 SEQ ID NO: 430 is the determined cDNA sequence for clone 27631.
SEQ ID NO: 431 is the determined cDNA sequence for clone 27632.

SEQ ID NO: 432 is the determined cDNA sequence for clone 27633.
SEQ ID NO: 433 is the determined cDNA sequence for clone 27635.
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SEQ ID NO: 435 is the determined cDNA sequence for clone 27637.
5 SEQ ID NO: 436 is the determined cDNA sequence for clone 27638.
SEQ ID NO: 437 is the determined cDNA sequence for clone 27639.
SEQ ID NO: 438 is the determined cDNA sequence for clone 27640.
SEQ ID NO: 439 is the determined cDNA sequence for clone 27641.
SEQ ID NO: 440 is the determined cDNA sequence for clone 27642.
10 SEQ ID NO: 441 is the determined cDNA sequence for clone 27644.
SEQ ID NO: 442 is the determined cDNA sequence for clone 27646.
SEQ ID NO: 443 is the determined cDNA sequence for clone 27647.
SEQ ID NO: 444 is the determined cDNA sequence for clone 27649.
SEQ ID NO: 445 is the determined cDNA sequence for clone 27650.
15 SEQ ID NO: 446 is the determined cDNA sequence for clone 27651.
SEQ ID NO: 447 is the determined cDNA sequence for clone 27652.
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SEQ ID NO: 450 is the determined cDNA sequence for clone 27657.
20 SEQ ID NO: 451 is the determined cDNA sequence for clone 27659.
SEQ ID NO: 452 is the determined cDNA sequence for clone 27665.
SEQ ID NO: 453 is the determined cDNA sequence for clone 27666.
SEQ ID NO: 454 is the determined cDNA sequence for clone 27668.
SEQ ID NO: 455 is the determined cDNA sequence for clone 27670.
25 SEQ ID NO: 456 is the determined cDNA sequence for clone 27671.
SEQ ID NO: 457 is the determined cDNA sequence for clone 27672.
SEQ ID NO: 458 is the determined cDNA sequence for clone 27674.
SEQ ID NO: 459 is the determined cDNA sequence for clone 27677.
SEQ ID NO: 460 is the determined cDNA sequence for clone 27681.
30 SEQ ID NO: 461 is the determined cDNA sequence for clone 27682.
SEQ ID NO: 462 is the determined cDNA sequence for clone 27683.

SEQ ID NO: 463 is the determined cDNA sequence for clone 27686.
SEQ ID NO: 464 is the determined cDNA sequence for clone 27688.
SEQ ID NO: 465 is the determined cDNA sequence for clone 27689.
SEQ ID NO: 466 is the determined cDNA sequence for clone 27690.
5 SEQ ID NO: 467 is the determined cDNA sequence for clone 27693.
SEQ ID NO: 468 is the determined cDNA sequence for clone 27699.
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SEQ ID NO: 470 is the determined cDNA sequence for clone 27702.
SEQ ID NO: 471 is the determined cDNA sequence for clone 27705.
10 SEQ ID NO: 472 is the determined cDNA sequence for clone 27706.
SEQ ID NO: 473 is the determined cDNA sequence for clone 27707.
SEQ ID NO: 474 is the determined cDNA sequence for clone 27708.
SEQ ID NO: 475 is the determined cDNA sequence for clone 27709.
SEQ ID NO: 476 is the determined cDNA sequence for clone 27710.
15 SEQ ID NO: 477 is the determined cDNA sequence for clone 27711.
SEQ ID NO: 478 is the determined cDNA sequence for clone 27712.
SEQ ID NO: 479 is the determined cDNA sequence for clone 27713.
SEQ ID NO: 480 is the determined cDNA sequence for clone 27714.
SEQ ID NO: 481 is the determined cDNA sequence for clone 27715.
20 SEQ ID NO: 482 is the determined cDNA sequence for clone 27716.
SEQ ID NO: 483 is the determined cDNA sequence for clone 27717.
SEQ ID NO: 484 is the determined cDNA sequence for clone 27718.
SEQ ID NO: 485 is the determined cDNA sequence for clone 27719.
SEQ ID NO: 486 is the determined cDNA sequence for clone 27720.
25 SEQ ID NO: 487 is the determined cDNA sequence for clone 27722.
SEQ ID NO: 488 is the determined cDNA sequence for clone 27723.
SEQ ID NO: 489 is the determined cDNA sequence for clone 27724.
SEQ ID NO: 490 is the determined cDNA sequence for clone 27726.
SEQ ID NO: 491 is the determined cDNA sequence for clone 25015.
30 SEQ ID NO: 492 is the determined cDNA sequence for clone 25016.
SEQ ID NO: 493 is the determined cDNA sequence for clone 25017.

SEQ ID NO: 494 is the determined cDNA sequence for clone 25018
SEQ ID NO: 495 is the determined cDNA sequence for clone 25030.
SEQ ID NO: 496 is the determined cDNA sequence for clone 25033.
SEQ ID NO: 497 is the determined cDNA sequence for clone 25034.
5 SEQ ID NO: 498 is the determined cDNA sequence for clone 25035.
SEQ ID NO: 499 is the determined cDNA sequence for clone 25036.
SEQ ID NO: 500 is the determined cDNA sequence for clone 25037.
SEQ ID NO: 501 is the determined cDNA sequence for clone 25038.
SEQ ID NO: 502 is the determined cDNA sequence for clone 25039.
10 SEQ ID NO: 503 is the determined cDNA sequence for clone 25040.
SEQ ID NO: 504 is the determined cDNA sequence for clone 25042.
SEQ ID NO: 505 is the determined cDNA sequence for clone 25043.
SEQ ID NO: 506 is the determined cDNA sequence for clone 25044.
SEQ ID NO: 507 is the determined cDNA sequence for clone 25045.
15 SEQ ID NO: 508 is the determined cDNA sequence for clone 25047.
SEQ ID NO: 509 is the determined cDNA sequence for clone 25048.
SEQ ID NO: 510 is the determined cDNA sequence for clone 25049.
SEQ ID NO: 511 is the determined cDNA sequence for clone 25185.
SEQ ID NO: 512 is the determined cDNA sequence for clone 25186.
20 SEQ ID NO: 513 is the determined cDNA sequence for clone 25187.
SEQ ID NO: 514 is the determined cDNA sequence for clone 25188.
SEQ ID NO: 515 is the determined cDNA sequence for clone 25189.
SEQ ID NO: 516 is the determined cDNA sequence for clone 25190.
SEQ ID NO: 517 is the determined cDNA sequence for clone 25193.
25 SEQ ID NO: 518 is the determined cDNA sequence for clone 25194.
SEQ ID NO: 519 is the determined cDNA sequence for clone 25196.
SEQ ID NO: 520 is the determined cDNA sequence for clone 25198.
SEQ ID NO: 521 is the determined cDNA sequence for clone 25199.
SEQ ID NO: 522 is the determined cDNA sequence for clone 25200.
30 SEQ ID NO: 523 is the determined cDNA sequence for clone 25202.
SEQ ID NO: 524 is the determined cDNA sequence for clone 25364.

SEQ ID NO: 525 is the determined cDNA sequence for clone 25366.
SEQ ID NO: 526 is the determined cDNA sequence for clone 25367.
SEQ ID NO: 527 is the determined cDNA sequence for clone 25368.
SEQ ID NO: 528 is the determined cDNA sequence for clone 25369.
5 SEQ ID NO: 529 is the determined cDNA sequence for clone 25370.
SEQ ID NO: 530 is the determined cDNA sequence for clone 25371.
SEQ ID NO: 531 is the determined cDNA sequence for clone 25372.
SEQ ID NO: 532 is the determined cDNA sequence for clone 25373.
SEQ ID NO: 533 is the determined cDNA sequence for clone 25374.
10 SEQ ID NO: 534 is the determined cDNA sequence for clone 25376.
SEQ ID NO: 535 is the determined cDNA sequence for clone 25377.
SEQ ID NO: 536 is the determined cDNA sequence for clone 25378.
SEQ ID NO: 537 is the determined cDNA sequence for clone 25379.
SEQ ID NO: 538 is the determined cDNA sequence for clone 25380.
15 SEQ ID NO: 539 is the determined cDNA sequence for clone 25381.
SEQ ID NO: 540 is the determined cDNA sequence for clone 25382.
SEQ ID NO: 541 is the determined cDNA sequence for clone 25383.
SEQ ID NO: 542 is the determined cDNA sequence for clone 25385.
SEQ ID NO: 543 is the determined cDNA sequence for clone 25386.
20 SEQ ID NO: 544 is the determined cDNA sequence for clone 25387.
SEQ ID NO: 545 is the determined cDNA sequence for clone 26013.
SEQ ID NO: 546 is the determined cDNA sequence for clone 26014.
SEQ ID NO: 547 is the determined cDNA sequence for clone 26016.
SEQ ID NO: 548 is the determined cDNA sequence for clone 26017.
25 SEQ ID NO: 549 is the determined cDNA sequence for clone 26018.
SEQ ID NO: 550 is the determined cDNA sequence for clone 26019.
SEQ ID NO: 551 is the determined cDNA sequence for clone 26020.
SEQ ID NO: 552 is the determined cDNA sequence for clone 26021.
SEQ ID NO: 553 is the determined cDNA sequence for clone 26022.
30 SEQ ID NO: 554 is the determined cDNA sequence for clone 26027.
SEQ ID NO: 555 is the determined cDNA sequence for clone 26197.

SEQ ID NO: 556 is the determined cDNA sequence for clone 26199.
SEQ ID NO: 557 is the determined cDNA sequence for clone 26201.
SEQ ID NO: 558 is the determined cDNA sequence for clone 26202.
SEQ ID NO: 559 is the determined cDNA sequence for clone 26203.
5 SEQ ID NO: 560 is the determined cDNA sequence for clone 26204.
SEQ ID NO: 561 is the determined cDNA sequence for clone 26205.
SEQ ID NO: 562 is the determined cDNA sequence for clone 26206.
SEQ ID NO: 563 is the determined cDNA sequence for clone 26208.
SEQ ID NO: 564 is the determined cDNA sequence for clone 26211.
10 SEQ ID NO: 565 is the determined cDNA sequence for clone 26212.
SEQ ID NO: 566 is the determined cDNA sequence for clone 26213.
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SEQ ID NO: 568 is the determined cDNA sequence for clone 26215.
SEQ ID NO: 569 is the determined cDNA sequence for clone 26216.
15 SEQ ID NO: 570 is the determined cDNA sequence for clone 26217.
SEQ ID NO: 571 is the determined cDNA sequence for clone 26218.
SEQ ID NO: 572 is the determined cDNA sequence for clone 26219.
SEQ ID NO: 573 is the determined cDNA sequence for clone 26220.
SEQ ID NO: 574 is the determined cDNA sequence for clone 26221.
20 SEQ ID NO: 575 is the determined cDNA sequence for clone 26224.
SEQ ID NO: 576 is the determined cDNA sequence for clone 26225.
SEQ ID NO: 577 is the determined cDNA sequence for clone 26226.
SEQ ID NO: 578 is the determined cDNA sequence for clone 26227.
SEQ ID NO: 579 is the determined cDNA sequence for clone 26228.
25 SEQ ID NO: 580 is the determined cDNA sequence for clone 26230.
SEQ ID NO: 581 is the determined cDNA sequence for clone 26231.
SEQ ID NO: 582 is the determined cDNA sequence for clone 26234.
SEQ ID NO: 583 is the determined cDNA sequence for clone 26236.
SEQ ID NO: 584 is the determined cDNA sequence for clone 26237.
30 SEQ ID NO: 585 is the determined cDNA sequence for clone 26239.
SEQ ID NO: 586 is the determined cDNA sequence for clone 26240.

SEQ ID NO: 587 is the determined cDNA sequence for clone 26241.
SEQ ID NO: 588 is the determined cDNA sequence for clone 26242.
SEQ ID NO: 589 is the determined cDNA sequence for clone 26246.
SEQ ID NO: 590 is the determined cDNA sequence for clone 26247.
5 SEQ ID NO: 591 is the determined cDNA sequence for clone 26248.
SEQ ID NO: 592 is the determined cDNA sequence for clone 26249.
SEQ ID NO: 593 is the determined cDNA sequence for clone 26250.
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10 SEQ ID NO: 596 is the determined cDNA sequence for clone 26253.
SEQ ID NO: 597 is the determined cDNA sequence for clone 26254.
SEQ ID NO: 598 is the determined cDNA sequence for clone 26255.
SEQ ID NO: 599 is the determined cDNA sequence for clone 26256.
SEQ ID NO: 600 is the determined cDNA sequence for clone 26257.
15 SEQ ID NO: 601 is the determined cDNA sequence for clone 26259.
SEQ ID NO: 602 is the determined cDNA sequence for clone 26260.
SEQ ID NO: 603 is the determined cDNA sequence for clone 26261.
SEQ ID NO: 604 is the determined cDNA sequence for clone 26262.
SEQ ID NO: 605 is the determined cDNA sequence for clone 26263.
20 SEQ ID NO: 606 is the determined cDNA sequence for clone 26264.
SEQ ID NO: 607 is the determined cDNA sequence for clone 26265.
SEQ ID NO: 608 is the determined cDNA sequence for clone 26266.
SEQ ID NO: 609 is the determined cDNA sequence for clone 26268.
SEQ ID NO: 610 is the determined cDNA sequence for clone 26269.
25 SEQ ID NO: 611 is the determined cDNA sequence for clone 26271.
SEQ ID NO: 612 is the determined cDNA sequence for clone 26273.
SEQ ID NO: 613 is the determined cDNA sequence for clone 26810.
SEQ ID NO: 614 is the determined cDNA sequence for clone 26811.
SEQ ID NO: 615 is the determined cDNA sequence for clone 26812.1.
30 SEQ ID NO: 616 is the determined cDNA sequence for clone 26812.2.
SEQ ID NO: 617 is the determined cDNA sequence for clone 26813.

SEQ ID NO: 618 is the determined cDNA sequence for clone 26814.
SEQ ID NO: 619 is the determined cDNA sequence for clone 26815.
SEQ ID NO: 620 is the determined cDNA sequence for clone 26816.
SEQ ID NO: 621 is the determined cDNA sequence for clone 26818.
5 SEQ ID NO: 622 is the determined cDNA sequence for clone 26819.
SEQ ID NO: 623 is the determined cDNA sequence for clone 26820.
SEQ ID NO: 624 is the determined cDNA sequence for clone 26821.
SEQ ID NO: 625 is the determined cDNA sequence for clone 26822.
SEQ ID NO: 626 is the determined cDNA sequence for clone 26824.
10 SEQ ID NO: 627 is the determined cDNA sequence for clone 26825.
SEQ ID NO: 628 is the determined cDNA sequence for clone 26826.
SEQ ID NO: 629 is the determined cDNA sequence for clone 26827.
SEQ ID NO: 630 is the determined cDNA sequence for clone 26829.
SEQ ID NO: 631 is the determined cDNA sequence for clone 26830.
15 SEQ ID NO: 632 is the determined cDNA sequence for clone 26831.
SEQ ID NO: 633 is the determined cDNA sequence for clone 26832.
SEQ ID NO: 634 is the determined cDNA sequence for clone 26835.
SEQ ID NO: 635 is the determined cDNA sequence for clone 26836.
SEQ ID NO: 636 is the determined cDNA sequence for clone 26837.
20 SEQ ID NO: 637 is the determined cDNA sequence for clone 26839.
SEQ ID NO: 638 is the determined cDNA sequence for clone 26841.
SEQ ID NO: 639 is the determined cDNA sequence for clone 26843.
SEQ ID NO: 640 is the determined cDNA sequence for clone 26844.
SEQ ID NO: 641 is the determined cDNA sequence for clone 26845.
25 SEQ ID NO: 642 is the determined cDNA sequence for clone 26846.
SEQ ID NO: 643 is the determined cDNA sequence for clone 26847.
SEQ ID NO: 644 is the determined cDNA sequence for clone 26848.
SEQ ID NO: 645 is the determined cDNA sequence for clone 26849.
SEQ ID NO: 646 is the determined cDNA sequence for clone 26850.
30 SEQ ID NO: 647 is the determined cDNA sequence for clone 26851.
SEQ ID NO: 648 is the determined cDNA sequence for clone 26852.

SEQ ID NO: 649 is the determined cDNA sequence for clone 26853.
SEQ ID NO: 650 is the determined cDNA sequence for clone 26854.
SEQ ID NO: 651 is the determined cDNA sequence for clone 26856.
SEQ ID NO: 652 is the determined cDNA sequence for clone 26857.
5 SEQ ID NO: 653 is the determined cDNA sequence for clone 26858.
SEQ ID NO: 654 is the determined cDNA sequence for clone 26859.
SEQ ID NO: 655 is the determined cDNA sequence for clone 26860.
SEQ ID NO: 656 is the determined cDNA sequence for clone 26862.
SEQ ID NO: 657 is the determined cDNA sequence for clone 26863.
10 SEQ ID NO: 658 is the determined cDNA sequence for clone 26864.
SEQ ID NO: 659 is the determined cDNA sequence for clone 26865.
SEQ ID NO: 660 is the determined cDNA sequence for clone 26867.
SEQ ID NO: 661 is the determined cDNA sequence for clone 26868.
SEQ ID NO: 662 is the determined cDNA sequence for clone 26871.
15 SEQ ID NO: 663 is the determined cDNA sequence for clone 26873.
SEQ ID NO: 664 is the determined cDNA sequence for clone 26875.
SEQ ID NO: 665 is the determined cDNA sequence for clone 26876.
SEQ ID NO: 666 is the determined cDNA sequence for clone 26877.
SEQ ID NO: 667 is the determined cDNA sequence for clone 26878.
20 SEQ ID NO: 668 is the determined cDNA sequence for clone 26880.
SEQ ID NO: 669 is the determined cDNA sequence for clone 26882.
SEQ ID NO: 670 is the determined cDNA sequence for clone 26883.
SEQ ID NO: 671 is the determined cDNA sequence for clone 26884.
SEQ ID NO: 672 is the determined cDNA sequence for clone 26885.
25 SEQ ID NO: 673 is the determined cDNA sequence for clone 26886.
SEQ ID NO: 674 is the determined cDNA sequence for clone 26887.
SEQ ID NO: 675 is the determined cDNA sequence for clone 26888.
SEQ ID NO: 676 is the determined cDNA sequence for clone 26889.
SEQ ID NO: 677 is the determined cDNA sequence for clone 26890.
30 SEQ ID NO: 678 is the determined cDNA sequence for clone 26892.
SEQ ID NO: 679 is the determined cDNA sequence for clone 26894.

SEQ ID NO: 680 is the determined cDNA sequence for clone 26895.
SEQ ID NO: 681 is the determined cDNA sequence for clone 26897.
SEQ ID NO: 682 is the determined cDNA sequence for clone 26898.
SEQ ID NO: 683 is the determined cDNA sequence for clone 26899.
5 SEQ ID NO: 684 is the determined cDNA sequence for clone 26900.
SEQ ID NO: 685 is the determined cDNA sequence for clone 26901.
SEQ ID NO: 686 is the determined cDNA sequence for clone 26903.
SEQ ID NO: 687 is the determined cDNA sequence for clone 26905.
SEQ ID NO: 688 is the determined cDNA sequence for clone 26906.
10 SEQ ID NO: 689 is the determined cDNA sequence for clone 26708.
SEQ ID NO: 690 is the determined cDNA sequence for clone 26709.
SEQ ID NO: 691 is the determined cDNA sequence for clone 26710.
SEQ ID NO: 692 is the determined cDNA sequence for clone 26711.
SEQ ID NO: 693 is the determined cDNA sequence for clone 26712.
15 SEQ ID NO: 694 is the determined cDNA sequence for clone 26713.
SEQ ID NO: 695 is the determined cDNA sequence for clone 26714.
SEQ ID NO: 696 is the determined cDNA sequence for clone 26715.
SEQ ID NO: 697 is the determined cDNA sequence for clone 26716.
SEQ ID NO: 698 is the determined cDNA sequence for clone 26717.
20 SEQ ID NO: 699 is the determined cDNA sequence for clone 26718.
SEQ ID NO: 700 is the determined cDNA sequence for clone 26719.
SEQ ID NO: 701 is the determined cDNA sequence for clone 26720.
SEQ ID NO: 702 is the determined cDNA sequence for clone 26721.
SEQ ID NO: 703 is the determined cDNA sequence for clone 26722.
25 SEQ ID NO: 704 is the determined cDNA sequence for clone 26723.
SEQ ID NO: 705 is the determined cDNA sequence for clone 26724.
SEQ ID NO: 706 is the determined cDNA sequence for clone 26725.
SEQ ID NO: 707 is the determined cDNA sequence for clone 26726.
SEQ ID NO: 708 is the determined cDNA sequence for clone 26727.
30 SEQ ID NO: 709 is the determined cDNA sequence for clone 26728.
SEQ ID NO: 710 is the determined cDNA sequence for clone 26729.

SEQ ID NO: 711 is the determined cDNA sequence for clone 26730.
SEQ ID NO: 712 is the determined cDNA sequence for clone 26731.
SEQ ID NO: 713 is the determined cDNA sequence for clone 26732.
SEQ ID NO: 714 is the determined cDNA sequence for clone 26733.1.
5 SEQ ID NO: 715 is the determined cDNA sequence for clone 26733.2.
SEQ ID NO: 716 is the determined cDNA sequence for clone 26734.
SEQ ID NO: 717 is the determined cDNA sequence for clone 26735.
SEQ ID NO: 718 is the determined cDNA sequence for clone 26736.
SEQ ID NO: 719 is the determined cDNA sequence for clone 26737.
10 SEQ ID NO: 720 is the determined cDNA sequence for clone 26738.
SEQ ID NO: 721 is the determined cDNA sequence for clone 26739.
SEQ ID NO: 722 is the determined cDNA sequence for clone 26741.
SEQ ID NO: 723 is the determined cDNA sequence for clone 26742.
SEQ ID NO: 724 is the determined cDNA sequence for clone 26743.
15 SEQ ID NO: 725 is the determined cDNA sequence for clone 26744.
SEQ ID NO: 726 is the determined cDNA sequence for clone 26745.
SEQ ID NO: 727 is the determined cDNA sequence for clone 26746.
SEQ ID NO: 728 is the determined cDNA sequence for clone 26747.
SEQ ID NO: 729 is the determined cDNA sequence for clone 26748.
20 SEQ ID NO: 730 is the determined cDNA sequence for clone 26749.
SEQ ID NO: 731 is the determined cDNA sequence for clone 26750.
SEQ ID NO: 732 is the determined cDNA sequence for clone 26751.
SEQ ID NO: 733 is the determined cDNA sequence for clone 26752.
SEQ ID NO: 734 is the determined cDNA sequence for clone 26753.
25 SEQ ID NO: 735 is the determined cDNA sequence for clone 26754.
SEQ ID NO: 736 is the determined cDNA sequence for clone 26755.
SEQ ID NO: 737 is the determined cDNA sequence for clone 26756.
SEQ ID NO: 738 is the determined cDNA sequence for clone 26757.
SEQ ID NO: 739 is the determined cDNA sequence for clone 26758.
30 SEQ ID NO: 740 is the determined cDNA sequence for clone 26759.
SEQ ID NO: 741 is the determined cDNA sequence for clone 26760.

SEQ ID NO: 742 is the determined cDNA sequence for clone 26761.
SEQ ID NO: 743 is the determined cDNA sequence for clone 26762.
SEQ ID NO: 744 is the determined cDNA sequence for clone 26763.
SEQ ID NO: 745 is the determined cDNA sequence for clone 26764.
5 SEQ ID NO: 746 is the determined cDNA sequence for clone 26765.
SEQ ID NO: 747 is the determined cDNA sequence for clone 26766.
SEQ ID NO: 748 is the determined cDNA sequence for clone 26767.
SEQ ID NO: 749 is the determined cDNA sequence for clone 26768.
SEQ ID NO: 750 is the determined cDNA sequence for clone 26769.
10 SEQ ID NO: 751 is the determined cDNA sequence for clone 26770.
SEQ ID NO: 752 is the determined cDNA sequence for clone 26771.
SEQ ID NO: 753 is the determined cDNA sequence for clone 26772.
SEQ ID NO: 754 is the determined cDNA sequence for clone 26773.
SEQ ID NO: 755 is the determined cDNA sequence for clone 26774.
15 SEQ ID NO: 756 is the determined cDNA sequence for clone 26775.
SEQ ID NO: 757 is the determined cDNA sequence for clone 26776.
SEQ ID NO: 758 is the determined cDNA sequence for clone 26777.
SEQ ID NO: 759 is the determined cDNA sequence for clone 26778.
SEQ ID NO: 760 is the determined cDNA sequence for clone 26779.
20 SEQ ID NO: 761 is the determined cDNA sequence for clone 26781.
SEQ ID NO: 762 is the determined cDNA sequence for clone 26782.
SEQ ID NO: 763 is the determined cDNA sequence for clone 26783.
SEQ ID NO: 764 is the determined cDNA sequence for clone 26784.
SEQ ID NO: 765 is the determined cDNA sequence for clone 26785.
25 SEQ ID NO: 766 is the determined cDNA sequence for clone 26786.
SEQ ID NO: 767 is the determined cDNA sequence for clone 26787.
SEQ ID NO: 768 is the determined cDNA sequence for clone 26788.
SEQ ID NO: 769 is the determined cDNA sequence for clone 26790.
SEQ ID NO: 770 is the determined cDNA sequence for clone 26791.
30 SEQ ID NO: 771 is the determined cDNA sequence for clone 26792.
SEQ ID NO: 772 is the determined cDNA sequence for clone 26793.

SEQ ID NO: 773 is the determined cDNA sequence for clone 26794.
SEQ ID NO: 774 is the determined cDNA sequence for clone 26795.
SEQ ID NO: 775 is the determined cDNA sequence for clone 26796.
SEQ ID NO: 776 is the determined cDNA sequence for clone 26797.
5 SEQ ID NO: 777 is the determined cDNA sequence for clone 26798.
SEQ ID NO: 778 is the determined cDNA sequence for clone 26800.
SEQ ID NO: 779 is the determined cDNA sequence for clone 26801.
SEQ ID NO: 780 is the determined cDNA sequence for clone 26802.
SEQ ID NO: 781 is the determined cDNA sequence for clone 26803.
10 SEQ ID NO: 782 is the determined cDNA sequence for clone 26804.
SEQ ID NO: 783 is the amino acid sequence for L773P.
SEQ ID NO: 784 is the determined DNA sequence of the L773P
expression construct.
SEQ ID NO: 785 is the determined DNA sequence of the L773PA
15 expression construct.
SEQ ID NO: 786 is a predicted amino acid sequence for L552S.
SEQ ID NO: 787 is a predicted amino acid sequence for L840P.
SEQ ID NO: 788 is the full-length cDNA sequence for L548S.
SEQ ID NO: 789 is the amino acid sequence encoded by SEQ ID NO:
20 788.
SEQ ID NO: 790 is an extended cDNA sequence for L552S.
SEQ ID NO: 791 is the predicted amino acid sequence encoded by the
cDNA sequence of SEQ ID NO: 790.
SEQ ID NO: 792 is the determined cDNA sequence for an isoform of
25 L552S.
SEQ ID NO: 793 is the predicted amino acid sequence encoded by SEQ
ID NO: 792.
SEQ ID NO: 794 is an extended cDNA sequence for L840P.
SEQ ID NO: 795 is the predicted amino acid sequence encoded by SEQ
30 DI NO: 794.
SEQ ID NO: 796 is an extended cDNA sequence for L801P.

SEQ ID NO: 797 is a first predicted amino acid sequence encoded by
SEQ ID NO: 796.

SEQ ID NO: 798 is a second predicted amino acid sequence encoded by
SEQ ID NO: 796.

5 SEQ ID NO: 799 is a third predicted amino acid sequence encoded by
SEQ ID NO: 796.

SEQ ID NO: 800 is the determined full-length sequence for L844P.

SEQ ID NO: 801 is the 5' consensus cDNA sequence for L551S.

SEQ ID NO: 802 is the 3' consensus cDNA sequence for L551S.

10 SEQ ID NO: 803 is the cDNA sequence for STY8.

SEQ ID NO: 804 is an extended cDNA sequence for L551S.

SEQ ID NO: 805 is the amino acid sequence for STY8.

SEQ ID NO: 806 is the extended amino acid sequence for L551S.

15 SEQ ID NO: 807 is the determined full-length cDNA sequence for
L773P.

SEQ ID NO: 808 is the full-length cDNA sequence of L552S.

SEQ ID NO: 809 is the full-length amino acid sequence of L552S.

SEQ ID NO: 810 is the determined cDNA sequence of clone 50989.

SEQ ID NO: 811 is the determined cDNA sequence of clone 50990.

20 SEQ ID NO: 812 is the determined cDNA sequence of clone 50992.

SEQ ID NO: 813-824 are the determined cDNA sequences for clones
isolated from lung tumor tissue.

SEQ ID NO: 825 is the determined cDNA sequence for the full-length
L551S clone 54305.

25 SEQ ID NO: 826 is the determined cDNA sequence for the full-length
L551S clone 54298.

SEQ ID NO: 827 is the full-length amino acid sequence for L551S.

DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for using the compositions, for example in the therapy and diagnosis of cancer, such as lung cancer. Certain illustrative compositions described
5 herein include lung tumor polypeptides, polynucleotides encoding such polypeptides, binding agents such as antibodies, antigen presenting cells (APCs) and/or immune system cells (*e.g.*, T cells). A "lung tumor protein," as the term is used herein, refers generally to a protein that is expressed in lung tumor cells at a level that is at least two fold, and preferably at least five fold, greater than the level of expression in a normal
10 tissue, as determined using a representative assay provided herein. Certain lung tumor proteins are tumor proteins that react detectably (within an immunoassay, such as an ELISA or Western blot) with antisera of a patient afflicted with lung cancer.

Therefore, in accordance with the above, and as described further below, the present invention provides illustrative polynucleotide compositions having
15 sequences set forth in SEQ ID NO: 1, 11-13, 15, 20, 23-27, 29, 30, 33, 34, 39, 41, 43-46, 51, 52, 57, 58, 60, 62, 65-67, 69-71, 74, 76, 79, 80, 84, 86, 89-92, 95, 97, 98, 101, 110, 111, 113-119, 121-128, 130-134, 136, 138, 139, 141, 143, 146-151, 153, 154, 157-160, 162-164, 167-178, 180, 181, 183, 186-190, 192, 193, 195-220, 224, 226-231, 234, 236, 237, 240, 241, 244-246, 248, 254, 255, 261, 262, 266, 270, 275, 280, 282, 283,
20 288, 289, 290, 292, 295, 301, 303, 304, 309, 311, 341-782, 784, 785, 790, 792, 794, 796, 800-804, 807, 808 and 810-826, illustrative polypeptide compositions having amino acid sequences set forth in SEQ ID NO: 786, 787, 791, 793, 795, 797-799, 806, 809 and 827, antibody compositions capable of binding such polypeptides, and numerous additional embodiments employing such compositions, for example in the
25 detection, diagnosis and/or therapy of human lung cancer.

POLYNUCLEOTIDE COMPOSITIONS

As used herein, the terms "DNA segment" and "polynucleotide" refer to a DNA molecule that has been isolated free of total genomic DNA of a particular species. Therefore, a DNA segment encoding a polypeptide refers to a DNA segment
30 that contains one or more coding sequences yet is substantially isolated away from, or

purified free from, total genomic DNA of the species from which the DNA segment is obtained. Included within the terms "DNA segment" and "polynucleotide" are DNA segments and smaller fragments of such segments, and also recombinant vectors, including, for example, plasmids, cosmids, phagemids, phage, viruses, and the like.

5 As will be understood by those skilled in the art, the DNA segments of this invention can include genomic sequences, extra-genomic and plasmid-encoded sequences and smaller engineered gene segments that express, or may be adapted to express, proteins, polypeptides, peptides and the like. Such segments may be naturally isolated, or modified synthetically by the hand of man.

10 "Isolated," as used herein, means that a polynucleotide is substantially away from other coding sequences, and that the DNA segment does not contain large portions of unrelated coding DNA, such as large chromosomal fragments or other functional genes or polypeptide coding regions. Of course, this refers to the DNA segment as originally isolated, and does not exclude genes or coding regions later added
15 to the segment by the hand of man.

As will be recognized by the skilled artisan, polynucleotides may be single-stranded (coding or antisense) or double-stranded, and may be DNA (genomic, cDNA or synthetic) or RNA molecules. RNA molecules include HnRNA molecules, which contain introns and correspond to a DNA molecule in a one-to-one manner, and
20 mRNA molecules, which do not contain introns. Additional coding or non-coding sequences may, but need not, be present within a polynucleotide of the present invention, and a polynucleotide may, but need not, be linked to other molecules and/or support materials.

Polynucleotides may comprise a native sequence (*i.e.*, an endogenous
25 sequence that encodes a lung tumor protein or a portion thereof) or may comprise a variant, or a biological or antigenic functional equivalent of such a sequence. Polynucleotide variants may contain one or more substitutions, additions, deletions and/or insertions, as further described below, preferably such that the immunogenicity of the encoded polypeptide is not diminished, relative to a native tumor protein. The
30 effect on the immunogenicity of the encoded polypeptide may generally be assessed as

described herein. The term "variants" also encompasses homologous genes of xenogenic origin.

When comparing polynucleotide or polypeptide sequences, two sequences are said to be "identical" if the sequence of nucleotides or amino acids in the
5 two sequences is the same when aligned for maximum correspondence, as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison window to identify and compare local regions of sequence similarity. A "comparison window" as used herein, refers to a segment of at least about
20 contiguous positions, usually 30 to about 75, 40 to about 50, in which a sequence
10 may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. This program embodies several
15 alignment schemes described in the following references: Dayhoff, M.O. (1978) A model of evolutionary change in proteins – Matrices for detecting distant relationships. In Dayhoff, M.O. (ed.) Atlas of Protein Sequence and Structure, National Biomedical Research Foundation, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) Unified Approach to Alignment and Phylogenies pp. 626-645 *Methods in Enzymology*
20 vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M. (1989) *CABIOS* 5:151-153; Myers, E.W. and Muller W. (1988) *CABIOS* 4:11-17; Robinson, E.D. (1971) *Comb. Theor* 11:105; Santou, N. Nes, M. (1987) *Mol. Biol. Evol.* 4:406-425; Sneath, P.H.A. and Sokal, R.R. (1973) *Numerical Taxonomy – the Principles and Practice of Numerical Taxonomy*, Freeman Press, San Francisco, CA; Wilbur, W.J. and
25 Lipman, D.J. (1983) *Proc. Natl. Acad. Sci. USA* 80:726-730.

Alternatively, optimal alignment of sequences for comparison may be conducted by the local identity algorithm of Smith and Waterman (1981) *Add. APL. Math* 2:482, by the identity alignment algorithm of Needleman and Wunsch (1970) *J. Mol. Biol.* 48:443, by the search for similarity methods of Pearson and Lipman (1988)
30 *Proc. Natl. Acad. Sci. USA* 85: 2444, by computerized implementations of these algorithms (GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics

Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, WI), or by inspection.

One preferred example of algorithms that are suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al.* (1977) *Nucl. Acids Res.* 25:3389-3402 and Altschul *et al.* (1990) *J. Mol. Biol.* 215:403-410, respectively. BLAST and BLAST 2.0 can be used, for example with the parameters described herein, to determine percent sequence identity for the polynucleotides and polypeptides of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. In one illustrative example, cumulative scores can be calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always >0) and N (penalty score for mismatching residues; always <0). For amino acid sequences, a scoring matrix can be used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) *Proc. Natl. Acad. Sci. USA* 89:10915) alignments, (B) of 50, expectation (E) of 10, M=5, N=-4 and a comparison of both strands.

Preferably, the "percentage of sequence identity" is determined by comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polynucleotide or polypeptide sequence in the comparison window may comprise additions or deletions (*i.e.*, gaps) of 20 percent or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference sequences (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid bases or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the

total number of positions in the reference sequence (*i.e.*, the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

Therefore, the present invention encompasses polynucleotide and polypeptide sequences having substantial identity to the sequences disclosed herein, for example those comprising at least 50% sequence identity, preferably at least 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% or higher, sequence identity compared to a polynucleotide or polypeptide sequence of this invention using the methods described herein, (*e.g.*, BLAST analysis using standard parameters, as described below). One skilled in this art will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning and the like.

In additional embodiments, the present invention provides isolated polynucleotides and polypeptides comprising various lengths of contiguous stretches of sequence identical to or complementary to one or more of the sequences disclosed herein. For example, polynucleotides are provided by this invention that comprise at least about 15, 20, 30, 40, 50, 75, 100, 150, 200, 300, 400, 500 or 1000 or more contiguous nucleotides of one or more of the sequences disclosed herein as well as all intermediate lengths there between. It will be readily understood that "intermediate lengths", in this context, means any length between the quoted values, such as 16, 17, 18, 19, *etc.*; 21, 22, 23, *etc.*; 30, 31, 32, *etc.*; 50, 51, 52, 53, *etc.*; 100, 101, 102, 103, *etc.*; 150, 151, 152, 153, *etc.*; including all integers through 200-500; 500-1,000, and the like.

The polynucleotides of the present invention, or fragments thereof, regardless of the length of the coding sequence itself, may be combined with other DNA sequences, such as promoters, polyadenylation signals, additional restriction enzyme sites, multiple cloning sites, other coding segments, and the like, such that their overall length may vary considerably. It is therefore contemplated that a nucleic acid fragment of almost any length may be employed, with the total length preferably being limited by the ease of preparation and use in the intended recombinant DNA protocol. For example, illustrative DNA segments with total lengths of about 10,000, about 5000,

about 3000, about 2,000, about 1,000, about 500, about 200, about 100, about 50 base pairs in length, and the like, (including all intermediate lengths) are contemplated to be useful in many implementations of this invention.

In other embodiments, the present invention is directed to polynucleotides that are capable of hybridizing under moderately stringent conditions to a polynucleotide sequence provided herein, or a fragment thereof, or a complementary sequence thereof. Hybridization techniques are well known in the art of molecular biology. For purposes of illustration, suitable moderately stringent conditions for testing the hybridization of a polynucleotide of this invention with other polynucleotides include prewashing in a solution of 5 X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0); hybridizing at 50°C-65°C, 5 X SSC, overnight; followed by washing twice at 65°C for 20 minutes with each of 2X, 0.5X and 0.2X SSC containing 0.1% SDS.

Moreover, it will be appreciated by those of ordinary skill in the art that, as a result of the degeneracy of the genetic code, there are many nucleotide sequences that encode a polypeptide as described herein. Some of these polynucleotides bear minimal homology to the nucleotide sequence of any native gene. Nonetheless, polynucleotides that vary due to differences in codon usage are specifically contemplated by the present invention. Further, alleles of the genes comprising the polynucleotide sequences provided herein are within the scope of the present invention. Alleles are endogenous genes that are altered as a result of one or more mutations, such as deletions, additions and/or substitutions of nucleotides. The resulting mRNA and protein may, but need not, have an altered structure or function. Alleles may be identified using standard techniques (such as hybridization, amplification and/or database sequence comparison).

PROBES AND PRIMERS

In other embodiments of the present invention, the polynucleotide sequences provided herein can be advantageously used as probes or primers for nucleic acid hybridization. As such, it is contemplated that nucleic acid segments that comprise a sequence region of at least about 15 nucleotide long contiguous sequence that has the

same sequence as, or is complementary to, a 15 nucleotide long contiguous sequence disclosed herein will find particular utility. Longer contiguous identical or complementary sequences, *e.g.*, those of about 20, 30, 40, 50, 100, 200, 500, 1000 (including all intermediate lengths) and even up to full length sequences will also be of use in certain embodiments.

The ability of such nucleic acid probes to specifically hybridize to a sequence of interest will enable them to be of use in detecting the presence of complementary sequences in a given sample. However, other uses are also envisioned, such as the use of the sequence information for the preparation of mutant species primers, or primers for use in preparing other genetic constructions.

Polynucleotide molecules having sequence regions consisting of contiguous nucleotide stretches of 10-14, 15-20, 30, 50, or even of 100-200 nucleotides or so (including intermediate lengths as well), identical or complementary to a polynucleotide sequence disclosed herein, are particularly contemplated as hybridization probes for use in, *e.g.*, Southern and Northern blotting. This would allow a gene product, or fragment thereof, to be analyzed, both in diverse cell types and also in various bacterial cells. The total size of fragment, as well as the size of the complementary stretch(es), will ultimately depend on the intended use or application of the particular nucleic acid segment. Smaller fragments will generally find use in hybridization embodiments, wherein the length of the contiguous complementary region may be varied, such as between about 15 and about 100 nucleotides, but larger contiguous complementarity stretches may be used, according to the length complementary sequences one wishes to detect.

The use of a hybridization probe of about 15-25 nucleotides in length allows the formation of a duplex molecule that is both stable and selective. Molecules having contiguous complementary sequences over stretches greater than 15 bases in length are generally preferred, though, in order to increase stability and selectivity of the hybrid, and thereby improve the quality and degree of specific hybrid molecules obtained. One will generally prefer to design nucleic acid molecules having complementary stretches of 15 to 25 contiguous nucleotides, or even longer where desired.

Hybridization probes may be selected from any portion of any of the sequences disclosed herein. All that is required is to review the sequence set forth in SEQ ID NO: 1, 11-13, 15, 20, 23-27, 29, 30, 33, 34, 39, 41, 43-46, 51, 52, 57, 58, 60, 62, 65-67, 69-71, 74, 76, 79, 80, 84, 86, 89-92, 95, 97, 98, 101, 110, 111, 113-119, 121-128, 130-134, 136, 138, 139, 141, 143, 146-151, 153, 154, 157-160, 162-164, 167-178, 180, 181, 183, 186-190, 192, 193, 195-220, 224, 226-231, 234, 236, 237, 240, 241, 244-246, 248, 254, 255, 261, 262, 266, 270, 275, 280, 282, 283, 288, 289, 290, 292, 295, 301, 303, 304, 309, 311, 341-782, 784, 785, 790, 792, 794, 796, 800-804, 807, 808 and 810-826, or to any continuous portion of the sequence, from about 15-25 nucleotides in length up to and including the full length sequence, that one wishes to utilize as a probe or primer. The choice of probe and primer sequences may be governed by various factors. For example, one may wish to employ primers from towards the termini of the total sequence.

Small polynucleotide segments or fragments may be readily prepared by, for example, directly synthesizing the fragment by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer. Also, fragments may be obtained by application of nucleic acid reproduction technology, such as the PCRTM technology of U. S. Patent 4,683,202 (incorporated herein by reference), by introducing selected sequences into recombinant vectors for recombinant production, and by other recombinant DNA techniques generally known to those of skill in the art of molecular biology.

The nucleotide sequences of the invention may be used for their ability to selectively form duplex molecules with complementary stretches of the entire gene or gene fragments of interest. Depending on the application envisioned, one will typically desire to employ varying conditions of hybridization to achieve varying degrees of selectivity of probe towards target sequence. For applications requiring high selectivity, one will typically desire to employ relatively stringent conditions to form the hybrids, *e.g.*, one will select relatively low salt and/or high temperature conditions, such as provided by a salt concentration of from about 0.02 M to about 0.15 M salt at temperatures of from about 50°C to about 70°C. Such selective conditions tolerate

little, if any, mismatch between the probe and the template or target strand, and would be particularly suitable for isolating related sequences.

Of course, for some applications, for example, where one desires to prepare mutants employing a mutant primer strand hybridized to an underlying
5 template, less stringent (reduced stringency) hybridization conditions will typically be needed in order to allow formation of the heteroduplex. In these circumstances, one may desire to employ salt conditions such as those of from about 0.15 M to about 0.9 M salt, at temperatures ranging from about 20°C to about 55°C. Cross-hybridizing species can thereby be readily identified as positively hybridizing signals with respect to control
10 hybridizations. In any case, it is generally appreciated that conditions can be rendered more stringent by the addition of increasing amounts of formamide, which serves to destabilize the hybrid duplex in the same manner as increased temperature. Thus, hybridization conditions can be readily manipulated, and thus will generally be a method of choice depending on the desired results.

15 POLYNUCLEOTIDE IDENTIFICATION AND CHARACTERIZATION

Polynucleotides may be identified, prepared and/or manipulated using any of a variety of well established techniques. For example, a polynucleotide may be identified, as described in more detail below, by screening a microarray of cDNAs for tumor-associated expression (*i.e.*, expression that is at least two fold greater in a tumor
20 than in normal tissue, as determined using a representative assay provided herein). Such screens may be performed, for example, using a Synteni microarray (Palo Alto, CA) according to the manufacturer's instructions (and essentially as described by Schena *et al.*, *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller *et al.*, *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997). Alternatively, polynucleotides may be
25 amplified from cDNA prepared from cells expressing the proteins described herein, such as lung tumor cells. Such polynucleotides may be amplified via polymerase chain reaction (PCR). For this approach, sequence-specific primers may be designed based on the sequences provided herein, and may be purchased or synthesized.

An amplified portion of a polynucleotide of the present invention may be
30 used to isolate a full length gene from a suitable library (*e.g.*, a lung tumor cDNA

library) using well known techniques. Within such techniques, a library (cDNA or genomic) is screened using one or more polynucleotide probes or primers suitable for amplification. Preferably, a library is size-selected to include larger molecules. Random primed libraries may also be preferred for identifying 5' and upstream regions of genes. Genomic libraries are preferred for obtaining introns and extending 5' sequences.

For hybridization techniques, a partial sequence may be labeled (*e.g.*, by nick-translation or end-labeling with ^{32}P) using well known techniques. A bacterial or bacteriophage library is then generally screened by hybridizing filters containing denatured bacterial colonies (or lawns containing phage plaques) with the labeled probe (see Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989). Hybridizing colonies or plaques are selected and expanded, and the DNA is isolated for further analysis. cDNA clones may be analyzed to determine the amount of additional sequence by, for example, PCR using a primer from the partial sequence and a primer from the vector. Restriction maps and partial sequences may be generated to identify one or more overlapping clones. The complete sequence may then be determined using standard techniques, which may involve generating a series of deletion clones. The resulting overlapping sequences can then assembled into a single contiguous sequence. A full length cDNA molecule can be generated by ligating suitable fragments, using well known techniques.

Alternatively, there are numerous amplification techniques for obtaining a full length coding sequence from a partial cDNA sequence. Within such techniques, amplification is generally performed via PCR. Any of a variety of commercially available kits may be used to perform the amplification step. Primers may be designed using, for example, software well known in the art. Primers are preferably 22-30 nucleotides in length, have a GC content of at least 50% and anneal to the target sequence at temperatures of about 68°C to 72°C. The amplified region may be sequenced as described above, and overlapping sequences assembled into a contiguous sequence.

One such amplification technique is inverse PCR (see Triglia *et al.*, *Nucl. Acids Res.* 16:8186, 1988), which uses restriction enzymes to generate a fragment

in the known region of the gene. The fragment is then circularized by intramolecular ligation and used as a template for PCR with divergent primers derived from the known region. Within an alternative approach, sequences adjacent to a partial sequence may be retrieved by amplification with a primer to a linker sequence and a primer specific to a known region. The amplified sequences are typically subjected to a second round of amplification with the same linker primer and a second primer specific to the known region. A variation on this procedure, which employs two primers that initiate extension in opposite directions from the known sequence, is described in WO 96/38591. Another such technique is known as "rapid amplification of cDNA ends" or RACE. This technique involves the use of an internal primer and an external primer, which hybridizes to a polyA region or vector sequence, to identify sequences that are 5' and 3' of a known sequence. Additional techniques include capture PCR (Lagerstrom *et al.*, *PCR Methods Applic.* 1:111-19, 1991) and walking PCR (Parker *et al.*, *Nucl. Acids. Res.* 19:3055-60, 1991). Other methods employing amplification may also be employed to obtain a full length cDNA sequence.

In certain instances, it is possible to obtain a full length cDNA sequence by analysis of sequences provided in an expressed sequence tag (EST) database, such as that available from GenBank. Searches for overlapping ESTs may generally be performed using well known programs (*e.g.*, NCBI BLAST searches), and such ESTs may be used to generate a contiguous full length sequence. Full length DNA sequences may also be obtained by analysis of genomic fragments.

POLYNUCLEOTIDE EXPRESSION IN HOST CELLS

In other embodiments of the invention, polynucleotide sequences or fragments thereof which encode polypeptides of the invention, or fusion proteins or functional equivalents thereof, may be used in recombinant DNA molecules to direct expression of a polypeptide in appropriate host cells. Due to the inherent degeneracy of the genetic code, other DNA sequences that encode substantially the same or a functionally equivalent amino acid sequence may be produced and these sequences may be used to clone and express a given polypeptide.

As will be understood by those of skill in the art, it may be advantageous in some instances to produce polypeptide-encoding nucleotide sequences possessing non-naturally occurring codons. For example, codons preferred by a particular prokaryotic or eukaryotic host can be selected to increase the rate of protein expression or to produce a recombinant RNA transcript having desirable properties, such as a half-life which is longer than that of a transcript generated from the naturally occurring sequence.

Moreover, the polynucleotide sequences of the present invention can be engineered using methods generally known in the art in order to alter polypeptide encoding sequences for a variety of reasons, including but not limited to, alterations which modify the cloning, processing, and/or expression of the gene product. For example, DNA shuffling by random fragmentation and PCR reassembly of gene fragments and synthetic oligonucleotides may be used to engineer the nucleotide sequences. In addition, site-directed mutagenesis may be used to insert new restriction sites, alter glycosylation patterns, change codon preference, produce splice variants, or introduce mutations, and so forth.

In another embodiment of the invention, natural, modified, or recombinant nucleic acid sequences may be ligated to a heterologous sequence to encode a fusion protein. For example, to screen peptide libraries for inhibitors of polypeptide activity, it may be useful to encode a chimeric protein that can be recognized by a commercially available antibody. A fusion protein may also be engineered to contain a cleavage site located between the polypeptide-encoding sequence and the heterologous protein sequence, so that the polypeptide may be cleaved and purified away from the heterologous moiety.

Sequences encoding a desired polypeptide may be synthesized, in whole or in part, using chemical methods well known in the art (see Caruthers, M. H. *et al.* (1980) *Nucl. Acids Res. Symp. Ser.* 215-223, Horn, T. *et al.* (1980) *Nucl. Acids Res. Symp. Ser.* 225-232). Alternatively, the protein itself may be produced using chemical methods to synthesize the amino acid sequence of a polypeptide, or a portion thereof. For example, peptide synthesis can be performed using various solid-phase techniques (Roberge, J. Y. *et al.* (1995) *Science* 269:202-204) and automated synthesis may be

achieved, for example, using the ABI 431A Peptide Synthesizer (Perkin Elmer, Palo Alto, CA).

A newly synthesized peptide may be substantially purified by preparative high performance liquid chromatography (*e.g.*, Creighton, T. (1983) Proteins, Structures and Molecular Principles, WH Freeman and Co., New York, N.Y.) or other comparable techniques available in the art. The composition of the synthetic peptides may be confirmed by amino acid analysis or sequencing (*e.g.*, the Edman degradation procedure). Additionally, the amino acid sequence of a polypeptide, or any part thereof, may be altered during direct synthesis and/or combined using chemical methods with sequences from other proteins, or any part thereof, to produce a variant polypeptide.

In order to express a desired polypeptide, the nucleotide sequences encoding the polypeptide, or functional equivalents, may be inserted into appropriate expression vector, *i.e.*, a vector which contains the necessary elements for the transcription and translation of the inserted coding sequence. Methods which are well known to those skilled in the art may be used to construct expression vectors containing sequences encoding a polypeptide of interest and appropriate transcriptional and translational control elements. These methods include *in vitro* recombinant DNA techniques, synthetic techniques, and *in vivo* genetic recombination. Such techniques are described in Sambrook, J. *et al.* (1989) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Plainview, N.Y., and Ausubel, F. M. *et al.* (1989) Current Protocols in Molecular Biology, John Wiley & Sons, New York, N.Y.

A variety of expression vector/host systems may be utilized to contain and express polynucleotide sequences. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with virus expression vectors (*e.g.*, baculovirus); plant cell systems transformed with virus expression vectors (*e.g.*, cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or with bacterial expression vectors (*e.g.*, Ti or pBR322 plasmids); or animal cell systems.

The "control elements" or "regulatory sequences" present in an expression vector are those non-translated regions of the vector--enhancers, promoters, 5' and 3' untranslated regions--which interact with host cellular proteins to carry out transcription and translation. Such elements may vary in their strength and specificity. Depending on the vector system and host utilized, any number of suitable transcription and translation elements, including constitutive and inducible promoters, may be used. For example, when cloning in bacterial systems, inducible promoters such as the hybrid lacZ promoter of the PBLUESCRIPT phagemid (Stratagene, La Jolla, Calif.) or PSPORT1 plasmid (Gibco BRL, Gaithersburg, MD) and the like may be used. In mammalian cell systems, promoters from mammalian genes or from mammalian viruses are generally preferred. If it is necessary to generate a cell line that contains multiple copies of the sequence encoding a polypeptide, vectors based on SV40 or EBV may be advantageously used with an appropriate selectable marker.

In bacterial systems, a number of expression vectors may be selected depending upon the use intended for the expressed polypeptide. For example, when large quantities are needed, for example for the induction of antibodies, vectors which direct high level expression of fusion proteins that are readily purified may be used. Such vectors include, but are not limited to, the multifunctional *E. coli* cloning and expression vectors such as BLUESCRIPT (Stratagene), in which the sequence encoding the polypeptide of interest may be ligated into the vector in frame with sequences for the amino-terminal Met and the subsequent 7 residues of .beta.-galactosidase so that a hybrid protein is produced; pIN vectors (Van Heeke, G. and S. M. Schuster (1989) *J. Biol. Chem.* 264:5503-5509); and the like. pGEX Vectors (Promega, Madison, Wis.) may also be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and can easily be purified from lysed cells by adsorption to glutathione-agarose beads followed by elution in the presence of free glutathione. Proteins made in such systems may be designed to include heparin, thrombin, or factor XA protease cleavage sites so that the cloned polypeptide of interest can be released from the GST moiety at will.

In the yeast, *Saccharomyces cerevisiae*, a number of vectors containing constitutive or inducible promoters such as alpha factor, alcohol oxidase, and PGH may

be used. For reviews, see Ausubel *et al.* (supra) and Grant *et al.* (1987) *Methods Enzymol.* 153:516-544.

In cases where plant expression vectors are used, the expression of sequences encoding polypeptides may be driven by any of a number of promoters. For example, viral promoters such as the 35S and 19S promoters of CaMV may be used alone or in combination with the omega leader sequence from TMV (Takamatsu, N. (1987) *EMBO J.* 6:307-311. Alternatively, plant promoters such as the small subunit of RUBISCO or heat shock promoters may be used (Coruzzi, G. *et al.* (1984) *EMBO J.* 3:1671-1680; Broglie, R. *et al.* (1984) *Science* 224:838-843; and Winter, J. *et al.* (1991) *Results Probl. Cell Differ.* 17:85-105). These constructs can be introduced into plant cells by direct DNA transformation or pathogen-mediated transfection. Such techniques are described in a number of generally available reviews (see, for example, Hobbs, S. or Murry, L. E. in McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York, N.Y.; pp. 191-196).

An insect system may also be used to express a polypeptide of interest. For example, in one such system, Autographa californica nuclear polyhedrosis virus (AcNPV) is used as a vector to express foreign genes in *Spodoptera frugiperda* cells or in *Trichoplusia* larvae. The sequences encoding the polypeptide may be cloned into a non-essential region of the virus, such as the polyhedrin gene, and placed under control of the polyhedrin promoter. Successful insertion of the polypeptide-encoding sequence will render the polyhedrin gene inactive and produce recombinant virus lacking coat protein. The recombinant viruses may then be used to infect, for example, *S. frugiperda* cells or *Trichoplusia* larvae in which the polypeptide of interest may be expressed (Engelhard, E. K. *et al.* (1994) *Proc. Natl. Acad. Sci.* 91 :3224-3227).

In mammalian host cells, a number of viral-based expression systems are generally available. For example, in cases where an adenovirus is used as an expression vector, sequences encoding a polypeptide of interest may be ligated into an adenovirus transcription/translation complex consisting of the late promoter and tripartite leader sequence. Insertion in a non-essential E1 or E3 region of the viral genome may be used to obtain a viable virus which is capable of expressing the polypeptide in infected host cells (Logan, J. and Shenk, T. (1984) *Proc. Natl. Acad. Sci.* 81:3655-3659). In addition,

transcription enhancers, such as the Rous sarcoma virus (RSV) enhancer, may be used to increase expression in mammalian host cells.

Specific initiation signals may also be used to achieve more efficient translation of sequences encoding a polypeptide of interest. Such signals include the
5 ATG initiation codon and adjacent sequences. In cases where sequences encoding the polypeptide, its initiation codon, and upstream sequences are inserted into the appropriate expression vector, no additional transcriptional or translational control signals may be needed. However, in cases where only coding sequence, or a portion thereof, is inserted, exogenous translational control signals including the ATG initiation
10 codon should be provided. Furthermore, the initiation codon should be in the correct reading frame to ensure translation of the entire insert. Exogenous translational elements and initiation codons may be of various origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of enhancers which are appropriate for the particular cell system which is used, such as those described in the
15 literature (Scharf, D. *et al.* (1994) *Results Probl. Cell Differ.* 20:125-162).

In addition, a host cell strain may be chosen for its ability to modulate the expression of the inserted sequences or to process the expressed protein in the desired fashion. Such modifications of the polypeptide include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation, and acylation.
20 Post-translational processing which cleaves a "prepro" form of the protein may also be used to facilitate correct insertion, folding and/or function. Different host cells such as CHO, HeLa, MDCK, HEK293, and WI38, which have specific cellular machinery and characteristic mechanisms for such post-translational activities, may be chosen to ensure the correct modification and processing of the foreign protein.

25 For long-term, high-yield production of recombinant proteins, stable expression is generally preferred. For example, cell lines which stably express a polynucleotide of interest may be transformed using expression vectors which may contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. Following the introduction
30 of the vector, cells may be allowed to grow for 1-2 days in an enriched media before they are switched to selective media. The purpose of the selectable marker is to confer

resistance to selection, and its presence allows growth and recovery of cells which successfully express the introduced sequences. Resistant clones of stably transformed cells may be proliferated using tissue culture techniques appropriate to the cell type.

Any number of selection systems may be used to recover transformed
5 cell lines. These include, but are not limited to, the herpes simplex virus thymidine kinase (Wigler, M. *et al.* (1977) *Cell* 11:223-32) and adenine phosphoribosyltransferase (Lowy, I. *et al.* (1990) *Cell* 22:817-23) genes which can be employed in tk.sup.- or aprt.sup.- cells, respectively. Also, antimetabolite, antibiotic or herbicide resistance can be used as the basis for selection; for example, dhfr which confers resistance to
10 methotrexate (Wigler, M. *et al.* (1980) *Proc. Natl. Acad. Sci.* 77:3567-70); npt, which confers resistance to the aminoglycosides, neomycin and G-418 (Colbere-Garapin, F. *et al.* (1981) *J. Mol. Biol.* 150:1-14); and als or pat, which confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively (Murry, *supra*). Additional selectable genes have been described, for example, trpB, which allows cells
15 to utilize indole in place of tryptophan, or hisD, which allows cells to utilize histinol in place of histidine (Hartman, S. C. and R. C. Mulligan (1988) *Proc. Natl. Acad. Sci.* 85:8047-51). Recently, the use of visible markers has gained popularity with such markers as anthocyanins, beta-glucuronidase and its substrate GUS, and luciferase and its substrate luciferin, being widely used not only to identify transformants, but also to
20 quantify the amount of transient or stable protein expression attributable to a specific vector system (Rhodes, C. A. *et al.* (1995) *Methods Mol. Biol.* 55:121-131).

Although the presence/absence of marker gene expression suggests that the gene of interest is also present, its presence and expression may need to be confirmed. For example, if the sequence encoding a polypeptide is inserted within a
25 marker gene sequence, recombinant cells containing sequences can be identified by the absence of marker gene function. Alternatively, a marker gene can be placed in tandem with a polypeptide-encoding sequence under the control of a single promoter. Expression of the marker gene in response to induction or selection usually indicates expression of the tandem gene as well.

30 Alternatively, host cells which contain and express a desired polynucleotide sequence may be identified by a variety of procedures known to those of

skill in the art. These procedures include, but are not limited to, DNA-DNA or DNA-RNA hybridizations and protein bioassay or immunoassay techniques which include membrane, solution, or chip based technologies for the detection and/or quantification of nucleic acid or protein.

5 A variety of protocols for detecting and measuring the expression of polynucleotide-encoded products, using either polyclonal or monoclonal antibodies specific for the product are known in the art. Examples include enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA), and fluorescence activated cell sorting (FACS). A two-site, monoclonal-based immunoassay utilizing monoclonal
10 antibodies reactive to two non-interfering epitopes on a given polypeptide may be preferred for some applications, but a competitive binding assay may also be employed. These and other assays are described, among other places, in Hampton, R. *et al.* (1990; Serological Methods, a Laboratory Manual, APS Press, St Paul. Minn.) and Maddox, D. E. *et al.* (1983; *J. Exp. Med.* 158:1211-1216).

15 A wide variety of labels and conjugation techniques are known by those skilled in the art and may be used in various nucleic acid and amino acid assays. Means for producing labeled hybridization or PCR probes for detecting sequences related to polynucleotides include oligolabeling, nick translation, end-labeling or PCR amplification using a labeled nucleotide. Alternatively, the sequences, or any portions
20 thereof may be cloned into a vector for the production of an mRNA probe. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes in vitro by addition of an appropriate RNA polymerase such as T7, T3, or SP6 and labeled nucleotides. These procedures may be conducted using a variety of commercially available kits. Suitable reporter molecules or labels, which may be used
25 include radionuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents as well as substrates, cofactors, inhibitors, magnetic particles, and the like.

 Host cells transformed with a polynucleotide sequence of interest may be cultured under conditions suitable for the expression and recovery of the protein from cell culture. The protein produced by a recombinant cell may be secreted or contained
30 intracellularly depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides of the

invention may be designed to contain signal sequences which direct secretion of the encoded polypeptide through a prokaryotic or eukaryotic cell membrane. Other recombinant constructions may be used to join sequences encoding a polypeptide of interest to nucleotide sequence encoding a polypeptide domain which will facilitate
5 purification of soluble proteins. Such purification facilitating domains include, but are not limited to, metal chelating peptides such as histidine-tryptophan modules that allow purification on immobilized metals, protein A domains that allow purification on immobilized immunoglobulin, and the domain utilized in the FLAGS extension/affinity purification system (Immunex Corp., Seattle, Wash.). The inclusion of cleavable linker
10 sequences such as those specific for Factor XA or enterokinase (Invitrogen, San Diego, Calif.) between the purification domain and the encoded polypeptide may be used to facilitate purification. One such expression vector provides for expression of a fusion protein containing a polypeptide of interest and a nucleic acid encoding 6 histidine residues preceding a thioredoxin or an enterokinase cleavage site. The histidine residues
15 facilitate purification on IMIAC (immobilized metal ion affinity chromatography) as described in Porath, J. *et al.* (1992, *Prot. Exp. Purif.* 3:263-281) while the enterokinase cleavage site provides a means for purifying the desired polypeptide from the fusion protein. A discussion of vectors which contain fusion proteins is provided in Kroll, D. J. *et al.* (1993; *DNA Cell Biol.* 12:441-453).

20 In addition to recombinant production methods, polypeptides of the invention, and fragments thereof, may be produced by direct peptide synthesis using solid-phase techniques (Merrifield J. (1963) *J. Am. Chem. Soc.* 85:2149-2154). Protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be achieved, for example, using Applied Biosystems 431A Peptide
25 Synthesizer (Perkin Elmer). Alternatively, various fragments may be chemically synthesized separately and combined using chemical methods to produce the full length molecule.

SITE-SPECIFIC MUTAGENESIS

Site-specific mutagenesis is a technique useful in the preparation of
30 individual peptides, or biologically functional equivalent polypeptides, through specific

mutagenesis of the underlying polynucleotides that encode them. The technique, well-known to those of skill in the art, further provides a ready ability to prepare and test sequence variants, for example, incorporating one or more of the foregoing considerations, by introducing one or more nucleotide sequence changes into the DNA.

- 5 Site-specific mutagenesis allows the production of mutants through the use of specific oligonucleotide sequences which encode the DNA sequence of the desired mutation, as well as a sufficient number of adjacent nucleotides, to provide a primer sequence of sufficient size and sequence complexity to form a stable duplex on both sides of the deletion junction being traversed. Mutations may be employed in a selected
10 polynucleotide sequence to improve, alter, decrease, modify, or otherwise change the properties of the polynucleotide itself, and/or alter the properties, activity, composition, stability, or primary sequence of the encoded polypeptide.

In certain embodiments of the present invention, the inventors contemplate the mutagenesis of the disclosed polynucleotide sequences to alter one or
15 more properties of the encoded polypeptide, such as the antigenicity of a polypeptide vaccine. The techniques of site-specific mutagenesis are well-known in the art, and are widely used to create variants of both polypeptides and polynucleotides. For example, site-specific mutagenesis is often used to alter a specific portion of a DNA molecule. In such embodiments, a primer comprising typically about 14 to about 25 nucleotides or so
20 in length is employed, with about 5 to about 10 residues on both sides of the junction of the sequence being altered.

As will be appreciated by those of skill in the art, site-specific mutagenesis techniques have often employed a phage vector that exists in both a single stranded and double stranded form. Typical vectors useful in site-directed mutagenesis
25 include vectors such as the M13 phage. These phage are readily commercially-available and their use is generally well-known to those skilled in the art. Double-stranded plasmids are also routinely employed in site directed mutagenesis that eliminates the step of transferring the gene of interest from a plasmid to a phage.

In general, site-directed mutagenesis in accordance herewith is
30 performed by first obtaining a single-stranded vector or melting apart of two strands of a double-stranded vector that includes within its sequence a DNA sequence that

encodes the desired peptide. An oligonucleotide primer bearing the desired mutated sequence is prepared, generally synthetically. This primer is then annealed with the single-stranded vector, and subjected to DNA polymerizing enzymes such as *E. coli* polymerase I Klenow fragment, in order to complete the synthesis of the mutation-bearing strand. Thus, a heteroduplex is formed wherein one strand encodes the original non-mutated sequence and the second strand bears the desired mutation. This heteroduplex vector is then used to transform appropriate cells, such as *E. coli* cells, and clones are selected which include recombinant vectors bearing the mutated sequence arrangement.

10 The preparation of sequence variants of the selected peptide-encoding DNA segments using site-directed mutagenesis provides a means of producing potentially useful species and is not meant to be limiting as there are other ways in which sequence variants of peptides and the DNA sequences encoding them may be obtained. For example, recombinant vectors encoding the desired peptide sequence
15 may be treated with mutagenic agents, such as hydroxylamine, to obtain sequence variants. Specific details regarding these methods and protocols are found in the teachings of Maloy *et al.*, 1994; Segal, 1976; Prokop and Bajpai, 1991; Kuby, 1994; and Maniatis *et al.*, 1982, each incorporated herein by reference, for that purpose.

As used herein, the term "oligonucleotide directed mutagenesis
20 procedure" refers to template-dependent processes and vector-mediated propagation which result in an increase in the concentration of a specific nucleic acid molecule relative to its initial concentration, or in an increase in the concentration of a detectable signal, such as amplification. As used herein, the term "oligonucleotide directed mutagenesis procedure" is intended to refer to a process that involves the
25 template-dependent extension of a primer molecule. The term template dependent process refers to nucleic acid synthesis of an RNA or a DNA molecule wherein the sequence of the newly synthesized strand of nucleic acid is dictated by the well-known rules of complementary base pairing (see, for example, Watson, 1987). Typically, vector mediated methodologies involve the introduction of the nucleic acid fragment
30 into a DNA or RNA vector, the clonal amplification of the vector, and the recovery of

the amplified nucleic acid fragment. Examples of such methodologies are provided by U. S. Patent No. 4,237,224, specifically incorporated herein by reference in its entirety.

POLYNUCLEOTIDE AMPLIFICATION TECHNIQUES

A number of template dependent processes are available to amplify the target sequences of interest present in a sample. One of the best known amplification methods is the polymerase chain reaction (PCR™) which is described in detail in U.S. Patent Nos. 4,683,195, 4,683,202 and 4,800,159, each of which is incorporated herein by reference in its entirety. Briefly, in PCR™, two primer sequences are prepared which are complementary to regions on opposite complementary strands of the target sequence. An excess of deoxynucleoside triphosphates is added to a reaction mixture along with a DNA polymerase (*e.g.*, *Taq* polymerase). If the target sequence is present in a sample, the primers will bind to the target and the polymerase will cause the primers to be extended along the target sequence by adding on nucleotides. By raising and lowering the temperature of the reaction mixture, the extended primers will dissociate from the target to form reaction products, excess primers will bind to the target and to the reaction product and the process is repeated. Preferably reverse transcription and PCR™ amplification procedure may be performed in order to quantify the amount of mRNA amplified. Polymerase chain reaction methodologies are well known in the art.

Another method for amplification is the ligase chain reaction (referred to as LCR), disclosed in Eur. Pat. Appl. Publ. No. 320,308 (specifically incorporated herein by reference in its entirety). In LCR, two complementary probe pairs are prepared, and in the presence of the target sequence, each pair will bind to opposite complementary strands of the target such that they abut. In the presence of a ligase, the two probe pairs will link to form a single unit. By temperature cycling, as in PCR™, bound ligated units dissociate from the target and then serve as "target sequences" for ligation of excess probe pairs. U.S. Patent No. 4,883,750, incorporated herein by reference in its entirety, describes an alternative method of amplification similar to LCR for binding probe pairs to a target sequence.

Qbeta Replicase, described in PCT Intl. Pat. Appl. Publ. No. PCT/US87/00880, incorporated herein by reference in its entirety, may also be used as still another amplification method in the present invention. In this method, a replicative sequence of RNA that has a region complementary to that of a target is added to a
5 sample in the presence of an RNA polymerase. The polymerase will copy the replicative sequence that can then be detected.

An isothermal amplification method, in which restriction endonucleases and ligases are used to achieve the amplification of target molecules that contain nucleotide 5'-[α -thio]triphosphates in one strand of a restriction site (Walker *et al.*,
10 1992, incorporated herein by reference in its entirety), may also be useful in the amplification of nucleic acids in the present invention.

Strand Displacement Amplification (SDA) is another method of carrying out isothermal amplification of nucleic acids which involves multiple rounds of strand displacement and synthesis, *i.e.* nick translation. A similar method, called Repair Chain
15 Reaction (RCR) is another method of amplification which may be useful in the present invention and is involves annealing several probes throughout a region targeted for amplification, followed by a repair reaction in which only two of the four bases are present. The other two bases can be added as biotinylated derivatives for easy detection. A similar approach is used in SDA.

20 Sequences can also be detected using a cyclic probe reaction (CPR). In CPR, a probe having a 3' and 5' sequences of non-target DNA and an internal or "middle" sequence of the target protein specific RNA is hybridized to DNA which is present in a sample. Upon hybridization, the reaction is treated with RNaseH, and the products of the probe are identified as distinctive products by generating a signal that is
25 released after digestion. The original template is annealed to another cycling probe and the reaction is repeated. Thus, CPR involves amplifying a signal generated by hybridization of a probe to a target gene specific expressed nucleic acid.

Still other amplification methods described in Great Britain Pat. Appl. No. 2 202 328, and in PCT Intl. Pat. Appl. Publ. No. PCT/US89/01025, each of which
30 is incorporated herein by reference in its entirety, may be used in accordance with the present invention. In the former application, "modified" primers are used in a PCR-

like, template and enzyme dependent synthesis. The primers may be modified by labeling with a capture moiety (*e.g.*, biotin) and/or a detector moiety (*e.g.*, enzyme). In the latter application, an excess of labeled probes is added to a sample. In the presence of the target sequence, the probe binds and is cleaved catalytically. After cleavage, the target sequence is released intact to be bound by excess probe. Cleavage of the labeled probe signals the presence of the target sequence.

Other nucleic acid amplification procedures include transcription-based amplification systems (TAS) (Kwoh *et al.*, 1989; PCT Intl. Pat. Appl. Publ. No. WO 88/10315, incorporated herein by reference in its entirety), including nucleic acid sequence based amplification (NASBA) and 3SR. In NASBA, the nucleic acids can be prepared for amplification by standard phenol/chloroform extraction, heat denaturation of a sample, treatment with lysis buffer and minispin columns for isolation of DNA and RNA or guanidinium chloride extraction of RNA. These amplification techniques involve annealing a primer that has sequences specific to the target sequence. Following polymerization, DNA/RNA hybrids are digested with RNase H while double stranded DNA molecules are heat-denatured again. In either case the single stranded DNA is made fully double stranded by addition of second target-specific primer, followed by polymerization. The double stranded DNA molecules are then multiply transcribed by a polymerase such as T7 or SP6. In an isothermal cyclic reaction, the RNAs are reverse transcribed into DNA, and transcribed once again with a polymerase such as T7 or SP6. The resulting products, whether truncated or complete, indicate target-specific sequences.

Eur. Pat. Appl. Publ. No. 329,822, incorporated herein by reference in its entirety, disclose a nucleic acid amplification process involving cyclically synthesizing single-stranded RNA ("ssRNA"), ssDNA, and double-stranded DNA (dsDNA), which may be used in accordance with the present invention. The ssRNA is a first template for a first primer oligonucleotide, which is elongated by reverse transcriptase (RNA-dependent DNA polymerase). The RNA is then removed from resulting DNA:RNA duplex by the action of ribonuclease H (RNase H, an RNase specific for RNA in a duplex with either DNA or RNA). The resultant ssDNA is a second template for a second primer, which also includes the sequences of an RNA polymerase

promoter (exemplified by T7 RNA polymerase) 5' to its homology to its template. This primer is then extended by DNA polymerase (exemplified by the large "Klenow" fragment of *E. coli* DNA polymerase I), resulting as a double-stranded DNA ("dsDNA") molecule, having a sequence identical to that of the original RNA between
5 the primers and having additionally, at one end, a promoter sequence. This promoter sequence can be used by the appropriate RNA polymerase to make many RNA copies of the DNA. These copies can then re-enter the cycle leading to very swift amplification. With proper choice of enzymes, this amplification can be done isothermally without addition of enzymes at each cycle. Because of the cyclical nature
10 of this process, the starting sequence can be chosen to be in the form of either DNA or RNA.

PCT Intl. Pat. Appl. Publ. No. WO 89/06700, incorporated herein by reference in its entirety, disclose a nucleic acid sequence amplification scheme based on the hybridization of a promoter/primer sequence to a target single-stranded DNA
15 ("ssDNA") followed by transcription of many RNA copies of the sequence. This scheme is not cyclic; *i.e.* new templates are not produced from the resultant RNA transcripts. Other amplification methods include "RACE" (Frohman, 1990), and "one-sided PCR" (Ohara, 1989) which are well-known to those of skill in the art.

Methods based on ligation of two (or more) oligonucleotides in the
20 presence of nucleic acid having the sequence of the resulting "di-oligonucleotide", thereby amplifying the di-oligonucleotide (Wu and Dean, 1996, incorporated herein by reference in its entirety), may also be used in the amplification of DNA sequences of the present invention.

BIOLOGICAL FUNCTIONAL EQUIVALENTS

25 Modification and changes may be made in the structure of the polynucleotides and polypeptides of the present invention and still obtain a functional molecule that encodes a polypeptide with desirable characteristics. As mentioned above, it is often desirable to introduce one or more mutations into a specific polynucleotide sequence. In certain circumstances, the resulting encoded polypeptide

sequence is altered by this mutation, or in other cases, the sequence of the polypeptide is unchanged by one or more mutations in the encoding polynucleotide.

When it is desirable to alter the amino acid sequence of a polypeptide to create an equivalent, or even an improved, second-generation molecule, the amino acid
5 changes may be achieved by changing one or more of the codons of the encoding DNA sequence, according to Table 1.

For example, certain amino acids may be substituted for other amino acids in a protein structure without appreciable loss of interactive binding capacity with structures such as, for example, antigen-binding regions of antibodies or binding sites
10 on substrate molecules. Since it is the interactive capacity and nature of a protein that defines that protein's biological functional activity, certain amino acid sequence substitutions can be made in a protein sequence, and, of course, its underlying DNA coding sequence, and nevertheless obtain a protein with like properties. It is thus contemplated by the inventors that various changes may be made in the peptide
15 sequences of the disclosed compositions, or corresponding DNA sequences which encode said peptides without appreciable loss of their biological utility or activity.

TABLE 1

Amino Acids			Codons						
Alanine	Ala	A	GCA	GCC	GCG	GCU			
Cysteine	Cys	C	UGC	UGU					
Aspartic acid	Asp	D	GAC	GAU					
Glutamic acid	Glu	E	GAA	GAG					
Phenylalanine	Phe	F	UUC	UUU					
Glycine	Gly	G	GGA	GGC	GGG	GGU			
Histidine	His	H	CAC	CAU					
Isoleucine	Ile	I	AUA	AUC	AUU				
Lysine	Lys	K	AAA	AAG					
Leucine	Leu	L	UUA	UUG	CUA	CUC	CUG	CUU	
Methionine	Met	M	AUG						
Asparagine	Asn	N	AAC	AAU					
Proline	Pro	P	CCA	CCC	CCG	CCU			
Glutamine	Gln	Q	CAA	CAG					
Arginine	Arg	R	AGA	AGG	CGA	CGC	CGG	CGU	
Serine	Ser	S	AGC	AGU	UCA	UCC	UCG	UCU	
Threonine	Thr	T	ACA	ACC	ACG	ACU			
Valine	Val	V	GUA	GUC	GUG	GUU			
Tryptophan	Trp	W	UGG						
Tyrosine	Tyr	Y	UAC	UAU					

In making such changes, the hydropathic index of amino acids may be considered. The importance of the hydropathic amino acid index in conferring

5 interactive biologic function on a protein is generally understood in the art (Kyte and Doolittle, 1982, incorporated herein by reference). It is accepted that the relative hydropathic character of the amino acid contributes to the secondary structure of the resultant protein, which in turn defines the interaction of the protein with other

10 molecules, for example, enzymes, substrates, receptors, DNA, antibodies, antigens, and the like. Each amino acid has been assigned a hydropathic index on the basis of its hydrophobicity and charge characteristics (Kyte and Doolittle, 1982). These values are:

isoleucine (+4.5); valine (+4.2); leucine (+3.8); phenylalanine (+2.8); cysteine/cystine (+2.5); methionine (+1.9); alanine (+1.8); glycine (−0.4); threonine (−0.7); serine (−0.8); tryptophan (−0.9); tyrosine (−1.3); proline (−1.6); histidine (−3.2); glutamate (−3.5); glutamine (−3.5); aspartate (−3.5); asparagine (−3.5); lysine (−3.9); and arginine (−4.5).

It is known in the art that certain amino acids may be substituted by other amino acids having a similar hydropathic index or score and still result in a protein with similar biological activity, *i.e.* still obtain a biological functionally equivalent protein. In making such changes, the substitution of amino acids whose hydropathic indices are within ± 2 is preferred, those within ± 1 are particularly preferred, and those within ± 0.5 are even more particularly preferred. It is also understood in the art that the substitution of like amino acids can be made effectively on the basis of hydrophilicity. U. S. Patent 4,554,101 (specifically incorporated herein by reference in its entirety), states that the greatest local average hydrophilicity of a protein, as governed by the hydrophilicity of its adjacent amino acids, correlates with a biological property of the protein.

As detailed in U. S. Patent 4,554,101, the following hydrophilicity values have been assigned to amino acid residues: arginine (+3.0); lysine (+3.0); aspartate (+3.0 \pm 1); glutamate (+3.0 \pm 1); serine (+0.3); asparagine (+0.2); glutamine (+0.2); glycine (0); threonine (−0.4); proline (−0.5 \pm 1); alanine (−0.5); histidine (−0.5); cysteine (−1.0); methionine (−1.3); valine (−1.5); leucine (−1.8); isoleucine (−1.8); tyrosine (−2.3); phenylalanine (−2.5); tryptophan (−3.4). It is understood that an amino acid can be substituted for another having a similar hydrophilicity value and still obtain a biologically equivalent, and in particular, an immunologically equivalent protein. In such changes, the substitution of amino acids whose hydrophilicity values are within ± 2 is preferred, those within ± 1 are particularly preferred, and those within ± 0.5 are even more particularly preferred.

As outlined above, amino acid substitutions are generally therefore based on the relative similarity of the amino acid side-chain substituents, for example, their hydrophobicity, hydrophilicity, charge, size, and the like. Exemplary substitutions that take various of the foregoing characteristics into consideration are well known to those

of skill in the art and include: arginine and lysine; glutamate and aspartate; serine and threonine; glutamine and asparagine; and valine, leucine and isoleucine.

In addition, any polynucleotide may be further modified to increase stability *in vivo*. Possible modifications include, but are not limited to, the addition of
5 flanking sequences at the 5' and/or 3' ends; the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages in the backbone; and/or the inclusion of nontraditional bases such as inosine, queosine and wybutosine, as well as acetyl-methyl-, thio- and other modified forms of adenine, cytidine, guanine, thymine and uridine.

10 IN VIVO POLYNUCLEOTIDE DELIVERY TECHNIQUES

In additional embodiments, genetic constructs comprising one or more of the polynucleotides of the invention are introduced into cells *in vivo*. This may be achieved using any of a variety of well known approaches, several of which are outlined below for the purpose of illustration.

15 1. ADENOVIRUS

One of the preferred methods for *in vivo* delivery of one or more nucleic acid sequences involves the use of an adenovirus expression vector. "Adenovirus expression vector" is meant to include those constructs containing adenovirus sequences sufficient to (a) support packaging of the construct and (b) to express a
20 polynucleotide that has been cloned therein in a sense or antisense orientation. Of course, in the context of an antisense construct, expression does not require that the gene product be synthesized.

The expression vector comprises a genetically engineered form of an adenovirus. Knowledge of the genetic organization of adenovirus, a 36 kb, linear,
25 double-stranded DNA virus, allows substitution of large pieces of adenoviral DNA with foreign sequences up to 7 kb (Grunhaus and Horwitz, 1992). In contrast to retrovirus, the adenoviral infection of host cells does not result in chromosomal integration because adenoviral DNA can replicate in an episomal manner without potential genotoxicity. Also, adenoviruses are structurally stable, and no genome rearrangement

has been detected after extensive amplification. Adenovirus can infect virtually all epithelial cells regardless of their cell cycle stage. So far, adenoviral infection appears to be linked only to mild disease such as acute respiratory disease in humans.

Adenovirus is particularly suitable for use as a gene transfer vector because of its mid-sized genome, ease of manipulation, high titer, wide target-cell range and high infectivity. Both ends of the viral genome contain 100-200 base pair inverted repeats (ITRs), which are *cis* elements necessary for viral DNA replication and packaging. The early (E) and late (L) regions of the genome contain different transcription units that are divided by the onset of viral DNA replication. The E1 region (E1A and E1B) encodes proteins responsible for the regulation of transcription of the viral genome and a few cellular genes. The expression of the E2 region (E2A and E2B) results in the synthesis of the proteins for viral DNA replication. These proteins are involved in DNA replication, late gene expression and host cell shut-off (Renan, 1990). The products of the late genes, including the majority of the viral capsid proteins, are expressed only after significant processing of a single primary transcript issued by the major late promoter (MLP). The MLP, (located at 16.8 m.u.) is particularly efficient during the late phase of infection, and all the mRNA's issued from this promoter possess a 5'-tripartite leader (TPL) sequence which makes them preferred mRNA's for translation.

In a current system, recombinant adenovirus is generated from homologous recombination between shuttle vector and provirus vector. Due to the possible recombination between two proviral vectors, wild-type adenovirus may be generated from this process. Therefore, it is critical to isolate a single clone of virus from an individual plaque and examine its genomic structure.

Generation and propagation of the current adenovirus vectors, which are replication deficient, depend on a unique helper cell line, designated 293, which was transformed from human embryonic kidney cells by Ad5 DNA fragments and constitutively expresses E1 proteins (Graham *et al.*, 1977). Since the E3 region is dispensable from the adenovirus genome (Jones and Shenk, 1978), the current adenovirus vectors, with the help of 293 cells, carry foreign DNA in either the E1, the D3 or both regions (Graham and Prevec, 1991). In nature, adenovirus can package

approximately 105% of the wild-type genome (Ghosh-Choudhury *et al.*, 1987), providing capacity for about 2 extra kB of DNA. Combined with the approximately 5.5 kB of DNA that is replaceable in the E1 and E3 regions, the maximum capacity of the current adenovirus vector is under 7.5 kB, or about 15% of the total length of the vector. More than 80% of the adenovirus viral genome remains in the vector backbone and is the source of vector-borne cytotoxicity. Also, the replication deficiency of the E1-deleted virus is incomplete. For example, leakage of viral gene expression has been observed with the currently available vectors at high multiplicities of infection (MOI) (Mulligan, 1993).

Helper cell lines may be derived from human cells such as human embryonic kidney cells, muscle cells, hematopoietic cells or other human embryonic mesenchymal or epithelial cells. Alternatively, the helper cells may be derived from the cells of other mammalian species that are permissive for human adenovirus. Such cells include, *e.g.*, Vero cells or other monkey embryonic mesenchymal or epithelial cells. As stated above, the currently preferred helper cell line is 293.

Recently, Racher *et al.* (1995) disclosed improved methods for culturing 293 cells and propagating adenovirus. In one format, natural cell aggregates are grown by inoculating individual cells into 1 liter siliconized spinner flasks (Techne, Cambridge, UK) containing 100-200 ml of medium. Following stirring at 40 rpm, the cell viability is estimated with trypan blue. In another format, Fibra-Cel microcarriers (Bibby Sterlin, Stone, UK) (5 g/l) is employed as follows. A cell inoculum, resuspended in 5 ml of medium, is added to the carrier (50 ml) in a 250 ml Erlenmeyer flask and left stationary, with occasional agitation, for 1 to 4 h. The medium is then replaced with 50 ml of fresh medium and shaking initiated. For virus production, cells are allowed to grow to about 80% confluence, after which time the medium is replaced (to 25% of the final volume) and adenovirus added at an MOI of 0.05. Cultures are left stationary overnight, following which the volume is increased to 100% and shaking commenced for another 72 h.

Other than the requirement that the adenovirus vector be replication defective, or at least conditionally defective, the nature of the adenovirus vector is not believed to be crucial to the successful practice of the invention. The adenovirus may

be of any of the 42 different known serotypes or subgroups A-F. Adenovirus type 5 of subgroup C is the preferred starting material in order to obtain a conditional replication-defective adenovirus vector for use in the present invention, since Adenovirus type 5 is a human adenovirus about which a great deal of biochemical and genetic information is known, and it has historically been used for most constructions employing adenovirus as a vector.

As stated above, the typical vector according to the present invention is replication defective and will not have an adenovirus E1 region. Thus, it will be most convenient to introduce the polynucleotide encoding the gene of interest at the position from which the E1-coding sequences have been removed. However, the position of insertion of the construct within the adenovirus sequences is not critical to the invention. The polynucleotide encoding the gene of interest may also be inserted in lieu of the deleted E3 region in E3 replacement vectors as described by Karlsson *et al.* (1986) or in the E4 region where a helper cell line or helper virus complements the E4 defect.

Adenovirus is easy to grow and manipulate and exhibits broad host range *in vitro* and *in vivo*. This group of viruses can be obtained in high titers, *e.g.*, 10^9 - 10^{11} plaque-forming units per ml, and they are highly infective. The life cycle of adenovirus does not require integration into the host cell genome. The foreign genes delivered by adenovirus vectors are episomal and, therefore, have low genotoxicity to host cells. No side effects have been reported in studies of vaccination with wild-type adenovirus (Couch *et al.*, 1963; Top *et al.*, 1971), demonstrating their safety and therapeutic potential as *in vivo* gene transfer vectors.

Adenovirus vectors have been used in eukaryotic gene expression (Levrero *et al.*, 1991; Gomez-Foix *et al.*, 1992) and vaccine development (Grunhaus and Horwitz, 1992; Graham and Prevec, 1992). Recently, animal studies suggested that recombinant adenovirus could be used for gene therapy (Stratford-Perricaudet and Perricaudet, 1991; Stratford-Perricaudet *et al.*, 1990; Rich *et al.*, 1993). Studies in administering recombinant adenovirus to different tissues include trachea instillation (Rosenfeld *et al.*, 1991; Rosenfeld *et al.*, 1992), muscle injection (Ragot *et al.*, 1993),

peripheral intravenous injections (Herz and Gerard, 1993) and stereotactic inoculation into the brain (Le Gal La Salle *et al.*, 1993).

2. RETROVIRUSES

The retroviruses are a group of single-stranded RNA viruses characterized by an ability to convert their RNA to double-stranded DNA in infected cells by a process of reverse-transcription (Coffin, 1990). The resulting DNA then stably integrates into cellular chromosomes as a provirus and directs synthesis of viral proteins. The integration results in the retention of the viral gene sequences in the recipient cell and its descendants. The retroviral genome contains three genes, gag, pol, and env that code for capsid proteins, polymerase enzyme, and envelope components, respectively. A sequence found upstream from the gag gene contains a signal for packaging of the genome into virions. Two long terminal repeat (LTR) sequences are present at the 5' and 3' ends of the viral genome. These contain strong promoter and enhancer sequences and are also required for integration in the host cell genome (Coffin, 1990).

In order to construct a retroviral vector, a nucleic acid encoding one or more oligonucleotide or polynucleotide sequences of interest is inserted into the viral genome in the place of certain viral sequences to produce a virus that is replication-defective. In order to produce virions, a packaging cell line containing the gag, pol, and env genes but without the LTR and packaging components is constructed (Mann *et al.*, 1983). When a recombinant plasmid containing a cDNA, together with the retroviral LTR and packaging sequences is introduced into this cell line (by calcium phosphate precipitation for example), the packaging sequence allows the RNA transcript of the recombinant plasmid to be packaged into viral particles, which are then secreted into the culture media (Nicolas and Rubenstein, 1988; Temin, 1986; Mann *et al.*, 1983). The media containing the recombinant retroviruses is then collected, optionally concentrated, and used for gene transfer. Retroviral vectors are able to infect a broad variety of cell types. However, integration and stable expression require the division of host cells (Paskind *et al.*, 1975).

A novel approach designed to allow specific targeting of retrovirus vectors was recently developed based on the chemical modification of a retrovirus by the chemical addition of lactose residues to the viral envelope. This modification could permit the specific infection of hepatocytes *via* sialoglycoprotein receptors.

5 A different approach to targeting of recombinant retroviruses was designed in which biotinylated antibodies against a retroviral envelope protein and against a specific cell receptor were used. The antibodies were coupled *via* the biotin components by using streptavidin (Roux *et al.*, 1989). Using antibodies against major histocompatibility complex class I and class II antigens, they demonstrated the infection
10 of a variety of human cells that bore those surface antigens with an ecotropic virus *in vitro* (Roux *et al.*, 1989).

3. ADENO-ASSOCIATED VIRUSES

AAV (Ridgeway, 1988; Hermonat and Muzyczka, 1984) is a parovirus, discovered as a contamination of adenoviral stocks. It is a ubiquitous virus (antibodies
15 are present in 85% of the US human population) that has not been linked to any disease. It is also classified as a dependovirus, because its replications is dependent on the presence of a helper virus, such as adenovirus. Five serotypes have been isolated, of which AAV-2 is the best characterized. AAV has a single-stranded linear DNA that is encapsidated into capsid proteins VP1, VP2 and VP3 to form an icosahedral virion of
20 20 to 24 nm in diameter (Muzyczka and McLaughlin, 1988).

The AAV DNA is approximately 4.7 kilobases long. It contains two open reading frames and is flanked by two ITRs. There are two major genes in the AAV genome: *rep* and *cap*. The *rep* gene codes for proteins responsible for viral replications, whereas *cap* codes for capsid protein VP1-3. Each ITR forms a T-shaped
25 hairpin structure. These terminal repeats are the only essential *cis* components of the AAV for chromosomal integration. Therefore, the AAV can be used as a vector with all viral coding sequences removed and replaced by the cassette of genes for delivery. Three viral promoters have been identified and named p5, p19, and p40, according to their map position. Transcription from p5 and p19 results in production of rep proteins,

and transcription from p40 produces the capsid proteins (Hermonat and Muzyczka, 1984).

There are several factors that prompted researchers to study the possibility of using rAAV as an expression vector. One is that the requirements for delivering a gene to integrate into the host chromosome are surprisingly few. It is necessary to have the 145-bp ITRs, which are only 6% of the AAV genome. This leaves room in the vector to assemble a 4.5-kb DNA insertion. While this carrying capacity may prevent the AAV from delivering large genes, it is amply suited for delivering the antisense constructs of the present invention.

AAV is also a good choice of delivery vehicles due to its safety. There is a relatively complicated rescue mechanism: not only wild type adenovirus but also AAV genes are required to mobilize rAAV. Likewise, AAV is not pathogenic and not associated with any disease. The removal of viral coding sequences minimizes immune reactions to viral gene expression, and therefore, rAAV does not evoke an inflammatory response.

4. OTHER VIRAL VECTORS AS EXPRESSION CONSTRUCTS

Other viral vectors may be employed as expression constructs in the present invention for the delivery of oligonucleotide or polynucleotide sequences to a host cell. Vectors derived from viruses such as vaccinia virus (Ridgeway, 1988; Coupar *et al.*, 1988), lentiviruses, polio viruses and herpes viruses may be employed. They offer several attractive features for various mammalian cells (Friedmann, 1989; Ridgeway, 1988; Coupar *et al.*, 1988; Horwich *et al.*, 1990).

With the recent recognition of defective hepatitis B viruses, new insight was gained into the structure-function relationship of different viral sequences. *In vitro* studies showed that the virus could retain the ability for helper-dependent packaging and reverse transcription despite the deletion of up to 80% of its genome (Horwich *et al.*, 1990). This suggested that large portions of the genome could be replaced with foreign genetic material. The hepatotropism and persistence (integration) were particularly attractive properties for liver-directed gene transfer. Chang *et al.* (1991) introduced the chloramphenicol acetyltransferase (CAT) gene into duck hepatitis B

virus genome in the place of the polymerase, surface, and pre-surface coding sequences. It was cotransfected with wild-type virus into an avian hepatoma cell line. Culture media containing high titers of the recombinant virus were used to infect primary duckling hepatocytes. Stable CAT gene expression was detected for at least 24 days after transfection (Chang *et al.*, 1991).

5. NON-VIRAL VECTORS

In order to effect expression of the oligonucleotide or polynucleotide sequences of the present invention, the expression construct must be delivered into a cell. This delivery may be accomplished *in vitro*, as in laboratory procedures for transforming cells lines, or *in vivo* or *ex vivo*, as in the treatment of certain disease states. As described above, one preferred mechanism for delivery is *via* viral infection where the expression construct is encapsulated in an infectious viral particle.

Once the expression construct has been delivered into the cell the nucleic acid encoding the desired oligonucleotide or polynucleotide sequences may be positioned and expressed at different sites. In certain embodiments, the nucleic acid encoding the construct may be stably integrated into the genome of the cell. This integration may be in the specific location and orientation *via* homologous recombination (gene replacement) or it may be integrated in a random, non-specific location (gene augmentation). In yet further embodiments, the nucleic acid may be stably maintained in the cell as a separate, episomal segment of DNA. Such nucleic acid segments or "episomes" encode sequences sufficient to permit maintenance and replication independent of or in synchronization with the host cell cycle. How the expression construct is delivered to a cell and where in the cell the nucleic acid remains is dependent on the type of expression construct employed.

In certain embodiments of the invention, the expression construct comprising one or more oligonucleotide or polynucleotide sequences may simply consist of naked recombinant DNA or plasmids. Transfer of the construct may be performed by any of the methods mentioned above which physically or chemically permeabilize the cell membrane. This is particularly applicable for transfer *in vitro* but it may be applied to *in vivo* use as well. Dubensky *et al.* (1984) successfully injected

polyomavirus DNA in the form of calcium phosphate precipitates into liver and spleen of adult and newborn mice demonstrating active viral replication and acute infection. Benvenisty and Reshef (1986) also demonstrated that direct intraperitoneal injection of calcium phosphate-precipitated plasmids results in expression of the transfected genes.

- 5 It is envisioned that DNA encoding a gene of interest may also be transferred in a similar manner *in vivo* and express the gene product.

Another embodiment of the invention for transferring a naked DNA expression construct into cells may involve particle bombardment. This method depends on the ability to accelerate DNA-coated microprojectiles to a high velocity
10 allowing them to pierce cell membranes and enter cells without killing them (Klein *et al.*, 1987). Several devices for accelerating small particles have been developed. One such device relies on a high voltage discharge to generate an electrical current, which in turn provides the motive force (Yang *et al.*, 1990). The microprojectiles used have consisted of biologically inert substances such as tungsten or gold beads.

- 15 Selected organs including the liver, skin, and muscle tissue of rats and mice have been bombarded *in vivo* (Yang *et al.*, 1990; Zelenin *et al.*, 1991). This may require surgical exposure of the tissue or cells, to eliminate any intervening tissue between the gun and the target organ, *i.e. ex vivo* treatment. Again, DNA encoding a particular gene may be delivered *via* this method and still be incorporated by the present
20 invention.

ANTISENSE OLIGONUCLEOTIDES

- The end result of the flow of genetic information is the synthesis of protein. DNA is transcribed by polymerases into messenger RNA and translated on the ribosome to yield a folded, functional protein. Thus there are several steps along the
25 route where protein synthesis can be inhibited. The native DNA segment coding for a polypeptide described herein, as all such mammalian DNA strands, has two strands: a sense strand and an antisense strand held together by hydrogen bonding. The messenger RNA coding for polypeptide has the same nucleotide sequence as the sense DNA strand except that the DNA thymidine is replaced by uridine. Thus, synthetic

antisense nucleotide sequences will bind to a mRNA and inhibit expression of the protein encoded by that mRNA.

The targeting of antisense oligonucleotides to mRNA is thus one mechanism to shut down protein synthesis, and, consequently, represents a powerful and targeted therapeutic approach. For example, the synthesis of polygalacturonase and the muscarine type 2 acetylcholine receptor are inhibited by antisense oligonucleotides directed to their respective mRNA sequences (U. S. Patent 5,739,119 and U. S. Patent 5,759,829, each specifically incorporated herein by reference in its entirety). Further, examples of antisense inhibition have been demonstrated with the nuclear protein cyclin, the multiple drug resistance gene (MDG1), ICAM-1, E-selectin, STK-1, striatal GABA_A receptor and human EGF (Jaskulski *et al.*, 1988; Vasanthakumar and Ahmed, 1989; Peris *et al.*, 1998; U. S. Patent 5,801,154; U. S. Patent 5,789,573; U. S. Patent 5,718,709 and U. S. Patent 5,610,288, each specifically incorporated herein by reference in its entirety). Antisense constructs have also been described that inhibit and can be used to treat a variety of abnormal cellular proliferations, *e.g.* cancer (U. S. Patent 5,747,470; U. S. Patent 5,591,317 and U. S. Patent 5,783,683, each specifically incorporated herein by reference in its entirety).

Therefore, in exemplary embodiments, the invention provides oligonucleotide sequences that comprise all, or a portion of, any sequence that is capable of specifically binding to polynucleotide sequence described herein, or a complement thereof. In one embodiment, the antisense oligonucleotides comprise DNA or derivatives thereof. In another embodiment, the oligonucleotides comprise RNA or derivatives thereof. In a third embodiment, the oligonucleotides are modified DNAs comprising a phosphorothioated modified backbone. In a fourth embodiment, the oligonucleotide sequences comprise peptide nucleic acids or derivatives thereof. In each case, preferred compositions comprise a sequence region that is complementary, and more preferably substantially-complementary, and even more preferably, completely complementary to one or more portions of polynucleotides disclosed herein.

Selection of antisense compositions specific for a given gene sequence is based upon analysis of the chosen target sequence (*i.e.* in these illustrative examples the rat and human sequences) and determination of secondary structure, T_m , binding

energy, relative stability, and antisense compositions were selected based upon their relative inability to form dimers, hairpins, or other secondary structures that would reduce or prohibit specific binding to the target mRNA in a host cell.

Highly preferred target regions of the mRNA, are those which are at or
5 near the AUG translation initiation codon, and those sequences which were substantially complementary to 5' regions of the mRNA. These secondary structure analyses and target site selection considerations were performed using v.4 of the OLIGO primer analysis software (Rychlik, 1997) and the BLASTN 2.0.5 algorithm software (Altschul *et al.*, 1997).

10 The use of an antisense delivery method employing a short peptide vector, termed MPG (27 residues), is also contemplated. The MPG peptide contains a hydrophobic domain derived from the fusion sequence of HIV gp41 and a hydrophilic domain from the nuclear localization sequence of SV40 T-antigen (Morris *et al.*, 1997). It has been demonstrated that several molecules of the MPG peptide coat the antisense
15 oligonucleotides and can be delivered into cultured mammalian cells in less than 1 hour with relatively high efficiency (90%). Further, the interaction with MPG strongly increases both the stability of the oligonucleotide to nuclease and the ability to cross the plasma membrane (Morris *et al.*, 1997).

RIBOZYMES

20 Although proteins traditionally have been used for catalysis of nucleic acids, another class of macromolecules has emerged as useful in this endeavor. Ribozymes are RNA-protein complexes that cleave nucleic acids in a site-specific fashion. Ribozymes have specific catalytic domains that possess endonuclease activity (Kim and Cech, 1987; Gerlach *et al.*, 1987; Forster and Symons, 1987). For example, a
25 large number of ribozymes accelerate phosphoester transfer reactions with a high degree of specificity, often cleaving only one of several phosphoesters in an oligonucleotide substrate (Cech *et al.*, 1981; Michel and Westhof, 1990; Reinhold-Hurek and Shub, 1992). This specificity has been attributed to the requirement that the substrate bind via specific base-pairing interactions to the internal guide sequence
30 ("IGS") of the ribozyme prior to chemical reaction.

Ribozyme catalysis has primarily been observed as part of sequence-specific cleavage/ligation reactions involving nucleic acids (Joyce, 1989; Cech *et al.*, 1981). For example, U. S. Patent No. 5,354,855 (specifically incorporated herein by reference) reports that certain ribozymes can act as endonucleases with a sequence
5 specificity greater than that of known ribonucleases and approaching that of the DNA restriction enzymes. Thus, sequence-specific ribozyme-mediated inhibition of gene expression may be particularly suited to therapeutic applications (Scanlon *et al.*, 1991; Sarver *et al.*, 1990). Recently, it was reported that ribozymes elicited genetic changes in some cells lines to which they were applied; the altered genes included the oncogenes
10 H-*ras*, c-*fos* and genes of HIV. Most of this work involved the modification of a target mRNA, based on a specific mutant codon that is cleaved by a specific ribozyme.

Six basic varieties of naturally-occurring enzymatic RNAs are known presently. Each can catalyze the hydrolysis of RNA phosphodiester bonds *in trans* (and thus can cleave other RNA molecules) under physiological conditions. In general,
15 enzymatic nucleic acids act by first binding to a target RNA. Such binding occurs through the target binding portion of a enzymatic nucleic acid which is held in close proximity to an enzymatic portion of the molecule that acts to cleave the target RNA. Thus, the enzymatic nucleic acid first recognizes and then binds a target RNA through complementary base-pairing, and once bound to the correct site, acts enzymatically to
20 cut the target RNA. Strategic cleavage of such a target RNA will destroy its ability to direct synthesis of an encoded protein. After an enzymatic nucleic acid has bound and cleaved its RNA target, it is released from that RNA to search for another target and can repeatedly bind and cleave new targets.

The enzymatic nature of a ribozyme is advantageous over many
25 technologies, such as antisense technology (where a nucleic acid molecule simply binds to a nucleic acid target to block its translation) since the concentration of ribozyme necessary to affect a therapeutic treatment is lower than that of an antisense oligonucleotide. This advantage reflects the ability of the ribozyme to act enzymatically. Thus, a single ribozyme molecule is able to cleave many molecules of
30 target RNA. In addition, the ribozyme is a highly specific inhibitor, with the specificity of inhibition depending not only on the base pairing mechanism of binding to the target

RNA, but also on the mechanism of target RNA cleavage. Single mismatches, or base-substitutions, near the site of cleavage can completely eliminate catalytic activity of a ribozyme. Similar mismatches in antisense molecules do not prevent their action (Woolf *et al.*, 1992). Thus, the specificity of action of a ribozyme is greater than that of
5 an antisense oligonucleotide binding the same RNA site.

The enzymatic nucleic acid molecule may be formed in a hammerhead, hairpin, a hepatitis δ virus, group I intron or RNaseP RNA (in association with an RNA guide sequence) or Neurospora VS RNA motif. Examples of hammerhead motifs are described by Rossi *et al.* (1992). Examples of hairpin motifs are described by Hampel
10 *et al.* (Eur. Pat. Appl. Publ. No. EP 0360257), Hampel and Tritz (1989), Hampel *et al.* (1990) and U. S. Patent 5,631,359 (specifically incorporated herein by reference). An example of the hepatitis δ virus motif is described by Perrotta and Been (1992); an example of the RNaseP motif is described by Guerrier-Takada *et al.* (1983); Neurospora VS RNA ribozyme motif is described by Collins (Saville and Collins,
15 1990; Saville and Collins, 1991; Collins and Olive, 1993); and an example of the Group I intron is described in (U. S. Patent 4,987,071, specifically incorporated herein by reference). All that is important in an enzymatic nucleic acid molecule of this invention is that it has a specific substrate binding site which is complementary to one or more of the target gene RNA regions, and that it have nucleotide sequences within or
20 surrounding that substrate binding site which impart an RNA cleaving activity to the molecule. Thus the ribozyme constructs need not be limited to specific motifs mentioned herein.

In certain embodiments, it may be important to produce enzymatic cleaving agents which exhibit a high degree of specificity for the RNA of a desired
25 target, such as one of the sequences disclosed herein. The enzymatic nucleic acid molecule is preferably targeted to a highly conserved sequence region of a target mRNA. Such enzymatic nucleic acid molecules can be delivered exogenously to specific cells as required. Alternatively, the ribozymes can be expressed from DNA or RNA vectors that are delivered to specific cells.

30 Small enzymatic nucleic acid motifs (*e.g.*, of the hammerhead or the hairpin structure) may also be used for exogenous delivery. The simple structure of

these molecules increases the ability of the enzymatic nucleic acid to invade targeted regions of the mRNA structure. Alternatively, catalytic RNA molecules can be expressed within cells from eukaryotic promoters (e.g., Scanlon *et al.*, 1991; Kashani-Sabet *et al.*, 1992; Dropulic *et al.*, 1992; Weerasinghe *et al.*, 1991; Ojwang *et al.*, 1992; 5 Chen *et al.*, 1992; Sarver *et al.*, 1990). Those skilled in the art realize that any ribozyme can be expressed in eukaryotic cells from the appropriate DNA vector. The activity of such ribozymes can be augmented by their release from the primary transcript by a second ribozyme (Int. Pat. Appl. Publ. No. WO 93/23569, and Int. Pat. Appl. Publ. No. WO 94/02595, both hereby incorporated by reference; Ohkawa *et al.*, 10 1992; Taira *et al.*, 1991; and Ventura *et al.*, 1993).

Ribozymes may be added directly, or can be complexed with cationic lipids, lipid complexes, packaged within liposomes, or otherwise delivered to target cells. The RNA or RNA complexes can be locally administered to relevant tissues *ex vivo*, or *in vivo* through injection, aerosol inhalation, infusion pump or stent, with or 15 without their incorporation in biopolymers.

Ribozymes may be designed as described in Int. Pat. Appl. Publ. No. WO 93/23569 and Int. Pat. Appl. Publ. No. WO 94/02595, each: specifically incorporated herein by reference) and synthesized to be tested *in vitro* and *in vivo*, as described. Such ribozymes can also be optimized for delivery. While specific 20 examples are provided, those in the art will recognize that equivalent RNA targets in other species can be utilized when necessary.

Hammerhead or hairpin ribozymes may be individually analyzed by computer folding (Jaeger *et al.*, 1989) to assess whether the ribozyme sequences fold into the appropriate secondary structure. Those ribozymes with unfavorable 25 intramolecular interactions between the binding arms and the catalytic core are eliminated from consideration. Varying binding arm lengths can be chosen to optimize activity. Generally, at least 5 or so bases on each arm are able to bind to, or otherwise interact with, the target RNA.

Ribozymes of the hammerhead or hairpin motif may be designed to 30 anneal to various sites in the mRNA message, and can be chemically synthesized. The method of synthesis used follows the procedure for normal RNA synthesis as described

in Usman *et al.* (1987) and in Scaringe *et al.* (1990) and makes use of common nucleic acid protecting and coupling groups, such as dimethoxytrityl at the 5'-end, and phosphoramidites at the 3'-end. Average stepwise coupling yields are typically >98%. Hairpin ribozymes may be synthesized in two parts and annealed to reconstruct an active ribozyme (Chowrira and Burke, 1992). Ribozymes may be modified extensively to enhance stability by modification with nuclease resistant groups, for example, 2'-amino, 2'-C-allyl, 2'-fluoro, 2'-O-methyl, 2'-H (for a review see *e.g.*, Usman and Cedergren, 1992). Ribozymes may be purified by gel electrophoresis using general methods or by high pressure liquid chromatography and resuspended in water.

Ribozyme activity can be optimized by altering the length of the ribozyme binding arms, or chemically synthesizing ribozymes with modifications that prevent their degradation by serum ribonucleases (see *e.g.*, Int. Pat. Appl. Publ. No. WO 92/07065; Perrault *et al.*, 1990; Pieken *et al.*, 1991; Usman and Cedergren, 1992; Int. Pat. Appl. Publ. No. WO 93/15187; Int. Pat. Appl. Publ. No. WO 91/03162; Eur. Pat. Appl. Publ. No. 92110298.4; U. S. Patent 5,334,711; and Int. Pat. Appl. Publ. No. WO 94/13688, which describe various chemical modifications that can be made to the sugar moieties of enzymatic RNA molecules), modifications which enhance their efficacy in cells, and removal of stem II bases to shorten RNA synthesis times and reduce chemical requirements.

Sullivan *et al.* (Int. Pat. Appl. Publ. No. WO 94/02595) describes the general methods for delivery of enzymatic RNA molecules. Ribozymes may be administered to cells by a variety of methods known to those familiar to the art, including, but not restricted to, encapsulation in liposomes, by iontophoresis, or by incorporation into other vehicles, such as hydrogels, cyclodextrins, biodegradable nanocapsules, and bioadhesive microspheres. For some indications, ribozymes may be directly delivered *ex vivo* to cells or tissues with or without the aforementioned vehicles. Alternatively, the RNA/vehicle combination may be locally delivered by direct inhalation, by direct injection or by use of a catheter, infusion pump or stent. Other routes of delivery include, but are not limited to, intravascular, intramuscular, subcutaneous or joint injection, aerosol inhalation, oral (tablet or pill form), topical, systemic, ocular, intraperitoneal and/or intrathecal delivery. More detailed descriptions

of ribozyme delivery and administration are provided in Int. Pat. Appl. Publ. No. WO 94/02595 and Int. Pat. Appl. Publ. No. WO 93/23569, each specifically incorporated herein by reference.

Another means of accumulating high concentrations of a ribozyme(s) within cells is to incorporate the ribozyme-encoding sequences into a DNA expression vector. Transcription of the ribozyme sequences are driven from a promoter for eukaryotic RNA polymerase I (pol I), RNA polymerase II (pol II), or RNA polymerase III (pol III). Transcripts from pol II or pol III promoters will be expressed at high levels in all cells; the levels of a given pol II promoter in a given cell type will depend on the nature of the gene regulatory sequences (enhancers, silencers, *etc.*) present nearby. Prokaryotic RNA polymerase promoters may also be used, providing that the prokaryotic RNA polymerase enzyme is expressed in the appropriate cells (Elroy-Stein and Moss, 1990; Gao and Huang, 1993; Lieber *et al.*, 1993; Zhou *et al.*, 1990). Ribozymes expressed from such promoters can function in mammalian cells (*e.g.* Kashani-Saber *et al.*, 1992; Ojwang *et al.*, 1992; Chen *et al.*, 1992; Yu *et al.*, 1993; L'Huillier *et al.*, 1992; Lisiewicz *et al.*, 1993). Such transcription units can be incorporated into a variety of vectors for introduction into mammalian cells, including but not restricted to, plasmid DNA vectors, viral DNA vectors (such as adenovirus or adeno-associated vectors), or viral RNA vectors (such as retroviral, semliki forest virus, sindbis virus vectors).

Ribozymes may be used as diagnostic tools to examine genetic drift and mutations within diseased cells. They can also be used to assess levels of the target RNA molecule. The close relationship between ribozyme activity and the structure of the target RNA allows the detection of mutations in any region of the molecule which alters the base-pairing and three-dimensional structure of the target RNA. By using multiple ribozymes, one may map nucleotide changes which are important to RNA structure and function *in vitro*, as well as in cells and tissues. Cleavage of target RNAs with ribozymes may be used to inhibit gene expression and define the role (essentially) of specified gene products in the progression of disease. In this manner, other genetic targets may be defined as important mediators of the disease. These studies will lead to better treatment of the disease progression by affording the possibility of combinational

therapies (e.g., multiple ribozymes targeted to different genes, ribozymes coupled with known small molecule inhibitors, or intermittent treatment with combinations of ribozymes and/or other chemical or biological molecules). Other *in vitro* uses of ribozymes are well known in the art, and include detection of the presence of mRNA
5 associated with an IL-5 related condition. Such RNA is detected by determining the presence of a cleavage product after treatment with a ribozyme using standard methodology.

PEPTIDE NUCLEIC ACIDS

In certain embodiments, the inventors contemplate the use of peptide
10 nucleic acids (PNAs) in the practice of the methods of the invention. PNA is a DNA mimic in which the nucleobases are attached to a pseudopeptide backbone (Good and Nielsen, 1997). PNA is able to be utilized in a number methods that traditionally have used RNA or DNA. Often PNA sequences perform better in techniques than the corresponding RNA or DNA sequences and have utilities that are not inherent to RNA
15 or DNA. A review of PNA including methods of making, characteristics of, and methods of using, is provided by Corey (1997) and is incorporated herein by reference. As such, in certain embodiments, one may prepare PNA sequences that are complementary to one or more portions of the ACE mRNA sequence, and such PNA compositions may be used to regulate, alter, decrease, or reduce the translation of ACE-
20 specific mRNA, and thereby alter the level of ACE activity in a host cell to which such PNA compositions have been administered.

PNAs have 2-aminoethyl-glycine linkages replacing the normal phosphodiester backbone of DNA (Nielsen *et al.*, 1991; Hanvey *et al.*, 1992; Hyrup and Nielsen, 1996; Neilsen, 1996). This chemistry has three important consequences:
25 firstly, in contrast to DNA or phosphorothioate oligonucleotides, PNAs are neutral molecules; secondly, PNAs are achiral, which avoids the need to develop a stereoselective synthesis; and thirdly, PNA synthesis uses standard Boc (Dueholm *et al.*, 1994) or Fmoc (Thomson *et al.*, 1995) protocols for solid-phase peptide synthesis, although other methods, including a modified Merrifield method, have been used
30 (Christensen *et al.*, 1995).

PNA monomers or ready-made oligomers are commercially available from PerSeptive Biosystems (Framingham, MA). PNA syntheses by either Boc or Fmoc protocols are straightforward using manual or automated protocols (Norton *et al.*, 1995). The manual protocol lends itself to the production of chemically modified PNAs or the simultaneous synthesis of families of closely related PNAs.

As with peptide synthesis, the success of a particular PNA synthesis will depend on the properties of the chosen sequence. For example, while in theory PNAs can incorporate any combination of nucleotide bases, the presence of adjacent purines can lead to deletions of one or more residues in the product. In expectation of this difficulty, it is suggested that, in producing PNAs with adjacent purines, one should repeat the coupling of residues likely to be added inefficiently. This should be followed by the purification of PNAs by reverse-phase high-pressure liquid chromatography (Norton *et al.*, 1995) providing yields and purity of product similar to those observed during the synthesis of peptides.

Modifications of PNAs for a given application may be accomplished by coupling amino acids during solid-phase synthesis or by attaching compounds that contain a carboxylic acid group to the exposed N-terminal amine. Alternatively, PNAs can be modified after synthesis by coupling to an introduced lysine or cysteine. The ease with which PNAs can be modified facilitates optimization for better solubility or for specific functional requirements. Once synthesized, the identity of PNAs and their derivatives can be confirmed by mass spectrometry. Several studies have made and utilized modifications of PNAs (Norton *et al.*, 1995; Haaima *et al.*, 1996; Stetsenko *et al.*, 1996; Petersen *et al.*, 1995; Ulmann *et al.*, 1996; Koch *et al.*, 1995; Orum *et al.*, 1995; Footer *et al.*, 1996; Griffith *et al.*, 1995; Kremsky *et al.*, 1996; Pardridge *et al.*, 1995; Boffa *et al.*, 1995; Landsdorp *et al.*, 1996; Gambacorti-Passerini *et al.*, 1996; Armitage *et al.*, 1997; Seeger *et al.*, 1997; Ruskowski *et al.*, 1997). U.S. Patent No. 5,700,922 discusses PNA-DNA-PNA chimeric molecules and their uses in diagnostics, modulating protein in organisms, and treatment of conditions susceptible to therapeutics.

In contrast to DNA and RNA, which contain negatively charged linkages, the PNA backbone is neutral. In spite of this dramatic alteration, PNAs

recognize complementary DNA and RNA by Watson-Crick pairing (Egholm *et al.*, 1993), validating the initial modeling by Nielsen *et al.* (1991). PNAs lack 3' to 5' polarity and can bind in either parallel or antiparallel fashion, with the antiparallel mode being preferred (Egholm *et al.*, 1993).

5 Hybridization of DNA oligonucleotides to DNA and RNA is destabilized by electrostatic repulsion between the negatively charged phosphate backbones of the complementary strands. By contrast, the absence of charge repulsion in PNA-DNA or PNA-RNA duplexes increases the melting temperature (T_m) and reduces the dependence of T_m on the concentration of mono- or divalent cations
10 (Nielsen *et al.*, 1991). The enhanced rate and affinity of hybridization are significant because they are responsible for the surprising ability of PNAs to perform strand invasion of complementary sequences within relaxed double-stranded DNA. In addition, the efficient hybridization at inverted repeats suggests that PNAs can recognize secondary structure effectively within double-stranded DNA. Enhanced
15 recognition also occurs with PNAs immobilized on surfaces, and Wang *et al.* have shown that support-bound PNAs can be used to detect hybridization events (Wang *et al.*, 1996).

One might expect that tight binding of PNAs to complementary sequences would also increase binding to similar (but not identical) sequences, reducing
20 the sequence specificity of PNA recognition. As with DNA hybridization, however, selective recognition can be achieved by balancing oligomer length and incubation temperature. Moreover, selective hybridization of PNAs is encouraged by PNA-DNA hybridization being less tolerant of base mismatches than DNA-DNA hybridization. For example, a single mismatch within a 16 bp PNA-DNA duplex can reduce the T_m by
25 up to 15°C (Egholm *et al.*, 1993). This high level of discrimination has allowed the development of several PNA-based strategies for the analysis of point mutations (Wang *et al.*, 1996; Carlsson *et al.*, 1996; Thiede *et al.*, 1996; Webb and Hurskainen, 1996; Perry-O'Keefe *et al.*, 1996).

High-affinity binding provides clear advantages for molecular
30 recognition and the development of new applications for PNAs. For example, 11-13 nucleotide PNAs inhibit the activity of telomerase, a ribonucleo-protein that extends

telomere ends using an essential RNA template, while the analogous DNA oligomers do not (Norton *et al.*, 1996).

Neutral PNAs are more hydrophobic than analogous DNA oligomers, and this can lead to difficulty solubilizing them at neutral pH, especially if the PNAs have a high purine content or if they have the potential to form secondary structures. Their solubility can be enhanced by attaching one or more positive charges to the PNA termini (Nielsen *et al.*, 1991).

Findings by Allfrey and colleagues suggest that strand invasion will occur spontaneously at sequences within chromosomal DNA (Boffa *et al.*, 1995; Boffa *et al.*, 1996). These studies targeted PNAs to triplet repeats of the nucleotides CAG and used this recognition to purify transcriptionally active DNA (Boffa *et al.*, 1995) and to inhibit transcription (Boffa *et al.*, 1996). This result suggests that if PNAs can be delivered within cells then they will have the potential to be general sequence-specific regulators of gene expression. Studies and reviews concerning the use of PNAs as antisense and anti-gene agents include Nielsen *et al.* (1993b), Hanvey *et al.* (1992), and Good and Nielsen (1997). Koppelhus *et al.* (1997) have used PNAs to inhibit HIV-1 inverse transcription, showing that PNAs may be used for antiviral therapies.

Methods of characterizing the antisense binding properties of PNAs are discussed in Rose (1993) and Jensen *et al.* (1997). Rose uses capillary gel electrophoresis to determine binding of PNAs to their complementary oligonucleotide, measuring the relative binding kinetics and stoichiometry. Similar types of measurements were made by Jensen *et al.* using BIAcore™ technology.

Other applications of PNAs include use in DNA strand invasion (Nielsen *et al.*, 1991), antisense inhibition (Hanvey *et al.*, 1992), mutational analysis (Orum *et al.*, 1993), enhancers of transcription (Mollegaard *et al.*, 1994), nucleic acid purification (Orum *et al.*, 1995), isolation of transcriptionally active genes (Boffa *et al.*, 1995), blocking of transcription factor binding (Vickers *et al.*, 1995), genome cleavage (Veselkov *et al.*, 1996), biosensors (Wang *et al.*, 1996), *in situ* hybridization (Thisted *et al.*, 1996), and in a alternative to Southern blotting (Perry-O'Keefe, 1996).

POLYPEPTIDE COMPOSITIONS

The present invention, in other aspects, provides polypeptide compositions. Generally, a polypeptide of the invention will be an isolated polypeptide (or an epitope, variant, or active fragment thereof) derived from a mammalian species.

5 Preferably, the polypeptide is encoded by a polynucleotide sequence disclosed herein or a sequence which hybridizes under moderately stringent conditions to a polynucleotide sequence disclosed herein. Alternatively, the polypeptide may be defined as a polypeptide which comprises a contiguous amino acid sequence from an amino acid sequence disclosed herein, or which polypeptide comprises an entire amino acid
10 sequence disclosed herein.

In the present invention, a polypeptide composition is also understood to comprise one or more polypeptides that are immunologically reactive with antibodies generated against a polypeptide of the invention, particularly a polypeptide having the amino acid sequence disclosed in SEQ ID NO: 786, 787, 791, 793, 795, 797-799, 806
15 or 809, or to active fragments, or to variants or biological functional equivalents thereof.

Likewise, a polypeptide composition of the present invention is understood to comprise one or more polypeptides that are capable of eliciting antibodies that are immunologically reactive with one or more polypeptides encoded by one or
20 more contiguous nucleic acid sequences contained in SEQ ID NO: 1, 11-13, 15, 20, 23-27, 29, 30, 33, 34, 39, 41, 43-46, 51, 52, 57, 58, 60, 62, 65-67, 69-71, 74, 76, 79, 80, 84, 86, 89-92, 95, 97, 98, 101, 110, 111, 113-119, 121-128, 130-134, 136, 138, 139, 141, 143, 146-151, 153, 154, 157-160, 162-164, 167-178, 180, 181, 183, 186-190, 192, 193, 195-220, 224, 226-231, 234, 236, 237, 240, 241, 244-246, 248, 254, 255, 261, 262, 266,
25 270, 275, 280, 282, 283, 288, 289, 290, 292, 295, 301, 303, 304, 309, 311, 341-782, 784, 785, 790, 792, 794, 796, 800-804, 807, 808 and 810-826, or to active fragments, or to variants thereof, or to one or more nucleic acid sequences which hybridize to one or more of these sequences under conditions of moderate to high stringency. Particularly illustrative polypeptides include the amino acid sequences disclosed in SEQ ID NO:
30 786, 787, 791, 793, 795, 797-799, 806, 809 and 827.

As used herein, an active fragment of a polypeptide includes a whole or a portion of a polypeptide which is modified by conventional techniques, *e.g.*, mutagenesis, or by addition, deletion, or substitution, but which active fragment exhibits substantially the same structure function, antigenicity, etc., as a polypeptide as described herein.

In certain illustrative embodiments, the polypeptides of the invention will comprise at least an immunogenic portion of a lung tumor protein or a variant thereof, as described herein. As noted above, a "lung tumor protein" is a protein that is expressed by lung tumor cells. Proteins that are lung tumor proteins also react detectably within an immunoassay (such as an ELISA) with antisera from a patient with lung cancer. Polypeptides as described herein may be of any length. Additional sequences derived from the native protein and/or heterologous sequences may be present, and such sequences may (but need not) possess further immunogenic or antigenic properties.

An "immunogenic portion," as used herein is a portion of a protein that is recognized (*i.e.*, specifically bound) by a B-cell and/or T-cell surface antigen receptor. Such immunogenic portions generally comprise at least 5 amino acid residues, more preferably at least 10, and still more preferably at least 20 amino acid residues of a lung tumor protein or a variant thereof. Certain preferred immunogenic portions include peptides in which an N-terminal leader sequence and/or transmembrane domain have been deleted. Other preferred immunogenic portions may contain a small N- and/or C-terminal deletion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids), relative to the mature protein.

Immunogenic portions may generally be identified using well known techniques, such as those summarized in Paul, *Fundamental Immunology*, 3rd ed., 243-247 (Raven Press, 1993) and references cited therein. Such techniques include screening polypeptides for the ability to react with antigen-specific antibodies, antisera and/or T-cell lines or clones. As used herein, antisera and antibodies are "antigen-specific" if they specifically bind to an antigen (*i.e.*, they react with the protein in an ELISA or other immunoassay, and do not react detectably with unrelated proteins). Such antisera and antibodies may be prepared as described herein, and using well

known techniques. An immunogenic portion of a native lung tumor protein is a portion that reacts with such antisera and/or T-cells at a level that is not substantially less than the reactivity of the full length polypeptide (e.g., in an ELISA and/or T-cell reactivity assay). Such immunogenic portions may react within such assays at a level that is similar to or greater than the reactivity of the full length polypeptide. Such screens may generally be performed using methods well known to those of ordinary skill in the art, such as those described in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. For example, a polypeptide may be immobilized on a solid support and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, ¹²⁵I-labeled Protein A.

As noted above, a composition may comprise a variant of a native lung tumor protein. A polypeptide "variant," as used herein, is a polypeptide that differs from a native lung tumor protein in one or more substitutions, deletions, additions and/or insertions, such that the immunogenicity of the polypeptide is not substantially diminished. In other words, the ability of a variant to react with antigen-specific antisera may be enhanced or unchanged, relative to the native protein, or may be diminished by less than 50%, and preferably less than 20%, relative to the native protein. Such variants may generally be identified by modifying one of the above polypeptide sequences and evaluating the reactivity of the modified polypeptide with antigen-specific antibodies or antisera as described herein. Preferred variants include those in which one or more portions, such as an N-terminal leader sequence or transmembrane domain, have been removed. Other preferred variants include variants in which a small portion (e.g., 1-30 amino acids, preferably 5-15 amino acids) has been removed from the N- and/or C-terminal of the mature protein.

Polypeptide variants encompassed by the present invention include those exhibiting at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or more identity (determined as described above) to the polypeptides disclosed herein.

Preferably, a variant contains conservative substitutions. A "conservative substitution" is one in which an amino acid is substituted for another

amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydropathic nature of the polypeptide to be substantially unchanged. Amino acid substitutions may generally be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity and/or the amphipathic nature of the residues. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine and arginine; and amino acids with uncharged polar head groups having similar hydrophilicity values include leucine, isoleucine and valine; glycine and alanine; asparagine and glutamine; and serine, threonine, phenylalanine and tyrosine. Other groups of amino acids that may represent conservative changes include: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his. A variant may also, or alternatively, contain nonconservative changes. In a preferred embodiment, variant polypeptides differ from a native sequence by substitution, deletion or addition of five amino acids or fewer. Variants may also (or alternatively) be modified by, for example, the deletion or addition of amino acids that have minimal influence on the immunogenicity, secondary structure and hydropathic nature of the polypeptide.

As noted above, polypeptides may comprise a signal (or leader) sequence at the N-terminal end of the protein, which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (e.g., poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

Polypeptides may be prepared using any of a variety of well known techniques. Recombinant polypeptides encoded by DNA sequences as described above may be readily prepared from the DNA sequences using any of a variety of expression vectors known to those of ordinary skill in the art. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast, and higher eukaryotic cells, such as mammalian cells and plant cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian

cell line such as COS or CHO. Supernatants from suitable host/vector systems which secrete recombinant protein or polypeptide into culture media may be first concentrated using a commercially available filter. Following concentration, the concentrate may be applied to a suitable purification matrix such as an affinity matrix or an ion exchange
5 resin. Finally, one or more reverse phase HPLC steps can be employed to further purify a recombinant polypeptide.

Portions and other variants having less than about 100 amino acids, and generally less than about 50 amino acids, may also be generated by synthetic means, using techniques well known to those of ordinary skill in the art. For example, such
10 polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. See Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems
15 Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

Within certain specific embodiments, a polypeptide may be a fusion protein that comprises multiple polypeptides as described herein, or that comprises at least one polypeptide as described herein and an unrelated sequence, such as a known
20 tumor protein. A fusion partner may, for example, assist in providing T helper epitopes (an immunological fusion partner), preferably T helper epitopes recognized by humans, or may assist in expressing the protein (an expression enhancer) at higher yields than the native recombinant protein. Certain preferred fusion partners are both immunological and expression enhancing fusion partners. Other fusion partners may be
25 selected so as to increase the solubility of the protein or to enable the protein to be targeted to desired intracellular compartments. Still further fusion partners include affinity tags, which facilitate purification of the protein.

Fusion proteins may generally be prepared using standard techniques, including chemical conjugation. Preferably, a fusion protein is expressed as a
30 recombinant protein, allowing the production of increased levels, relative to a non-fused protein, in an expression system. Briefly, DNA sequences encoding the polypeptide

components may be assembled separately, and ligated into an appropriate expression vector. The 3' end of the DNA sequence encoding one polypeptide component is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide component so that the reading frames of the sequences are in phase.

- 5 This permits translation into a single fusion protein that retains the biological activity of both component polypeptides.

A peptide linker sequence may be employed to separate the first and second polypeptide components by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is
10 incorporated into the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with
15 the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea *et al.*, *Gene* 40:39-46, 1985; Murphy *et al.*, *Proc. Natl. Acad. Sci. USA* 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S.
20 Patent No. 4,751,180. The linker sequence may generally be from 1 to about 50 amino acids in length. Linker sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable
25 transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons required to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

- 30 Fusion proteins are also provided. Such proteins comprise a polypeptide as described herein together with an unrelated immunogenic protein. Preferably the

immunogenic protein is capable of eliciting a recall response. Examples of such proteins include tetanus, tuberculosis and hepatitis proteins (*see, for example, Stoute et al. New Engl. J. Med., 336:86-91, 1997*).

Within preferred embodiments, an immunological fusion partner is
5 derived from protein D, a surface protein of the gram-negative bacterium *Haemophilus influenza B* (WO 91/18926). Preferably, a protein D derivative comprises approximately the first third of the protein (*e.g.*, the first N-terminal 100-110 amino acids), and a protein D derivative may be lipidated. Within certain preferred
10 embodiments, the first 109 residues of a Lipoprotein D fusion partner is included on the N-terminus to provide the polypeptide with additional exogenous T-cell epitopes and to increase the expression level in *E. coli* (thus functioning as an expression enhancer). The lipid tail ensures optimal presentation of the antigen to antigen presenting cells. Other fusion partners include the non-structural protein from influenzae virus, NS1 (hemagglutinin). Typically, the N-terminal 81 amino acids are used, although different
15 fragments that include T-helper epitopes may be used.

In another embodiment, the immunological fusion partner is the protein known as LYTA, or a portion thereof (preferably a C-terminal portion). LYTA is derived from *Streptococcus pneumoniae*, which synthesizes an N-acetyl-L-alanine amidase known as amidase LYTA (encoded by the *LytA* gene; *Gene* 43:265-292,
20 1986). LYTA is an autolysin that specifically degrades certain bonds in the peptidoglycan backbone. The C-terminal domain of the LYTA protein is responsible for the affinity to the choline or to some choline analogues such as DEAE. This property has been exploited for the development of *E. coli* C-LYTA expressing plasmids useful for expression of fusion proteins. Purification of hybrid proteins
25 containing the C-LYTA fragment at the amino terminus has been described (*see Biotechnology* 10:795-798, 1992). Within a preferred embodiment, a repeat portion of LYTA may be incorporated into a fusion protein. A repeat portion is found in the C-terminal region starting at residue 178. A particularly preferred repeat portion incorporates residues 188-305.

30 In general, polypeptides (including fusion proteins) and polynucleotides as described herein are isolated. An "isolated" polypeptide or polynucleotide is one that

is removed from its original environment. For example, a naturally-occurring protein is isolated if it is separated from some or all of the coexisting materials in the natural system. Preferably, such polypeptides are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure. A polynucleotide is
5 considered to be isolated if, for example, it is cloned into a vector that is not a part of the natural environment.

BINDING AGENTS

The present invention further provides agents, such as antibodies and antigen-binding fragments thereof, that specifically bind to a lung tumor protein. As
10 used herein, an antibody, or antigen-binding fragment thereof, is said to "specifically bind" to a lung tumor protein if it reacts at a detectable level (within, for example, an ELISA) with a lung tumor protein, and does not react detectably with unrelated proteins under similar conditions. As used herein, "binding" refers to a noncovalent association between two separate molecules such that a complex is formed. The ability to bind may
15 be evaluated by, for example, determining a binding constant for the formation of the complex. The binding constant is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In general, two compounds are said to "bind," in the context of the present invention, when the binding constant for complex formation exceeds about 10^3 L/mol. The binding constant may be
20 determined using methods well known in the art.

Binding agents may be further capable of differentiating between patients with and without a cancer, such as lung cancer, using the representative assays provided herein. In other words, antibodies or other binding agents that bind to a lung tumor protein will generate a signal indicating the presence of a cancer in at least about
25 20% of patients with the disease, and will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without the cancer. To determine whether a binding agent satisfies this requirement, biological samples (e.g., blood, sera, sputum, urine and/or tumor biopsies) from patients with and without a cancer (as determined using standard clinical tests) may be assayed as described herein
30 for the presence of polypeptides that bind to the binding agent. It will be apparent that a

statistically significant number of samples with and without the disease should be assayed. Each binding agent should satisfy the above criteria; however, those of ordinary skill in the art will recognize that binding agents may be used in combination to improve sensitivity.

5 Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome, with or without a peptide component, an RNA molecule or a polypeptide. In a preferred embodiment, a binding agent is an antibody or an antigen-binding fragment thereof. Antibodies may be prepared by any of a variety of techniques known to those of ordinary skill in the art. See, e.g., Harlow
10 and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, antibodies can be produced by cell culture techniques, including the generation of monoclonal antibodies as described herein, or via transfection of antibody genes into suitable bacterial or mammalian cell hosts, in order to allow for the production of recombinant antibodies. In one technique, an immunogen comprising the polypeptide
15 is initially injected into any of a wide variety of mammals (e.g., mice, rats, rabbits, sheep or goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The
20 immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

25 Monoclonal antibodies specific for an antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (i.e., reactivity with the polypeptide of interest). Such cell lines may
30 be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a

myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid
5 cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and their culture supernatants tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

10 Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by
15 conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

Within certain embodiments, the use of antigen-binding fragments of antibodies may be preferred. Such fragments include Fab fragments, which may be
20 prepared using standard techniques. Briefly, immunoglobulins may be purified from rabbit serum by affinity chromatography on Protein A bead columns (Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988) and digested by papain to yield Fab and Fc fragments. The Fab and Fc fragments may be separated by affinity chromatography on protein A bead columns.

25 Monoclonal antibodies of the present invention may be coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include ^{90}Y , ^{123}I , ^{125}I , ^{131}I , ^{186}Re , ^{188}Re , ^{211}At , and ^{212}Bi . Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers
30 include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria

toxin, cholera toxin, gelonin, *Pseudomonas* exotoxin, *Shigella* toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (*e.g.*, covalently bonded) to a suitable monoclonal antibody either directly or indirectly (*e.g.*, via a linker group). A
5 direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulfhydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (*e.g.*, a halide) on the other.

10 Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in
15 chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker
20 group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U.S. Patent No. 4,671,958, to Rodwell *et al.*

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a
25 linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (*e.g.*, U.S. Patent No. 4,489,710, to Spitler), by irradiation of a photolabile bond (*e.g.*, U.S. Patent No. 4,625,014, to Senter *et al.*), by hydrolysis of
30 derivatized amino acid side chains (*e.g.*, U.S. Patent No. 4,638,045, to Kohn *et al.*), by

serum complement-mediated hydrolysis (*e.g.*, U.S. Patent No. 4,671,958, to Rodwell *et al.*), and acid-catalyzed hydrolysis (*e.g.*, U.S. Patent No. 4,569,789, to Blattler *et al.*).

It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In
5 another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers that provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

10 A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (*e.g.*, U.S. Patent No. 4,507,234, to Kato *et al.*), peptides and polysaccharides such as aminodextran (*e.g.*, U.S. Patent No. 4,699,784, to Shih *et al.*). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a
15 liposome vesicle (*e.g.*, U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing nitrogen and sulfur
20 atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison *et al.* discloses representative chelating compounds and their synthesis.

A variety of routes of administration for the antibodies and immunoconjugates may be used. Typically, administration will be intravenous,
25 intramuscular, subcutaneous or in the bed of a resected tumor. It will be evident that the precise dose of the antibody/immunoconjugate will vary depending upon the antibody used, the antigen density on the tumor, and the rate of clearance of the antibody.

T CELLS

Immunotherapeutic compositions may also, or alternatively, comprise T cells specific for a lung tumor protein. Such cells may generally be prepared *in vitro* or *ex vivo*, using standard procedures. For example, T cells may be isolated from bone marrow, peripheral blood, or a fraction of bone marrow or peripheral blood of a patient, using a commercially available cell separation system, such as the Isolex™ System, available from Nexell Therapeutics, Inc. (Irvine, CA; see also U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). Alternatively, T cells may be derived from related or unrelated humans, non-human mammals, cell lines or cultures.

T cells may be stimulated with a lung tumor polypeptide, polynucleotide encoding a lung tumor polypeptide and/or an antigen presenting cell (APC) that expresses such a polypeptide. Such stimulation is performed under conditions and for a time sufficient to permit the generation of T cells that are specific for the polypeptide. Preferably, a lung tumor polypeptide or polynucleotide is present within a delivery vehicle, such as a microsphere, to facilitate the generation of specific T cells.

T cells are considered to be specific for a lung tumor polypeptide if the T cells specifically proliferate, secrete cytokines or kill target cells coated with the polypeptide or expressing a gene encoding the polypeptide. T cell specificity may be evaluated using any of a variety of standard techniques. For example, within a chromium release assay or proliferation assay, a stimulation index of more than two fold increase in lysis and/or proliferation, compared to negative controls, indicates T cell specificity. Such assays may be performed, for example, as described in Chen *et al.*, *Cancer Res.* 54:1065-1070, 1994. Alternatively, detection of the proliferation of T cells may be accomplished by a variety of known techniques. For example, T cell proliferation can be detected by measuring an increased rate of DNA synthesis (*e.g.*, by pulse-labeling cultures of T cells with tritiated thymidine and measuring the amount of tritiated thymidine incorporated into DNA). Contact with a lung tumor polypeptide (100 ng/ml - 100 µg/ml, preferably 200 ng/ml - 25 µg/ml) for 3 - 7 days should result in at least a two fold increase in proliferation of the T cells. Contact as described above for 2-3 hours should result in activation of the T cells, as measured using standard

cytokine assays in which a two fold increase in the level of cytokine release (*e.g.*, TNF or IFN- γ) is indicative of T cell activation (*see* Coligan *et al.*, Current Protocols in Immunology, vol. 1, Wiley Interscience (Greene 1998)). T cells that have been activated in response to a lung tumor polypeptide, polynucleotide or polypeptide-expressing APC may be CD4⁺ and/or CD8⁺. Lung tumor protein-specific T cells may be expanded using standard techniques. Within preferred embodiments, the T cells are derived from a patient, a related donor or an unrelated donor, and are administered to the patient following stimulation and expansion.

For therapeutic purposes, CD4⁺ or CD8⁺ T cells that proliferate in response to a lung tumor polypeptide, polynucleotide or APC can be expanded in number either *in vitro* or *in vivo*. Proliferation of such T cells *in vitro* may be accomplished in a variety of ways. For example, the T cells can be re-exposed to a lung tumor polypeptide, or a short peptide corresponding to an immunogenic portion of such a polypeptide, with or without the addition of T cell growth factors, such as interleukin-2, and/or stimulator cells that synthesize a lung tumor polypeptide. Alternatively, one or more T cells that proliferate in the presence of a lung tumor protein can be expanded in number by cloning. Methods for cloning cells are well known in the art, and include limiting dilution.

PHARMACEUTICAL COMPOSITIONS

In additional embodiments, the present invention concerns formulation of one or more of the polynucleotide, polypeptide, T-cell and/or antibody compositions disclosed herein in pharmaceutically-acceptable solutions for administration to a cell or an animal, either alone, or in combination with one or more other modalities of therapy.

It will also be understood that, if desired, the nucleic acid segment, RNA, DNA or PNA compositions that express a polypeptide as disclosed herein may be administered in combination with other agents as well, such as, *e.g.*, other proteins or polypeptides or various pharmaceutically-active agents. In fact, there is virtually no limit to other components that may also be included, given that the additional agents do not cause a significant adverse effect upon contact with the target cells or host tissues. The compositions may thus be delivered along with various other agents as required in

the particular instance. Such compositions may be purified from host cells or other biological sources, or alternatively may be chemically synthesized as described herein. Likewise, such compositions may further comprise substituted or derivatized RNA or DNA compositions.

5 Formulation of pharmaceutically-acceptable excipients and carrier solutions is well-known to those of skill in the art, as is the development of suitable dosing and treatment regimens for using the particular compositions described herein in a variety of treatment regimens, including *e.g.*, oral, parenteral, intravenous, intranasal, and intramuscular administration and formulation.

10 1. ORAL DELIVERY

 In certain applications, the pharmaceutical compositions disclosed herein may be delivered *via* oral administration to an animal. As such, these compositions may be formulated with an inert diluent or with an assimilable edible carrier, or they may be enclosed in hard- or soft-shell gelatin capsule, or they may be compressed into
15 tablets, or they may be incorporated directly with the food of the diet.

 The active compounds may even be incorporated with excipients and used in the form of ingestible tablets, buccal tables, troches, capsules, elixirs, suspensions, syrups, wafers, and the like (Mathiowitz *et al.*, 1997; Hwang *et al.*, 1998; U. S. Patent 5,641,515; U. S. Patent 5,580,579 and U. S. Patent 5,792,451, each
20 specifically incorporated herein by reference in its entirety). The tablets, troches, pills, capsules and the like may also contain the following: a binder, as gum tragacanth, acacia, cornstarch, or gelatin; excipients, such as dicalcium phosphate; a disintegrating agent, such as corn starch, potato starch, alginic acid and the like; a lubricant, such as magnesium stearate; and a sweetening agent, such as sucrose, lactose or saccharin may
25 be added or a flavoring agent, such as peppermint, oil of wintergreen, or cherry flavoring. When the dosage unit form is a capsule, it may contain, in addition to materials of the above type, a liquid carrier. Various other materials may be present as coatings or to otherwise modify the physical form of the dosage unit. For instance, tablets, pills, or capsules may be coated with shellac, sugar, or both. A syrup or elixir
30 may contain the active compound sucrose as a sweetening agent methyl and

propylparabens as preservatives, a dye and flavoring, such as cherry or orange flavor. Of course, any material used in preparing any dosage unit form should be pharmaceutically pure and substantially non-toxic in the amounts employed. In addition, the active compounds may be incorporated into sustained-release preparation
5 and formulations.

Typically, these formulations may contain at least about 0.1% of the active compound or more, although the percentage of the active ingredient(s) may, of course, be varied and may conveniently be between about 1 or 2% and about 60% or 70% or more of the weight or volume of the total formulation. Naturally, the amount of
10 active compound(s) in each therapeutically useful composition may be prepared in such a way that a suitable dosage will be obtained in any given unit dose of the compound. Factors such as solubility, bioavailability, biological half-life, route of administration, product shelf life, as well as other pharmacological considerations will be contemplated by one skilled in the art of preparing such pharmaceutical formulations, and as such, a
15 variety of dosages and treatment regimens may be desirable.

For oral administration the compositions of the present invention may alternatively be incorporated with one or more excipients in the form of a mouthwash, dentifrice, buccal tablet, oral spray, or sublingual orally-administered formulation. For example, a mouthwash may be prepared incorporating the active ingredient in the
20 required amount in an appropriate solvent, such as a sodium borate solution (Dobell's Solution). Alternatively, the active ingredient may be incorporated into an oral solution such as one containing sodium borate, glycerin and potassium bicarbonate, or dispersed in a dentifrice, or added in a therapeutically-effective amount to a composition that may include water, binders, abrasives, flavoring agents, foaming agents, and humectants.
25 Alternatively the compositions may be fashioned into a tablet or solution form that may be placed under the tongue or otherwise dissolved in the mouth.

2. INJECTABLE DELIVERY

In certain circumstances it will be desirable to deliver the pharmaceutical compositions disclosed herein parenterally, intravenously, intramuscularly, or even
30 intraperitoneally as described in U. S. Patent 5,543,158; U. S. Patent 5,641,515 and U.

S. Patent 5,399,363 (each specifically incorporated herein by reference in its entirety). Solutions of the active compounds as free base or pharmacologically acceptable salts may be prepared in water suitably mixed with a surfactant, such as hydroxypropylcellulose. Dispersions may also be prepared in glycerol, liquid
5 polyethylene glycols, and mixtures thereof and in oils. Under ordinary conditions of storage and use, these preparations contain a preservative to prevent the growth of microorganisms.

The pharmaceutical forms suitable for injectable use include sterile aqueous solutions or dispersions and sterile powders for the extemporaneous
10 preparation of sterile injectable solutions or dispersions (U. S. Patent 5,466,468, specifically incorporated herein by reference in its entirety). In all cases the form must be sterile and must be fluid to the extent that easy syringability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms, such as bacteria and fungi. The carrier can be
15 a solvent or dispersion medium containing, for example, water, ethanol, polyol (e.g., glycerol, propylene glycol, and liquid polyethylene glycol, and the like), suitable mixtures thereof, and/or vegetable oils. Proper fluidity may be maintained, for example, by the use of a coating, such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. The prevention of
20 the action of microorganisms can be facilitated by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, sorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars or sodium chloride. Prolonged absorption of the injectable compositions can be brought about by the use in the compositions of agents delaying absorption, for
25 example, aluminum monostearate and gelatin.

For parenteral administration in an aqueous solution, for example, the solution should be suitably buffered if necessary and the liquid diluent first rendered isotonic with sufficient saline or glucose. These particular aqueous solutions are especially suitable for intravenous, intramuscular, subcutaneous and intraperitoneal
30 administration. In this connection, a sterile aqueous medium that can be employed will be known to those of skill in the art in light of the present disclosure. For example, one

dosage may be dissolved in 1 ml of isotonic NaCl solution and either added to 1000 ml of hypodermoclysis fluid or injected at the proposed site of infusion, (see for example, "Remington's Pharmaceutical Sciences" 15th Edition, pages 1035-1038 and 1570-1580). Some variation in dosage will necessarily occur depending on the condition of
5 the subject being treated. The person responsible for administration will, in any event, determine the appropriate dose for the individual subject. Moreover, for human administration, preparations should meet sterility, pyrogenicity, and the general safety and purity standards as required by FDA Office of Biologics standards.

Sterile injectable solutions are prepared by incorporating the active
10 compounds in the required amount in the appropriate solvent with various of the other ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the various sterilized active ingredients into a sterile vehicle which contains the basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the
15 preparation of sterile injectable solutions, the preferred methods of preparation are vacuum-drying and freeze-drying techniques which yield a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

The compositions disclosed herein may be formulated in a neutral or salt
20 form. Pharmaceutically-acceptable salts, include the acid addition salts (formed with the free amino groups of the protein) and which are formed with inorganic acids such as, for example, hydrochloric or phosphoric acids, or such organic acids as acetic, oxalic, tartaric, mandelic, and the like. Salts formed with the free carboxyl groups can also be derived from inorganic bases such as, for example, sodium, potassium,
25 ammonium, calcium, or ferric hydroxides, and such organic bases as isopropylamine, trimethylamine, histidine, procaine and the like. Upon formulation, solutions will be administered in a manner compatible with the dosage formulation and in such amount as is therapeutically effective. The formulations are easily administered in a variety of dosage forms such as injectable solutions, drug-release capsules, and the like.

30 As used herein, "carrier" includes any and all solvents, dispersion media, vehicles, coatings, diluents, antibacterial and antifungal agents, isotonic and absorption

delaying agents, buffers, carrier solutions, suspensions, colloids, and the like. The use of such media and agents for pharmaceutical active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active ingredient, its use in the therapeutic compositions is contemplated. Supplementary
5 active ingredients can also be incorporated into the compositions.

The phrase "pharmaceutically-acceptable" refers to molecular entities and compositions that do not produce an allergic or similar untoward reaction when administered to a human. The preparation of an aqueous composition that contains a protein as an active ingredient is well understood in the art. Typically, such
10 compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid prior to injection can also be prepared. The preparation can also be emulsified.

3. NASAL DELIVERY

In certain embodiments, the pharmaceutical compositions may be
15 delivered by intranasal sprays, inhalation, and/or other aerosol delivery vehicles. Methods for delivering genes, nucleic acids, and peptide compositions directly to the lungs *via* nasal aerosol sprays has been described *e.g.*, in U. S. Patent 5,756,353 and U. S. Patent 5,804,212 (each specifically incorporated herein by reference in its entirety). Likewise, the delivery of drugs using intranasal microparticle resins (Takenaga *et al.*,
20 1998) and lysophosphatidyl-glycerol compounds (U. S. Patent 5,725,871, specifically incorporated herein by reference in its entirety) are also well-known in the pharmaceutical arts. Likewise, transmucosal drug delivery in the form of a polytetrafluoroethylene support matrix is described in U. S. Patent 5,780,045 (specifically incorporated herein by reference in its entirety).

25 4. LIPOSOME-, NANOCAPSULE-, AND MICROPARTICLE-MEDIATED DELIVERY

In certain embodiments, the inventors contemplate the use of liposomes, nanocapsules, microparticles, microspheres, lipid particles, vesicles, and the like, for the introduction of the compositions of the present invention into suitable host cells. In particular, the compositions of the present invention may be formulated for delivery

either encapsulated in a lipid particle, a liposome, a vesicle, a nanosphere, or a nanoparticle or the like.

Such formulations may be preferred for the introduction of pharmaceutically-acceptable formulations of the nucleic acids or constructs disclosed
5 herein. The formation and use of liposomes is generally known to those of skill in the art (see for example, Couvreur *et al.*, 1977; Couvreur, 1988; Lasic, 1998; which describes the use of liposomes and nanocapsules in the targeted antibiotic therapy for intracellular bacterial infections and diseases). Recently, liposomes were developed with improved serum stability and circulation half-times (Gabizon and
10 Papahadjopoulos, 1988; Allen and Choun, 1987; U. S. Patent 5,741,516, specifically incorporated herein by reference in its entirety). Further, various methods of liposome and liposome like preparations as potential drug carriers have been reviewed (Takakura, 1998; Chandran *et al.*, 1997; Margalit, 1995; U. S. Patent 5,567,434; U. S. Patent 5,552,157; U. S. Patent 5,565,213; U. S. Patent 5,738,868 and U. S. Patent 5,795,587,
15 each specifically incorporated herein by reference in its entirety).

Liposomes have been used successfully with a number of cell types that are normally resistant to transfection by other procedures including T cell suspensions, primary hepatocyte cultures and PC 12 cells (Renneisen *et al.*, 1990; Muller *et al.*, 1990). In addition, liposomes are free of the DNA length constraints that are typical of
20 viral-based delivery systems. Liposomes have been used effectively to introduce genes, drugs (Heath and Martin, 1986; Heath *et al.*, 1986; Balazsovits *et al.*, 1989; Fresta and Puglisi, 1996), radiotherapeutic agents (Pikul *et al.*, 1987), enzymes (Imaizumi *et al.*, 1990a; Imaizumi *et al.*, 1990b), viruses (Faller and Baltimore, 1984), transcription factors and allosteric effectors (Nicolau and Gersonde, 1979) into a variety of cultured
25 cell lines and animals. In addition, several successful clinical trails examining the effectiveness of liposome-mediated drug delivery have been completed (Lopez-Berestein *et al.*, 1985a; 1985b; Coune, 1988; Sculier *et al.*, 1988). Furthermore, several studies suggest that the use of liposomes is not associated with autoimmune responses, toxicity or gonadal localization after systemic delivery (Mori and Fukatsu, 1992).

30 Liposomes are formed from phospholipids that are dispersed in an aqueous medium and spontaneously form multilamellar concentric bilayer vesicles

(also termed multilamellar vesicles (MLVs). MLVs generally have diameters of from 25 nm to 4 μ m. Sonication of MLVs results in the formation of small unilamellar vesicles (SUVs) with diameters in the range of 200 to 500 Å, containing an aqueous solution in the core.

5 Liposomes bear resemblance to cellular membranes and are contemplated for use in connection with the present invention as carriers for the peptide compositions. They are widely suitable as both water- and lipid-soluble substances can be entrapped, *i.e.* in the aqueous spaces and within the bilayer itself, respectively. It is possible that the drug-bearing liposomes may even be employed for site-specific
10 delivery of active agents by selectively modifying the liposomal formulation.

 In addition to the teachings of Couvreur *et al.* (1977; 1988), the following information may be utilized in generating liposomal formulations. Phospholipids can form a variety of structures other than liposomes when dispersed in water, depending on the molar ratio of lipid to water. At low ratios the liposome is the
15 preferred structure. The physical characteristics of liposomes depend on pH, ionic strength and the presence of divalent cations. Liposomes can show low permeability to ionic and polar substances, but at elevated temperatures undergo a phase transition which markedly alters their permeability. The phase transition involves a change from a closely packed, ordered structure, known as the gel state, to a loosely packed, less-
20 ordered structure, known as the fluid state. This occurs at a characteristic phase-transition temperature and results in an increase in permeability to ions, sugars and drugs.

 In addition to temperature, exposure to proteins can alter the permeability of liposomes. Certain soluble proteins, such as cytochrome c, bind,
25 deform and penetrate the bilayer, thereby causing changes in permeability. Cholesterol inhibits this penetration of proteins, apparently by packing the phospholipids more tightly. It is contemplated that the most useful liposome formations for antibiotic and inhibitor delivery will contain cholesterol.

 The ability to trap solutes varies between different types of liposomes.
30 For example, MLVs are moderately efficient at trapping solutes, but SUVs are extremely inefficient. SUVs offer the advantage of homogeneity and reproducibility in

size distribution, however, and a compromise between size and trapping efficiency is offered by large unilamellar vesicles (LUVs). These are prepared by ether evaporation and are three to four times more efficient at solute entrapment than MLVs.

In addition to liposome characteristics, an important determinant in entrapping compounds is the physicochemical properties of the compound itself. Polar compounds are trapped in the aqueous spaces and nonpolar compounds bind to the lipid bilayer of the vesicle. Polar compounds are released through permeation or when the bilayer is broken, but nonpolar compounds remain affiliated with the bilayer unless it is disrupted by temperature or exposure to lipoproteins. Both types show maximum efflux rates at the phase transition temperature.

Liposomes interact with cells via four different mechanisms: endocytosis by phagocytic cells of the reticuloendothelial system such as macrophages and neutrophils; adsorption to the cell surface, either by nonspecific weak hydrophobic or electrostatic forces, or by specific interactions with cell-surface components; fusion with the plasma cell membrane by insertion of the lipid bilayer of the liposome into the plasma membrane, with simultaneous release of liposomal contents into the cytoplasm; and by transfer of liposomal lipids to cellular or subcellular membranes, or vice versa, without any association of the liposome contents. It often is difficult to determine which mechanism is operative and more than one may operate at the same time.

The fate and disposition of intravenously injected liposomes depend on their physical properties, such as size, fluidity, and surface charge. They may persist in tissues for h or days, depending on their composition, and half lives in the blood range from min to several h. Larger liposomes, such as MLVs and LUVs, are taken up rapidly by phagocytic cells of the reticuloendothelial system, but physiology of the circulatory system restrains the exit of such large species at most sites. They can exit only in places where large openings or pores exist in the capillary endothelium, such as the sinusoids of the liver or spleen. Thus, these organs are the predominate site of uptake. On the other hand, SUVs show a broader tissue distribution but still are sequestered highly in the liver and spleen. In general, this *in vivo* behavior limits the potential targeting of liposomes to only those organs and tissues accessible to their large size. These include the blood, liver, spleen, bone marrow, and lymphoid organs.

Targeting is generally not a limitation in terms of the present invention. However, should specific targeting be desired, methods are available for this to be accomplished. Antibodies may be used to bind to the liposome surface and to direct the antibody and its drug contents to specific antigenic receptors located on a particular cell-type surface. Carbohydrate determinants (glycoprotein or glycolipid cell-surface components that play a role in cell-cell recognition, interaction and adhesion) may also be used as recognition sites as they have potential in directing liposomes to particular cell types. Mostly, it is contemplated that intravenous injection of liposomal preparations would be used, but other routes of administration are also conceivable.

Alternatively, the invention provides for pharmaceutically-acceptable nanocapsule formulations of the compositions of the present invention. Nanocapsules can generally entrap compounds in a stable and reproducible way (Henry-Michelland *et al.*, 1987; Quintanar-Guerrero *et al.*, 1998; Douglas *et al.*, 1987). To avoid side effects due to intracellular polymeric overloading, such ultrafine particles (sized around 0.1 μm) should be designed using polymers able to be degraded *in vivo*. Biodegradable polyalkyl-cyanoacrylate nanoparticles that meet these requirements are contemplated for use in the present invention. Such particles may be easily made, as described (Couvreur *et al.*, 1980; 1988; zur Muhlen *et al.*, 1998; Zambaux *et al.* 1998; Pinto-Alphandry *et al.*, 1995 and U. S. Patent 5,145,684, specifically incorporated herein by reference in its entirety).

IMMUNOGENIC COMPOSITIONS

In certain preferred embodiments of the present invention, immunogenic compositions, or vaccines, are provided. The immunogenic compositions will generally comprise one or more pharmaceutical compositions, such as those discussed above, in combination with an immunostimulant. An immunostimulant may be any substance that enhances or potentiates an immune response (antibody and/or cell-mediated) to an exogenous antigen. Examples of immunostimulants include adjuvants, biodegradable microspheres (*e.g.*, polylactic galactide) and liposomes (into which the compound is incorporated; *see e.g.*, Fullerton, U.S. Patent No. 4,235,877). Vaccine preparation is generally described in, for example, M.F. Powell and M.J. Newman, eds., "Vaccine

Design (the subunit and adjuvant approach)," Plenum Press (NY, 1995).
Pharmaceutical compositions and immunogenic compositions, or vaccines, within the
scope of the present invention may also contain other compounds, which may be
biologically active or inactive. For example, one or more immunogenic portions of
5 other tumor antigens may be present, either incorporated into a fusion polypeptide or as
a separate compound, within the composition.

Illustrative immunogenic compositions may contain DNA encoding one
or more of the polypeptides as described above, such that the polypeptide is generated
in situ. As noted above, the DNA may be present within any of a variety of delivery
10 systems known to those of ordinary skill in the art, including nucleic acid expression
systems, bacteria and viral expression systems. Numerous gene delivery techniques are
well known in the art, such as those described by Rolland, *Crit. Rev. Therap. Drug
Carrier Systems* 15:143-198, 1998, and references cited therein. Appropriate nucleic
acid expression systems contain the necessary DNA sequences for expression in the
15 patient (such as a suitable promoter and terminating signal). Bacterial delivery systems
involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that
expresses an immunogenic portion of the polypeptide on its cell surface or secretes such
an epitope. In a preferred embodiment, the DNA may be introduced using a viral
expression system (*e.g.*, vaccinia or other pox virus, retrovirus, or adenovirus), which
20 may involve the use of a non-pathogenic (defective), replication competent virus.
Suitable systems are disclosed, for example, in Fisher-Hoch *et al.*, *Proc. Natl. Acad.
Sci. USA* 86:317-321, 1989; Flexner *et al.*, *Ann. N.Y. Acad. Sci.* 569:86-103, 1989;
Flexner *et al.*, *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and
5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242;
25 WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld *et al.*, *Science*
252:431-434, 1991; Kolls *et al.*, *Proc. Natl. Acad. Sci. USA* 91:215-219, 1994;
Kass-Eisler *et al.*, *Proc. Natl. Acad. Sci. USA* 90:11498-11502, 1993; Guzman *et al.*,
Circulation 88:2838-2848, 1993; and Guzman *et al.*, *Cir. Res.* 73:1202-1207, 1993.
Techniques for incorporating DNA into such expression systems are well known to
30 those of ordinary skill in the art. The DNA may also be "naked," as described, for
example, in Ulmer *et al.*, *Science* 259:1745-1749, 1993 and reviewed by Cohen,

Science 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells. It will be apparent that an immunogenic composition may comprise both a polynucleotide and a polypeptide component. Such immunogenic compositions may provide for an enhanced immune response.

It will be apparent that an immunogenic composition may contain pharmaceutically acceptable salts of the polynucleotides and polypeptides provided herein. Such salts may be prepared from pharmaceutically acceptable non-toxic bases, including organic bases (*e.g.*, salts of primary, secondary and tertiary amines and basic amino acids) and inorganic bases (*e.g.*, sodium, potassium, lithium, ammonium, calcium and magnesium salts).

While any suitable carrier known to those of ordinary skill in the art may be employed in the immunogenic compositions of this invention, the type of carrier will vary depending on the mode of administration. Compositions of the present invention may be formulated for any appropriate manner of administration, including for example, topical, oral, nasal, intravenous, intracranial, intraperitoneal, subcutaneous or intramuscular administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a fat, a wax or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable microspheres (*e.g.*, polylactate polyglycolate) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268; 5,075,109; 5,928,647; 5,811,128; 5,820,883; 5,853,763; 5,814,344 and 5,942,252. One may also employ a carrier comprising the particulate-protein complexes described in U.S. Patent No. 5,928,647, which are capable of inducing a class I-restricted cytotoxic T lymphocyte responses in a host.

Such compositions may also comprise buffers (*e.g.*, neutral buffered saline or phosphate buffered saline), carbohydrates (*e.g.*, glucose, mannose, sucrose or dextrans), mannitol, proteins, polypeptides or amino acids such as glycine, antioxidants,

bacteriostats, chelating agents such as EDTA or glutathione, adjuvants (e.g., aluminum hydroxide), solutes that render the formulation isotonic, hypotonic or weakly hypertonic with the blood of a recipient, suspending agents, thickening agents and/or preservatives. Alternatively, compositions of the present invention may be formulated as a lyophilizate. Compounds may also be encapsulated within liposomes using well known technology.

Any of a variety of immunostimulants may be employed in the immunogenic compositions of this invention. For example, an adjuvant may be included. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins. Suitable adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF or interleukin-2, -7, or -12, may also be used as adjuvants.

Within the immunogenic compositions provided herein, the adjuvant composition is preferably designed to induce an immune response predominantly of the Th1 type. High levels of Th1-type cytokines (e.g., IFN- γ , TNF α , IL-2 and IL-12) tend to favor the induction of cell mediated immune responses to an administered antigen. In contrast, high levels of Th2-type cytokines (e.g., IL-4, IL-5, IL-6 and IL-10) tend to favor the induction of humoral immune responses. Following application of an immunogenic composition as provided herein, a patient will support an immune response that includes Th1- and Th2-type responses. Within a preferred embodiment, in which a response is predominantly Th1-type, the level of Th1-type cytokines will increase to a greater extent than the level of Th2-type cytokines. The levels of these cytokines may be readily assessed using standard assays. For a review of the families of cytokines, see Mosmann and Coffman, *Ann. Rev. Immunol.* 7:145-173, 1989.

Preferred adjuvants for use in eliciting a predominantly Th1-type response include, for example, a combination of monophosphoryl lipid A, preferably 3-de-O-acylated monophosphoryl lipid A (3D-MPL), together with an aluminum salt. MPL adjuvants are available from Corixa Corporation (Seattle, WA; *see* US Patent
5 Nos. 4,436,727; 4,877,611; 4,866,034 and 4,912,094). CpG-containing oligonucleotides (in which the CpG dinucleotide is unmethylated) also induce a predominantly Th1 response. Such oligonucleotides are well known and are described, for example, in WO 96/02555, WO 99/33488 and U.S. Patent Nos. 6,008,200 and 5,856,462. Immunostimulatory DNA sequences are also described, for example, by
10 Sato *et al.*, *Science* 273:352, 1996. Another preferred adjuvant is a saponin, preferably QS21 (Aquila Biopharmaceuticals Inc., Framingham, MA), which may be used alone or in combination with other adjuvants. For example, an enhanced system involves the combination of a monophosphoryl lipid A and saponin derivative, such as the combination of QS21 and 3D-MPL as described in WO 94/00153, or a less reactogenic
15 composition where the QS21 is quenched with cholesterol, as described in WO 96/33739. Other preferred formulations comprise an oil-in-water emulsion and tocopherol. A particularly potent adjuvant formulation involving QS21, 3D-MPL and tocopherol in an oil-in-water emulsion is described in WO 95/17210.

Other preferred adjuvants include Montanide ISA 720 (Seppic, France),
20 SAF (Chiron, California, United States), ISCOMS (CSL), MF-59 (Chiron), the SBAS series of adjuvants (*e.g.*, SBAS-2 or SBAS-4, available from SmithKline Beecham, Rixensart, Belgium), Detox (Corixa, Hamilton, MT), RC-529 (Corixa, Hamilton, MT) and other aminoalkyl glucosaminide 4-phosphates (AGPs), such as those described in pending U.S. Patent Application Serial Nos. 08/853,826 and 09/074,720, the disclosures
25 of which are incorporated herein by reference in their entireties.

Any immunogenic composition provided herein may be prepared using well known methods that result in a combination of antigen, immune response enhancer and a suitable carrier or excipient. The compositions described herein may be administered as part of a sustained release formulation (*i.e.*, a formulation such as a
30 capsule, sponge or gel (composed of polysaccharides, for example) that effects a slow release of compound following administration). Such formulations may generally be

prepared using well known technology (*see, e.g., Coombes et al., Vaccine 14:1429-1438, 1996*) and administered by, for example, oral, rectal or subcutaneous implantation, or by implantation at the desired target site. Sustained-release formulations may contain a polypeptide, polynucleotide or antibody dispersed in a carrier matrix and/or contained within a reservoir surrounded by a rate controlling membrane.

Carriers for use within such formulations are biocompatible, and may also be biodegradable; preferably the formulation provides a relatively constant level of active component release. Such carriers include microparticles of poly(lactide-co-glycolide), polyacrylate, latex, starch, cellulose, dextran and the like. Other delayed-release carriers include supramolecular biovectors, which comprise a non-liquid hydrophilic core (*e.g., a cross-linked polysaccharide or oligosaccharide*) and, optionally, an external layer comprising an amphiphilic compound, such as a phospholipid (*see e.g., U.S. Patent No. 5,151,254 and PCT applications WO 94/20078, WO/94/23701 and WO 96/06638*). The amount of active compound contained within a sustained release formulation depends upon the site of implantation, the rate and expected duration of release and the nature of the condition to be treated or prevented.

Any of a variety of delivery vehicles may be employed within pharmaceutical compositions and immunogenic compositions to facilitate production of an antigen-specific immune response that targets tumor cells. Delivery vehicles include antigen presenting cells (APCs), such as dendritic cells, macrophages, B cells, monocytes and other cells that may be engineered to be efficient APCs. Such cells may, but need not, be genetically modified to increase the capacity for presenting the antigen, to improve activation and/or maintenance of the T cell response, to have anti-tumor effects *per se* and/or to be immunologically compatible with the receiver (*i.e., matched HLA haplotype*). APCs may generally be isolated from any of a variety of biological fluids and organs, including tumor and peritumoral tissues, and may be autologous, allogeneic, syngeneic or xenogeneic cells.

Certain preferred embodiments of the present invention use dendritic cells or progenitors thereof as antigen-presenting cells. Dendritic cells are highly potent APCs (Banchereau and Steinman, *Nature 392:245-251, 1998*) and have been shown to

be effective as a physiological adjuvant for eliciting prophylactic or therapeutic antitumor immunity (*see* Timmerman and Levy, *Ann. Rev. Med.* 50:507-529, 1999). In general, dendritic cells may be identified based on their typical shape (stellate *in situ*, with marked cytoplasmic processes (dendrites) visible *in vitro*), their ability to take up,
5 process and present antigens with high efficiency and their ability to activate naïve T cell responses. Dendritic cells may, of course, be engineered to express specific cell-surface receptors or ligands that are not commonly found on dendritic cells *in vivo* or *ex vivo*, and such modified dendritic cells are contemplated by the present invention. As an alternative to dendritic cells, secreted vesicles antigen-loaded dendritic cells (called
10 exosomes) may be used within a vaccine, or immunogenic composition (*see* Zitvogel *et al.*, *Nature Med.* 4:594-600, 1998).

Dendritic cells and progenitors may be obtained from peripheral blood, bone marrow, tumor-infiltrating cells, peritumoral tissues-infiltrating cells, lymph nodes, spleen, skin, umbilical cord blood or any other suitable tissue or fluid. For
15 example, dendritic cells may be differentiated *ex vivo* by adding a combination of cytokines such as GM-CSF, IL-4, IL-13 and/or TNF α to cultures of monocytes harvested from peripheral blood. Alternatively, CD34 positive cells harvested from peripheral blood, umbilical cord blood or bone marrow may be differentiated into dendritic cells by adding to the culture medium combinations of GM-CSF, IL-3, TNF α ,
20 CD40 ligand, LPS, flt3 ligand and/or other compound(s) that induce differentiation, maturation and proliferation of dendritic cells.

Dendritic cells are conveniently categorized as "immature" and "mature" cells, which allows a simple way to discriminate between two well characterized phenotypes. However, this nomenclature should not be construed to exclude all
25 possible intermediate stages of differentiation. Immature dendritic cells are characterized as APC with a high capacity for antigen uptake and processing, which correlates with the high expression of Fc γ receptor and mannose receptor. The mature phenotype is typically characterized by a lower expression of these markers, but a high expression of cell surface molecules responsible for T cell activation such as class I and
30 class II MHC, adhesion molecules (*e.g.*, CD54 and CD11) and costimulatory molecules (*e.g.*, CD40, CD80, CD86 and 4-1BB).

APCs may generally be transfected with a polynucleotide encoding a lung tumor protein (or portion or other variant thereof) such that the lung tumor polypeptide, or an immunogenic portion thereof, is expressed on the cell surface. Such transfection may take place *ex vivo*, and a composition comprising such transfected
5 cells may then be used for therapeutic purposes, as described herein. Alternatively, a gene delivery vehicle that targets a dendritic or other antigen presenting cell may be administered to a patient, resulting in transfection that occurs *in vivo*. *In vivo* and *ex vivo* transfection of dendritic cells, for example, may generally be performed using any methods known in the art, such as those described in WO 97/24447, or the gene gun
10 approach described by Mahvi *et al.*, *Immunology and cell Biology* 75:456-460, 1997. Antigen loading of dendritic cells may be achieved by incubating dendritic cells or progenitor cells with the lung tumor polypeptide, DNA (naked or within a plasmid vector) or RNA; or with antigen-expressing recombinant bacterium or viruses (*e.g.*, vaccinia, fowlpox, adenovirus or lentivirus vectors). Prior to loading, the polypeptide
15 may be covalently conjugated to an immunological partner that provides T cell help (*e.g.*, a carrier molecule). Alternatively, a dendritic cell may be pulsed with a non-conjugated immunological partner, separately or in the presence of the polypeptide.

Immunogenic compositions and pharmaceutical compositions may be presented in unit-dose or multi-dose containers, such as sealed ampoules or vials. Such
20 containers are preferably hermetically sealed to preserve sterility of the formulation until use. In general, formulations may be stored as suspensions, solutions or emulsions in oily or aqueous vehicles. Alternatively, an immunogenic or pharmaceutical composition may be stored in a freeze-dried condition requiring only the addition of a sterile liquid carrier immediately prior to use.

25 **CANCER THERAPY**

In further aspects of the present invention, the compositions described herein may be used for immunotherapy of cancer, such as lung cancer. Within such methods, compositions are typically administered to a patient. As used herein, a
“patient” refers to any warm-blooded animal, preferably a human. A patient may or
30 may not be afflicted with cancer. Accordingly, the above pharmaceutical compositions

and immunogenic compositions may be used to prevent the development of a cancer or to treat a patient afflicted with a cancer. A cancer may be diagnosed using criteria generally accepted in the art, including the presence of a malignant tumor. Pharmaceutical compositions and immunogenic compositions may be administered
5 either prior to or following surgical removal of primary tumors and/or treatment such as administration of radiotherapy or conventional chemotherapeutic drugs. Administration may be by any suitable method, including administration by intravenous, intraperitoneal, intramuscular, subcutaneous, intranasal, intradermal, anal, vaginal, topical and oral routes.

10 Within certain embodiments, immunotherapy may be active immunotherapy, in which treatment relies on the *in vivo* stimulation of the endogenous host immune system to react against tumors with the administration of immune response-modifying agents (such as polypeptides and polynucleotides as provided herein).

15 Within other embodiments, immunotherapy may be passive immunotherapy, in which treatment involves the delivery of agents with established tumor-immune reactivity (such as effector cells or antibodies) that can directly or indirectly mediate antitumor effects and does not necessarily depend on an intact host immune system. Examples of effector cells include T cells as discussed above, T
20 lymphocytes (such as CD8⁺ cytotoxic T lymphocytes and CD4⁺ T-helper tumor-infiltrating lymphocytes), killer cells (such as Natural Killer cells and lymphokine-activated killer cells), B cells and antigen-presenting cells (such as dendritic cells and macrophages) expressing a polypeptide provided herein. T cell receptors and antibody
25 receptors specific for the polypeptides recited herein may be cloned, expressed and transferred into other vectors or effector cells for adoptive immunotherapy. The polypeptides provided herein may also be used to generate antibodies or anti-idiotypic antibodies (as described above and in U.S. Patent No. 4,918,164) for passive immunotherapy.

Effector cells may generally be obtained in sufficient quantities for
30 adoptive immunotherapy by growth *in vitro*, as described herein. Culture conditions for expanding single antigen-specific effector cells to several billion in number with

retention of antigen recognition *in vivo* are well known in the art. Such *in vitro* culture conditions typically use intermittent stimulation with antigen, often in the presence of cytokines (such as IL-2) and non-dividing feeder cells. As noted above, immunoreactive polypeptides as provided herein may be used to rapidly expand
5 antigen-specific T cell cultures in order to generate a sufficient number of cells for immunotherapy. In particular, antigen-presenting cells, such as dendritic, macrophage, monocyte, fibroblast and/or B cells, may be pulsed with immunoreactive polypeptides or transfected with one or more polynucleotides using standard techniques well known in the art. For example, antigen-presenting cells can be transfected with a
10 polynucleotide having a promoter appropriate for increasing expression in a recombinant virus or other expression system. Cultured effector cells for use in therapy must be able to grow and distribute widely, and to survive long term *in vivo*. Studies have shown that cultured effector cells can be induced to grow *in vivo* and to survive long term in substantial numbers by repeated stimulation with antigen supplemented
15 with IL-2 (*see, for example, Cheever et al., Immunological Reviews 157:177, 1997*).

Alternatively, a vector expressing a polypeptide recited herein may be introduced into antigen presenting cells taken from a patient and clonally propagated *ex vivo* for transplant back into the same patient. Transfected cells may be reintroduced into the patient using any means known in the art, preferably in sterile form by
20 intravenous, intracavitary, intraperitoneal or intratumor administration.

Routes and frequency of administration of the therapeutic compositions described herein, as well as dosage, will vary from individual to individual, and may be readily established using standard techniques. In general, the pharmaceutical compositions and immunogenic compositions may be administered by injection (*e.g.*,
25 intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (*e.g.*, by aspiration) or orally. Preferably, between 1 and 10 doses may be administered over a 52 week period. Preferably, 6 doses are administered, at intervals of 1 month, and booster vaccinations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of a compound that,
30 when administered as described above, is capable of promoting an anti-tumor immune response, and is at least 10-50% above the basal (*i.e.*, untreated) level. Such response

can be monitored by measuring the anti-tumor antibodies in a patient or by vaccine-dependent generation of cytolytic effector cells capable of killing the patient's tumor cells *in vitro*. Such vaccines, or immunogenic compositions, should also be capable of causing an immune response that leads to an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial or longer disease-free survival) in vaccinated patients as compared to non-vaccinated patients. In general, for compositions comprising one or more polypeptides, the amount of each polypeptide present in a dose ranges from about 25 µg to 5 mg per kg of host. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.1 mL to about 5 mL.

10 In general, an appropriate dosage and treatment regimen provides the active compound(s) in an amount sufficient to provide therapeutic and/or prophylactic benefit. Such a response can be monitored by establishing an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial, or longer disease-free survival) in treated patients as compared to non-treated patients. Increases in preexisting immune responses to a lung tumor protein generally correlate with an improved clinical outcome. Such immune responses may generally be evaluated using standard proliferation, cytotoxicity or cytokine assays, which may be performed using samples obtained from a patient before and after treatment.

CANCER DETECTION AND DIAGNOSIS

20 In general, a cancer may be detected in a patient based on the presence of one or more lung tumor proteins and/or polynucleotides encoding such proteins in a biological sample (for example, blood, sera, sputum urine and/or tumor biopsies) obtained from the patient. In other words, such proteins may be used as markers to indicate the presence or absence of a cancer such as lung cancer. In addition, such proteins may be useful for the detection of other cancers. The binding agents provided herein generally permit detection of the level of antigen that binds to the agent in the biological sample. Polynucleotide primers and probes may be used to detect the level of mRNA encoding a tumor protein, which is also indicative of the presence or absence of a cancer. In general, a lung tumor sequence should be present at a level that is at least three fold higher in tumor tissue than in normal tissue

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There are a variety of assay formats known to those of ordinary skill in the art for using a binding agent to detect polypeptide markers in a sample. *See, e.g.,* Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, the presence or absence of a cancer in a patient may be determined by

5 (a) contacting a biological sample obtained from a patient with a binding agent; (b) detecting in the sample a level of polypeptide that binds to the binding agent; and (c) comparing the level of polypeptide with a predetermined cut-off value.

In a preferred embodiment, the assay involves the use of binding agent immobilized on a solid support to bind to and remove the polypeptide from the

10 remainder of the sample. The bound polypeptide may then be detected using a detection reagent that contains a reporter group and specifically binds to the binding agent/polypeptide complex. Such detection reagents may comprise, for example, a binding agent that specifically binds to the polypeptide or an antibody or other agent that specifically binds to the binding agent, such as an anti-immunoglobulin, protein G,

15 protein A or a lectin. Alternatively, a competitive assay may be utilized, in which a polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding agent after incubation of the binding agent with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding agent is indicative of the reactivity of the sample with the immobilized binding

20 agent. Suitable polypeptides for use within such assays include full length lung tumor proteins and portions thereof to which the binding agent binds, as described above.

The solid support may be any material known to those of ordinary skill in the art to which the tumor protein may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane.

25 Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply

30 described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption,

and covalent attachment (which may be a direct linkage between the agent and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, 5 in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10 µg, and preferably about 100 ng to about 1 µg, is sufficient to immobilize an 10 adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports 15 having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (*see, e.g.,* Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay. 20 This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a detection reagent (preferably a second antibody capable of binding to 25 a different site on the polypeptide) containing a reporter group is added. The amount of detection reagent that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically 30 blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20™ (Sigma Chemical Co., St. Louis, MO). The

immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation time) is a period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with lung cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20™. The second antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include those groups recited above.

The detection reagent is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound detection reagent is then removed and bound detection reagent is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of a cancer, such as lung cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In

one preferred embodiment, the cut-off value for the detection of a cancer is the average mean signal obtained when the immobilized antibody is incubated with samples from patients without the cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for the cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett *et al.*, *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for a cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the binding agent is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized binding agent as the sample passes through the membrane. A second, labeled binding agent then binds to the binding agent-polypeptide complex as a solution containing the second binding agent flows through the membrane. The detection of bound second binding agent may then be performed as described above. In the strip test format, one end of the membrane to which binding agent is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second binding agent and to the area of immobilized binding agent. Concentration of second binding agent at the area of immobilized antibody indicates the presence of a cancer. Typically, the concentration of second binding agent at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of binding agent immobilized

on the membrane is selected to generate 'a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferred binding agents for use in such assays are antibodies and antigen-binding
5 fragments thereof. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1 µg, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use
10 with the tumor proteins or binding agents of the present invention. The above descriptions are intended to be exemplary only. For example, it will be apparent to those of ordinary skill in the art that the above protocols may be readily modified to use lung tumor polypeptides to detect antibodies that bind to such polypeptides in a biological sample. The detection of such lung tumor protein specific antibodies may
15 correlate with the presence of a cancer.

A cancer may also, or alternatively, be detected based on the presence of T cells that specifically react with a lung tumor protein in a biological sample. Within certain methods, a biological sample comprising CD4⁺ and/or CD8⁺ T cells isolated from a patient is incubated with a lung tumor polypeptide, a polynucleotide encoding
20 such a polypeptide and/or an APC that expresses at least an immunogenic portion of such a polypeptide, and the presence or absence of specific activation of the T cells is detected. Suitable biological samples include, but are not limited to, isolated T cells. For example, T cells may be isolated from a patient by routine techniques (such as by Ficoll/Hypaque density gradient centrifugation of peripheral blood lymphocytes). T
25 cells may be incubated *in vitro* for 2-9 days (typically 4 days) at 37°C with polypeptide (e.g., 5 - 25 µg/ml). It may be desirable to incubate another aliquot of a T cell sample in the absence of lung tumor polypeptide to serve as a control. For CD4⁺ T cells, activation is preferably detected by evaluating proliferation of the T cells. For CD8⁺ T cells, activation is preferably detected by evaluating cytolytic activity. A level of
30 proliferation that is at least two fold greater and/or a level of cytolytic activity that is at

least 20% greater than in disease-free patients indicates the presence of a cancer in the patient.

As noted above, a cancer may also, or alternatively, be detected based on the level of mRNA encoding a lung tumor protein in a biological sample. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify a portion of a lung tumor cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for (*i.e.*, hybridizes to) a polynucleotide encoding the lung tumor protein. The amplified cDNA is then separated and detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes that specifically hybridize to a polynucleotide encoding a lung tumor protein may be used in a hybridization assay to detect the presence of polynucleotide encoding the tumor protein in a biological sample.

To permit hybridization under assay conditions, oligonucleotide primers and probes should comprise an oligonucleotide sequence that has at least about 60%, preferably at least about 75% and more preferably at least about 90%, identity to a portion of a polynucleotide encoding a lung tumor protein that is at least 10 nucleotides, and preferably at least 20 nucleotides, in length. Preferably, oligonucleotide primers and/or probes hybridize to a polynucleotide encoding a polypeptide described herein under moderately stringent conditions, as defined above. Oligonucleotide primers and/or probes which may be usefully employed in the diagnostic methods described herein preferably are at least 10-40 nucleotides in length. In a preferred embodiment, the oligonucleotide primers comprise at least 10 contiguous nucleotides, more preferably at least 15 contiguous nucleotides, of a DNA molecule having a sequence recited in SEQ ID NO: 1, 11-13, 15, 20, 23-27, 29, 30, 33, 34, 39, 41, 43-46, 51, 52, 57, 58, 60, 62, 65-67, 69-71, 74, 76, 79, 80, 84, 86, 89-92, 95, 97, 98, 101, 110, 111, 113-119, 121-128, 130-134, 136, 138, 139, 141, 143, 146-151, 153, 154, 157-160, 162-164, 167-178, 180, 181, 183, 186-190, 192, 193, 195-220, 224, 226-231, 234, 236, 237, 240, 241, 244-246, 248, 254, 255, 261, 262, 266, 270, 275, 280, 282, 283, 288, 289, 290, 292, 295, 301, 303, 304, 309, 311, 341-782, 784, 785, 790, 792, 794, 796, 800-804, 807, 808 or 810-826. Techniques for both PCR based assays and hybridization assays

are well known in the art (*see*, for example, Mullis *et al.*, *Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989).

One preferred assay employs RT-PCR, in which PCR is applied in conjunction with reverse transcription. Typically, RNA is extracted from a biological sample, such as biopsy tissue, and is reverse transcribed to produce cDNA molecules. PCR amplification using at least one specific primer generates a cDNA molecule, which may be separated and visualized using, for example, gel electrophoresis. Amplification may be performed on biological samples taken from a test patient and from an individual who is not afflicted with a cancer. The amplification reaction may be performed on several dilutions of cDNA spanning two orders of magnitude. A two-fold or greater increase in expression in several dilutions of the test patient sample as compared to the same dilutions of the non-cancerous sample is typically considered positive.

In another embodiment, the compositions described herein may be used as markers for the progression of cancer. In this embodiment, assays as described above for the diagnosis of a cancer may be performed over time, and the change in the level of reactive polypeptide(s) or polynucleotide(s) evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, a cancer is progressing in those patients in whom the level of polypeptide or polynucleotide detected increases over time. In contrast, the cancer is not progressing when the level of reactive polypeptide or polynucleotide either remains constant or decreases with time.

Certain *in vivo* diagnostic assays may be performed directly on a tumor. One such assay involves contacting tumor cells with a binding agent. The bound binding agent may then be detected directly or indirectly via a reporter group. Such binding agents may also be used in histological applications. Alternatively, polynucleotide probes may be used within such applications.

As noted above, to improve sensitivity, multiple lung tumor protein markers may be assayed within a given sample. It will be apparent that binding agents specific for different proteins provided herein may be combined within a single assay. Further, multiple primers or probes may be used concurrently. The selection of tumor

protein markers may be based on routine experiments to determine combinations that results in optimal sensitivity. In addition, or alternatively, assays for tumor proteins provided herein may be combined with assays for other known tumor antigens.

DIAGNOSTIC KITS

5 The present invention further provides kits for use within any of the above diagnostic methods. Such kits typically comprise two or more components necessary for performing a diagnostic assay. Components may be compounds, reagents, containers and/or equipment. For example, one container within a kit may contain a monoclonal antibody or fragment thereof that specifically binds to a lung
10 tumor protein. Such antibodies or fragments may be provided attached to a support material, as described above. One or more additional containers may enclose elements, such as reagents or buffers, to be used in the assay. Such kits may also, or alternatively, contain a detection reagent as described above that contains a reporter group suitable for direct or indirect detection of antibody binding.

15 Alternatively, a kit may be designed to detect the level of mRNA encoding a lung tumor protein in a biological sample. Such kits generally comprise at least one oligonucleotide probe or primer, as described above, that hybridizes to a polynucleotide encoding a lung tumor protein. Such an oligonucleotide may be used, for example, within a PCR or hybridization assay. Additional components that may be
20 present within such kits include a second oligonucleotide and/or a diagnostic reagent or container to facilitate the detection of a polynucleotide encoding a lung tumor protein.

The following Examples are offered by way of illustration and not by way of limitation.

EXAMPLE 1IDENTIFICATION AND CHARACTERIZATION OF LUNG
TUMOR PROTEIN cDNAS

5 This Example illustrates the identification of cDNA molecules encoding lung tumor proteins.

A. Isolation of cDNA Sequences from Lung Adenocarcinoma Libraries
using Conventional cDNA Library Subtraction

 A human lung adenocarcinoma cDNA expression library was
10 constructed from poly A⁺ RNA from patient tissues (# 40031486) using a Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning kit (BRL Life Technologies, Gaithersburg, MD) following the manufacturer's protocol. Specifically, lung carcinoma tissues were homogenized with polytron (Kinematica, Switzerland) and total RNA was extracted using Trizol reagent (BRL Life Technologies) as directed by the
15 manufacturer. The poly A⁺ RNA was then purified using an oligo dT cellulose column as described in Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989. First-strand cDNA was synthesized using the NotI/Oligo-dT18 primer. Double-stranded cDNA was synthesized, ligated with BstXI/EcoRI adaptors (Invitrogen, San Diego, CA) and
20 digested with NotI. Following size fractionation with cDNA size fractionation columns (BRL Life Technologies), the cDNA was ligated into the BstXI/NotI site of pcDNA3.1 (Invitrogen) and transformed into ElectroMax *E. coli* DH10B cells (BRL Life Technologies) by electroporation. A total of 3 x 10⁶ independent colonies were generated.

25 Using the same procedure, a normal human cDNA expression library was prepared from a panel of normal tissue specimens, including lung, liver, pancreas, skin, kidney, brain and resting PBMC.

 cDNA library subtraction was performed using the above lung adenocarcinoma and normal tissue cDNA libraries, as described by Hara *et al.* (*Blood*,
30 84:189-199, 1994) with some modifications. Specifically, a lung adenocarcinoma-

specific subtracted cDNA library was generated as follows. The normal tissue cDNA library (80 µg) was digested with BamHI and XhoI, followed by a filling-in reaction with DNA polymerase Klenow fragment. After phenol-chloroform extraction and ethanol precipitation, the DNA was dissolved in 133 µl of H₂O, heat-denatured and mixed with 133 µl (133 µg) of Photoprobe biotin (Vector Laboratories, Burlingame, CA). As recommended by the manufacturer, the resulting mixture was irradiated with a 270 W sunlamp on ice for 20 minutes. Additional Photoprobe biotin (67 µl) was added and the biotinylation reaction was repeated. After extraction with butanol five times, the DNA was ethanol-precipitated and dissolved in 23 µl H₂O. The resulting DNA, plus other highly redundant cDNA clones that were frequently recovered in previous lung subtractions formed the driver DNA.

To form the tracer DNA, 10 µg lung adenocarcinoma cDNA library was digested with NotI and SpeI, phenol chloroform extracted and passed through Chroma spin-400 columns (Clontech, Palo Alto, CA). Typically, 5 µg of cDNA was recovered after the sizing column. Following ethanol precipitation, the tracer DNA was dissolved in 5 µl H₂O. Tracer DNA was mixed with 15 µl driver DNA and 20 µl of 2 x hybridization buffer (1.5 M NaCl/10 mM EDTA/50 mM HEPES pH 7.5/0.2% sodium dodecyl sulfate), overlaid with mineral oil, and heat-denatured completely. The sample was immediately transferred into a 68 °C water bath and incubated for 20 hours (long hybridization [LH]). The reaction mixture was then subjected to a streptavidin treatment followed by phenol/chloroform extraction. This process was repeated three more times. Subtracted DNA was precipitated, dissolved in 12 µl H₂O, mixed with 8 µl driver DNA and 20 µl of 2 x hybridization buffer, and subjected to a hybridization at 68 °C for 2 hours (short hybridization [SH]). After removal of biotinylated double-stranded DNA, subtracted cDNA was ligated into NotI/SpeI site of chloramphenicol resistant pBCSK⁺ (Stratagene, La Jolla, CA) and transformed into ElectroMax *E. coli* DH10B cells by electroporation to generate a lung adenocarcinoma specific subtracted cDNA library, referred to as LAT-S1. Similarly, LAT-S2 was generated by including 23 genes that were over-expressed in the tracer as additional drivers.

A second human lung adenocarcinoma cDNA expression library was constructed using adenocarcinoma tissue from a second patient (# 86-66) and used to

prepare a second lung adenocarcinoma-specific subtracted cDNA library (referred to as LAT2-S2), as described above, using the same panel of normal tissues and the additional genes over-expressed in LAT-S1.

5 A third human metastatic lung adenocarcinoma library was constructed from a pool of two lung pleural effusions with lung and gastric adenocarcinoma origins. The subtracted cDNA library, Mets-sub2 was generated as described above using the same panel of normal tissues. However, the Mets-sub3 subtracted library was constructed by including 51 additional genes as drivers. These 51 genes were recovered in Mets-sub2, representing over-expressed housekeeping genes in the testers. As a
10 result, Mets-sub3 is more complexed and normalized.

A total of 16 cDNA fragments isolated from LAT-S1, 585 cDNA fragments isolated from LAT-S2, 568 cDNA clones from LAT2-S2, 15 cDNA clones from Mets-sub2 and 343 cDNA clones from Mets-sub3, described above, were colony PCR amplified and their mRNA expression levels in lung tumor, normal lung, and
15 various other normal and tumor tissues were determined using microarray technology (Incyte, Palo Alto, CA). Briefly, the PCR amplification products were dotted onto slides in an array format, with each product occupying a unique location in the array. mRNA was extracted from the tissue sample to be tested, reverse transcribed, and fluorescent-labeled cDNA probes were generated. The microarrays were probed with
20 the labeled cDNA probes, the slides scanned and fluorescence intensity was measured. This intensity correlates with the hybridization intensity. Seventy-three non-redundant cDNA clones, of which 42 were found to be unique, showed over-expression in lung tumors, with expression in normal tissues tested (lung, skin, lymph node, colon, liver, pancreas, breast, heart, bone marrow, large intestine, kidney, stomach, brain, small
25 intestine, bladder and salivary gland) being either undetectable, or at significantly lower levels compared to lung adenocarcinoma tumors. These clones were further characterized by DNA sequencing with a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A and/or Model 377 (Foster City, CA).

The sequences were compared to known sequences in the gene bank
30 using the EMBL GenBank databases (release 96). No significant homologies were found to the sequence provided in SEQ ID NO: 67, with no apparent homology to

previously identified expressed sequence tags (ESTs). The sequences of SEQ ID NO: 60, 62, 65, 66, 69-71, 74, 76, 79, 80, 84, 86, 89-92, 95, 97 and 98 were found to show some homology to previously identified expressed sequence tags (ESTs). The cDNA sequences of SEQ ID NO: 59, 61, 63, 64, 67, 68, 72, 73, 75, 77, 78, 81-83, 85, 87, 88, 93, 94, 96, 99 and 100 showed homology to previously identified genes. The full-length cDNA sequences for the clones of SEQ ID NO: 96 and 100 are provided in SEQ ID NO: 316 and 318, respectively. The amino acid sequences for the clones of SEQ ID NO: 59, 61, 63, 64, 68, 73, 82, 83, 94, 96 and 100 are provided in SEQ ID NO: 331, 328, 329, 332, 327, 333, 330, 326, 325, 324 and 335, respectively. A predicted amino acid sequence encoded by the sequence of SEQ ID NO: 69 (referred to as L552S) is provided in SEQ ID NO: 786.

Further studies led to the isolation of an extended cDNA sequence, and open reading frame, for L552S (SEQ ID NO: 790). The predicted amino acid sequence encoded by the cDNA sequence of SEQ ID NO: 790 is provided in SEQ ID NO: 791. The determined cDNA sequence of an isoform of L552S is provided in SEQ ID NO: 792, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 793. Subsequent studies led to the isolation of the full-length cDNA sequence of L552S (SEQ ID NO: 808). The corresponding amino acid sequence is provided in SEQ ID NO: 809. No homologies were found to the protein sequence of L552S. However, nucleotides 533-769 of the full-length cDNA sequence were found to show homology to a previously identified DNA sequence.

Full-length cloning efforts on L552S led to the isolation of three additional cDNA sequences (SEQ ID NO: 810-812) from a metastatic lung adenocarcinoma library. The sequence of SEQ ID NO: 810 was found to show some homology to previously identified human DNA sequences. The sequence of SEQ ID NO: 811 was found to show some homology to a previously identified DNA sequence. The sequence of SEQ ID NO: 812 was found to show some homology to previously identified ESTs.

The gene of SEQ ID NO: 84 (referred to as L551S) was determined by real-time RT-PCR analysis to be over-expressed in 2/9 primary adenocarcinomas and to be expressed at lower levels in 2/2 metastatic adenocarcinomas and 1/2 squamous cell

carcinomas. No expression was observed in normal tissues, with the exception of very low expression in normal stomach. Further studies on L551S led to the isolation of the 5' and 3' cDNA consensus sequences provided in SEQ ID NO: 801 and 802, respectively. The L551S 5' sequence was found to show some homology to the previously identified gene STY8 (cDNA sequence provided in SEQ ID NO: 803; corresponding amino acid sequence provided in SEQ ID NO: 805), which is a mitogen activated protein kinase phosphatase. However, no significant homologies were found to the 3' sequence of L551S. Subsequently, an extended cDNA sequence for L551S was isolated (SEQ ID NO: 804). The corresponding amino acid sequence is provided in SEQ ID NO: 806. Further studies led to the isolation of two independent full-length clones for L551S (referred to as 54298 and 54305). These two clones have five nucleotide differences compared to the STY8 DNA sequence. Two of these differences are single nucleotide polymorphisms which do not effect the encoded amino acid sequences. The other three nucleotide differences are consistent between the two L551S clones but lead to encoded amino acid sequences that are different from the STY8 protein sequence. The determined cDNA sequences for the L551S full-length clones 54305 and 54298 are provided in SEQ ID NO: 825 and 826, respectively, with the amino acid sequence for L551S being provided in SEQ ID NO: 827.

B. Isolation of cDNA Sequences from Lung Adenocarcinoma Libraries using PCR-Based cDNA Library Subtraction

cDNA clones from a PCR-based subtraction library, containing cDNA from a pool of two human lung primary adenocarcinomas subtracted against a pool of nine normal human tissue cDNAs including skin, colon, lung, esophagus, brain, kidney, spleen, pancreas and liver, (Clontech, Palo Alto, CA) were derived and submitted to a first round of PCR amplification. This library (referred to as ALT-1) was subjected to a second round of PCR amplification, following the manufacturer's protocol. The expression levels of 760 cDNA clones in lung tumor, normal lung, and various other normal and tumor tissues, were examined using microarray technology as described above. A total of 118 clones, of which 55 were unique, were found to be over-expressed in lung tumor tissue, with expression in normal tissues tested (lung, skin,

lymph node, colon, liver, pancreas, breast, heart, bone marrow, large intestine, kidney, stomach, brain, small intestine, bladder and salivary gland) being either undetectable, or at significantly lower levels. The sequences were compared to known sequences in the gene bank using the EMBL and GenBank databases (release 96). No significant
5 homologies (including ESTs) were found to the sequence provided in SEQ ID NO: 44. The sequences of SEQ ID NO: 1, 11, 13, 15, 20, 23-27, 29, 30, 33, 34, 39, 41, 43, 45, 46, 51 and 57 were found to show some homology to previously identified expressed sequence tags (ESTs). The cDNA sequences of SEQ ID NO: 2-10, 12, 14, 16-19, 21, 22, 28, 31, 32, 35-38, 40, 42, 44, 47-50, 52-56 and 58 showed homology to previously
10 identified genes. The full-length cDNA sequences for the clones of SEQ ID NO: 18, 22, 31, 35, 36 and 42 are provided in SEQ ID NO: 320, 319, 323, 321, 317, 321 and 322, respectively, with the corresponding amino acid sequences being provided in SEQ ID NO: 337, 336, 340, 338, 334, and 339, respectively.

Further studies led to the isolation of an extended cDNA sequence for
15 the clone of SEQ ID NO: 33 (referred to as L801P). This extended cDNA sequence (provided in SEQ ID NO: 796), was found to contain three potential open reading frames (ORFs). The predicted amino acid sequences encoded by these three ORFs are provided in SEQ ID NO: 797-799, respectively.

In subsequent studies, a full-length cDNA sequence for the clone of SEQ
20 ID NO: 44 (referred to as L844P) was isolated (provided in SEQ ID NO: 800). Comparison of this sequence with those in the public databases revealed that the 470 bases at the 5' end of the sequence show homology to the known gene dihydrodiol dehydrogenase, thus indicating that L844P is a novel transcript of the dihydrodiol dehydrogenase family having 2007 base pairs of previously unidentified 3'
25 untranslated region.

The predicted amino acid sequence encoded by the sequence of SEQ ID NO: 46 (referred to as L840P) is provided in SEQ ID NO: 787. An extended cDNA sequence for L840P, which was determined to include an open reading frame, is provided in SEQ ID NO: 794. The predicted amino acid sequence encoded by the
30 cDNA sequence of SEQ ID NO: 794 is provided in SEQ ID NO: 795. The full-length cDNA sequence for the clone of SEQ ID NO: 54 (referred to as L548S) is provided in

SEQ ID NO: 788, with the corresponding amino acid sequence being provided in SEQ ID NO: 789.

Northern blot analyses of the genes of SEQ ID NO: 25 and 46 (referred to as L839P and L840P, respectively) were remarkably similar. Both genes were expressed in 1/2 lung adenocarcinomas as two bands of 3.6 kb and 1.6 kb. No expression of L839P was observed in normal lung or trachea. No expression of L840P was observed in normal bone marrow, resting or activated PBMC, esophagus, or normal lung. Given the similar expression patterns, L839P and L840P may be derived from the same gene.

Further studies on L773P (SEQ ID NO: 58) resulted in the isolation of the extended consensus cDNA sequence provided in SEQ ID NO: 807.

Additional lung adenocarcinoma cDNA clones were isolated as follows. A cDNA library was prepared from a pool of two lung adenocarcinomas and subtracted against cDNA from a panel of normal tissues including lung, brain, liver, kidney, pancreas, skin, heart and spleen. The subtraction was performed using a PCR-based protocol (Clontech), which was modified to generate larger fragments. Within this protocol, tester and driver double stranded cDNA were separately digested with five restriction enzymes that recognize six-nucleotide restriction sites (MluI, MscI, PvuII, SalI and StuI). This digestion resulted in an average cDNA size of 600 bp, rather than the average size of 300 bp that results from digestion with RsaI according to the Clontech protocol. The ends of the restriction digested tester cDNA were filled in to generate blunt ends for adapter ligation. This modification did not affect the subtraction efficiency. Two tester populations were then created with different adapters, and the driver library remained without adapters. The tester and driver libraries were then hybridized using excess driver cDNA. In the first hybridization step, driver was separately hybridized with each of the two tester cDNA populations. This resulted in populations of (a) unhybridized tester cDNAs, (b) tester cDNAs hybridized to other tester cDNAs, (c) tester cDNAs hybridized to driver cDNAs and (d) unhybridized driver cDNAs. The two separate hybridization reactions were then combined, and rehybridized in the presence of additional denatured driver cDNA. Following this second hybridization, in addition to populations (a) through (d), a fifth population (e)

was generated in which tester cDNA with one adapter hybridized to tester cDNA with the second adapter. Accordingly, the second hybridization step resulted in enrichment of differentially expressed sequences which could be used as templates for PCR amplification with adaptor-specific primers.

5 The ends were then filled in, and PCR amplification was performed using adaptor-specific primers. Only population (e), which contained tester cDNA that did not hybridize to driver cDNA, was amplified exponentially. A second PCR amplification step was then performed, to reduce background and further enrich differentially expressed sequences.

10 Fifty-seven cDNA clones were isolated from the subtracted library (referred to as LAP1) and sequenced. The determined cDNA sequences for 16 of these clones are provided in SEQ ID NO: 101-116. The sequences of SEQ ID NO: 101 and 114 showed no significant homologies to previously identified sequences. The sequences of SEQ ID NO: 102-109 and 112 showed some similarity to previously
15 identified sequences, while the sequences of SEQ ID NO: 113, 115 and 116 showed some similarity to previously isolated ESTs.

C. Isolation of cDNA Sequences from Small Cell Lung Carcinoma Libraries using PCR-Based cDNA Library Subtraction

A subtracted cDNA library for small cell lung carcinoma (referred to as
20 SCL1) was prepared using essentially the modified PCR-based subtraction process described above. cDNA from small cell lung carcinoma was subtracted against cDNA from a panel of normal tissues, including normal lung, brain, kidney, liver, pancreas, skin, heart, lymph node and spleen. Both tester and driver poly A+ RNA were initially amplified using SMART PCR cDNA synthesis kit (Clontech, Palo Alto, CA). The
25 tester and driver double stranded cDNA were separately digested with five restriction enzymes (DraI, MscI, PvuII, SmaI, and StuI). These restriction enzymes generated blunt end cuts and the digestion resulted in an average insert size of 600 bp. Digestion with this set of restriction enzymes eliminates the step required to generate blunt ends by filling in of the cDNA ends. These modifications did not affect subtraction
30 efficiency.

Eighty-five clones were isolated and sequenced. The determined cDNA sequences for 31 of these clones are provided in SEQ ID NO: 117-147. The sequences of SEQ ID NO: 122, 124, 126, 127, 130, 131, 133, 136, 139 and 147 showed no significant homologies to previously identified sequences. The sequences of SEQ ID NO: 120, 129, 135, 137, 140, 142, 144 and 145 showed some similarity to previously identified gene sequences, while the sequences of SEQ ID NO: 114, 118, 119, 121, 123, 125, 128, 132, 134, 138, 141, 143 and 147 showed some similarity to previously isolated ESTs.

In further studies, three additional cDNA libraries were generated from poly A⁺ RNA from a single small cell lung carcinoma sample subtracted against a pool of poly A⁺ RNA from nine normal tissues (lung, brain, kidney, liver, pancreas, skin, heart pituitary gland and spleen). For the first library (referred to as SCL2), the subtraction was carried out essentially as described above for the LAP1 library, with the exception that the tester and driver were digested with PvuII, StuI, MscI and DraI. The ratio of tester and driver cDNA used was as recommended by Clontech. For the second library (referred to as SCL3), subtraction was performed essentially as for SCL2 except that cDNA for highly redundant clones identified from the SCL2 library was included in the driver cDNA. Construction of the SCL4 library was performed essentially as described for the SCL3 library except that a higher ratio of driver to tester was employed.

Each library was characterized by DNA sequencing and database analyses. The determined cDNA sequence for 35 clones isolated from the SCL2 library are provided in SEQ ID NO: 245-279, with the determined cDNA sequences for 21 clones isolated from the SCL3 library and for 15 clones isolated from the SCL4 library being provided in SEQ ID NO: 280-300 and 301-315, respectively. The sequences of SEQ ID NO: 246, 254, 261, 262, 304, 309 and 311 showed no significant homologies to previously identified sequences. The sequence of SEQ ID NO: 245, 248, 255, 266, 270, 275, 280, 282, 283, 288-290, 292, 295, 301 and 303 showed some homology to previously isolated ESTs, while the sequences of SEQ ID NO: 247, 249-253, 256-260, 263-265, 267-269, 271-274, 276-279, 281, 284-287, 291, 293, 294, 296-300, 302, 305-308, 310 and 312-315 showed some homology to previously identified gene sequences.

D. Isolation of cDNA Sequences from a Neuroendocrine Library using
PCR-Based cDNA Library Subtraction

Using the modified PCR-based subtraction process, essentially as described above for the LAP1 subtracted library, a subtracted cDNA library (referred to as MLN1) was derived from a lung neuroendocrine carcinoma that had metastasized to the subcarinal lymph node, by subtraction with a panel of nine normal tissues, including normal lung, brain, kidney, liver, pancreas, skin, heart, lymph node and spleen.

Ninety-one individual clones were isolated and sequenced. The determined cDNA sequences for 58 of these clones are provided in SEQ ID NO: 147-222. The sequences of SEQ ID NO: 150, 151, 154, 157, 158, 159, 160, 163, 174, 175, 178, 186-190, 192, 193, 195-200, 208-210, 212-215 and 220 showed no significant homologies to previously identified sequences. The sequences of SEQ ID NO: 152, 155, 156, 161, 165, 166, 176, 179, 182, 184, 185, 191, 194, 221 and 222 showed some similarity to previously identified gene sequences, while the sequences of SEQ ID NO: 148, 149, 153, 164, 167-173, 177, 180, 181, 183, 201-207, 211 and 216-219 showed some similarity to previously isolated ESTs.

The determined cDNA sequences of an additional 442 clones isolated from the MLN1 library are provided in SEQ ID NO: 341-782.

E. Isolation of cDNA Sequences from a Squamous Cell Lung Carcinoma
Library using PCR-Based cDNA Library Subtraction

A subtracted cDNA library for squamous cell lung carcinoma (referred to as SQL1) was prepared, essentially using the modified PCR-based subtraction process described above, except the tester and driver double stranded cDNA were separately digested with four restriction enzymes (DraI, MscI, PvuII and StuI) cDNA from a pool of two squamous cell lung carcinomas was subtracted against cDNA from a pool of 10 normal tissues, including normal lung, brain, kidney, liver, pancreas, skin, heart, spleen, esophagus and trachea.

Seventy-four clones were isolated and sequenced. The determined cDNA sequences for 22 of these clones are provided in SEQ ID NO: 223-244. The sequence of SEQ ID NO: 241 showed no significant homologies to previously

identified sequences. The sequences of SEQ ID NO: 223, 225, 232, 233, 235, 238, 239, 242 and 243 showed some similarity to previously identified gene sequences, while the sequences of SEQ ID NO: 224, 226-231, 234, 236, 237, 240, 241 and 244 showed some similarity to previously isolated ESTs.

5 The sequences of an additional 12 clones isolated during chracterization of cDNA libraries prepared from lung tumor tissue are provided in SEQ ID NO: 813-824. Comparison of these sequences with those in the GenBank database and the GeneSeq DNA database revealed no significant homologies to previously identified sequences.

10

EXAMPLE 2

SYNTHESIS OF POLYPEPTIDES

Polypeptides may be synthesized on a Perkin Elmer/Applied Biosystems
15 Division 430A peptide synthesizer using Fmoc chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following
20 cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0%-60% acetonitrile (containing 0.1% TFA) in water
25 (containing 0.1% TFA) may be used to elute the peptides. Following lyophilization of the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

EXAMPLE 3

PREPARATION OF ANTIBODIES AGAINST LUNG CANCER ANTIGENS

Polyclonal antibodies against the lung cancer antigen L773P (SEQ ID
5 NO: 783) were prepared as follows.

Rabbits were immunized with recombinant protein expressed in and
purified from *E. coli* as described above. For the initial immunization, 400 µg of
antigen combined with muramyl dipeptide (MDP) was injected subcutaneously (S.C.).
Animals were boosted S.C. 4 weeks later with 200 µg of antigen mixed with incomplete
10 Freund's Adjuvant (IFA). Subsequent boosts of 100 µg of antigen mixed with IFA
were injected S.C. as necessary to induce high antibody titer responses. Serum bleeds
from immunized rabbits were tested for L773P-specific reactivity using ELISA assays
with purified protein and showed strong reactivity to L773P. Polyclonal antibodies
against L773P were affinity purified from high titer polyclonal sera using purified
15 protein attached to a solid support.

EXAMPLE 4

PROTEIN EXPRESSION OF LUNG TUMOR-SPECIFIC ANTIGENS

20 Full-length L773P (amino acids 2-364 of SEQ ID NO: 783), with a 6X
His Tag, were subcloned into the pPDM expression vector and transformed into either
BL21 CodonPlus or BL21 pLysS host cells using standard techniques. High levels of
expression were observed in both cases. Similarly, the N-terminal portion of L773P
(amino acids 2-71 of SEQ ID NO: 783; referred to as L773PA), with a 6X His tag were
25 subcloned into the vector pPDM and transformed into BL21 CodonPlus host cells. Low
levels of expression were observed by N-terminal sequencing. The sequence of the
expressed constructs for L773P and L773PA are provided in SEQ ID NO: 784 and 785,
respectively.

30

From the foregoing it will be appreciated that, although specific embodiments of the invention have been described herein for purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention. Accordingly, the invention is not limited except as by the appended claims.

CLAIMS

What is claimed:

1. An isolated polypeptide, comprising at least an immunogenic portion of a lung tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(a) sequences recited in SEQ ID NOs: 1, 11-13, 15, 20, 23-27, 29, 30, 33, 34, 39, 41, 43-46, 51, 52, 57, 58, 60, 62, 65-67, 69-71, 74, 76, 79, 80, 84, 86, 89-92, 95, 97, 98, 101, 110, 111, 113-119, 121-128, 130-134, 136, 138, 139, 141, 143, 146-151, 153, 154, 157-160, 162-164, 167-178, 180, 181, 183, 186-190, 192, 193, 195-220, 224, 226-231, 234, 236, 237, 240, 241, 244-246, 248, 254, 255, 261, 262, 266, 270, 275, 280, 282, 283, 288, 289, 290, 292, 295, 301, 303, 304, 309, 311, 341-782, 784, 785, 790, 792, 794, 796, 800, 802, 804, 807, 808 and 811-826;

(b) sequences that hybridize to a sequence recited in any one of SEQ ID NOs: 1, 11-13, 15, 20, 23-27, 29, 30, 33, 34, 39, 41, 43-46, 51, 52, 57, 58, 60, 62, 65-67, 69-71, 74, 76, 79, 80, 84, 86, 89-92, 95, 97, 98, 101, 110, 111, 113-119, 121-128, 130-134, 136, 138, 139, 141, 143, 146-151, 153, 154, 157-160, 162-164, 167-178, 180, 181, 183, 186-190, 192, 193, 195-220, 224, 226-231, 234, 236, 237, 240, 241, 244-246, 248, 254, 255, 261, 262, 266, 270, 275, 280, 282, 283, 288, 289, 290, 292, 295, 301, 303, 304, 309, 311, 341-782, 784, 785, 790, 792, 794, 796, 800, 802, 804, 807, 808 and 811-826 under moderately stringent conditions; and

(c) complements of sequences of (a) or (b).

2. An isolated polypeptide according to claim 1, wherein the polypeptide comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs: 1, 11-13, 15, 20, 23-27, 29, 30, 33, 34, 39, 41, 43-46, 51, 52, 57, 58, 60, 62, 65-67, 69-71, 74, 76, 79, 80, 84, 86, 89-92, 95, 97, 98, 101, 110, 111, 113-119, 121-128, 130-134, 136, 138, 139, 141, 143, 146-151, 153, 154, 157-160, 162-164, 167-178, 180, 181, 183, 186-190, 192, 193, 195-220, 224, 226-231, 234, 236, 237, 240, 241, 244-246, 248, 254, 255, 261, 262, 266, 270, 275, 280, 282, 283, 288, 289, 290, 292, 295, 301, 303, 304, 309, 311, 341-

782, 784, 785, 790, 792, 794, 796, 800, 802, 804, 807, 808 and 811-826 or a complement of any of the foregoing polynucleotide sequences.

3. An isolated polypeptide comprising a sequence recited in any one of SEQ ID NOs: 786, 787, 791, 793, 795, 797-799, 806, 809 and 827.

4. An isolated polynucleotide encoding at least 15 amino acid residues of a lung tumor protein, or a variant thereof that differs in one or more substitutions, deletions, additions and/or insertions such that the ability of the variant to react with antigen-specific antisera is not substantially diminished, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide comprising a sequence recited in any one of SEQ ID NO: 1, 11-13, 15, 20, 23-27, 29, 30, 33, 34, 39, 41, 43-46, 51, 52, 57, 58, 60, 62, 65-67, 69-71, 74, 76, 79, 80, 84, 86, 89-92, 95, 97, 98, 101, 110, 111, 113-119, 121-128, 130-134, 136, 138, 139, 141, 143, 146-151, 153, 154, 157-160, 162-164, 167-178, 180, 181, 183, 186-190, 192, 193, 195-220, 224, 226-231, 234, 236, 237, 240, 241, 244-246, 248, 254, 255, 261, 262, 266, 270, 275, 280, 282, 283, 288, 289, 290, 292, 295, 301, 303, 304, 309, 311, 341-782, 784, 785, 790, 792, 794, 796, 800, 802, 804, 807, 808 and 811-826, or a complement of any of the foregoing sequences.

5. An isolated polynucleotide encoding a lung tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide comprising a sequence recited in any one of SEQ ID NOs: 1, 11-13, 15, 20, 23-27, 29, 30, 33, 34, 39, 41, 43-46, 51, 52, 57, 58, 60, 62, 65-67, 69-71, 74, 76, 79, 80, 84, 86, 89-92, 95, 97, 98, 101, 110, 111, 113-119, 121-128, 130-134, 136, 138, 139, 141, 143, 146-151, 153, 154, 157-160, 162-164, 167-178, 180, 181, 183, 186-190, 192, 193, 195-220, 224, 226-231, 234, 236, 237, 240, 241, 244-246, 248, 254, 255, 261, 262, 266, 270, 275, 280, 282, 283, 288, 289, 290, 292, 295, 301, 303, 304, 309, 311, 341-782, 784, 785, 790, 792, 794, 796, 800, 802, 804, 807, 808 and 811-826 or a complement of any of the foregoing sequences.

6. An isolated polynucleotide, comprising a sequence recited in any one of SEQ ID NOs: 1, 11-13, 15, 20, 23-27, 29, 30, 33, 34, 39, 41, 43-46, 51, 52, 57, 58, 60, 62, 65-67, 69-71, 74, 76, 79, 80, 84, 86, 89-92, 95, 97, 98, 101, 110, 111, 113-119, 121-128, 130-134, 136, 138, 139, 141, 143, 146-151, 153, 154, 157-160, 162-164, 167-178, 180, 181, 183, 186-190, 192, 193, 195-220, 224, 226-231, 234, 236, 237, 240, 241, 244-246, 248, 254, 255, 261, 262, 266, 270, 275, 280, 282, 283, 288, 289, 290, 292, 295, 301, 303, 304, 309, 311, 341-782, 784, 785, 790, 792, 794, 796, 800, 802, 804, 807, 808 and 811-826.

7. An isolated polynucleotide, comprising a sequence that hybridizes to a sequence recited in any one of SEQ ID NOs: 1, 11-13, 15, 20, 23-27, 29, 30, 33, 34, 39, 41, 43-46, 51, 52, 57, 58, 60, 62, 65-67, 69-71, 74, 76, 79, 80, 84, 86, 89-92, 95, 97, 98, 101, 110, 111, 113-119, 121-128, 130-134, 136, 138, 139, 141, 143, 146-151, 153, 154, 157-160, 162-164, 167-178, 180, 181, 183, 186-190, 192, 193, 195-220, 224, 226-231, 234, 236, 237, 240, 241, 244-246, 248, 254, 255, 261, 262, 266, 270, 275, 280, 282, 283, 288, 289, 290, 292, 295, 301, 303, 304, 309, 311, 341-782, 784, 785, 790, 792, 794, 796, 800, 802, 804, 807, 808 and 811-826 under moderately stringent conditions.

8. An isolated polynucleotide complementary to a polynucleotide according to any one of claims 4-7.

9. An expression vector, comprising a polynucleotide according to any one of claims 4-8.

10. A host cell transformed or transfected with an expression vector according to claim 9.

11. An isolated antibody, or antigen-binding fragment thereof, that specifically binds to a lung tumor protein that comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs: 1, 11-13, 15, 20, 23-27, 29, 30,

33, 34, 39, 41, 43-46, 51, 52, 57, 58, 60, 62, 65-67, 69-71, 74, 76, 79, 80, 84, 86, 89-92, 95, 97, 98, 101, 110, 111, 113-119, 121-128, 130-134, 136, 138, 139, 141, 143, 146-151, 153, 154, 157-160, 162-164, 167-178, 180, 181, 183, 186-190, 192, 193, 195-220, 224, 226-231, 234, 236, 237, 240, 241, 244-246, 248, 254, 255, 261, 262, 266, 270, 275, 280, 282, 283, 288, 289, 290, 292, 295, 301, 303, 304, 309, 311, 341-782, 784, 785, 790, 792, 794, 796, 800, 802, 804, 807, 808 and 811-826 or a complement of any of the foregoing polynucleotide sequences.

12. A fusion protein, comprising at least one polypeptide according to claim 1.

13. A fusion protein according to claim 12, wherein the fusion protein comprises an expression enhancer that increases expression of the fusion protein in a host cell transfected with a polynucleotide encoding the fusion protein.

14. A fusion protein according to claim 12, wherein the fusion protein comprises a T helper epitope that is not present within the polypeptide of claim 1.

15. A fusion protein according to claim 12, wherein the fusion protein comprises an affinity tag.

16. An isolated polynucleotide encoding a fusion protein according to claim 12.

17. A pharmaceutical composition, comprising a physiologically acceptable carrier and at least one component selected from the group consisting of:

- (a) a polypeptide according to claim 1;
- (b) a polynucleotide according to claim 4;
- (c) an antibody according to claim 11;
- (d) a fusion protein according to claim 12; and
- (e) a polynucleotide according to claim 16.

18. An immunogenic composition comprising an immunostimulant and at least one component selected from the group consisting of:

- (a) a polypeptide according to claim 1;
- (b) a polynucleotide according to claim 4;
- (c) an antibody according to claim 11;
- (d) a fusion protein according to claim 12; and
- (e) a polynucleotide according to claim 16.

19. An immunogenic composition according to claim 18, wherein the immunostimulant is an adjuvant.

20. An immunogenic composition according to any claim 18, wherein the immunostimulant induces a predominantly Type I response.

21. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a pharmaceutical composition according to claim 17.

22. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of an immunogenic composition according to claim 18.

23. A pharmaceutical composition comprising an antigen-presenting cell that expresses a polypeptide according to claim 1, in combination with a pharmaceutically acceptable carrier or excipient.

24. A pharmaceutical composition according to claim 23, wherein the antigen presenting cell is a dendritic cell or a macrophage.

25. An immunogenic composition comprising an antigen-presenting cell that expresses a polypeptide comprising at least an immunogenic portion of a lung tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(a) sequences recited in SEQ ID NOs: 1, 11-13, 15, 20, 23-27, 29, 30, 33, 34, 39, 41, 43-46, 51, 52, 57, 58, 60, 62, 65-67, 69-71, 74, 76, 79, 80, 84, 86, 89-92, 95, 97, 98, 101, 110, 111, 113-119, 121-128, 130-134, 136, 138, 139, 141, 143, 146-151, 153, 154, 157-160, 162-164, 167-178, 180, 181, 183, 186-190, 192, 193, 195-220, 224, 226-231, 234, 236, 237, 240, 241, 244-246, 248, 254, 255, 261, 262, 266, 270, 275, 280, 282, 283, 288, 289, 290, 292, 295, 301, 303, 304, 309, 311, 341-782, 784, 785, 790, 792, 794, 796, 800-804, 807, 808 and 810-826;

(b) sequences that hybridize to a sequence recited in any one of SEQ ID NOs: 1, 11-13, 15, 20, 23-27, 29, 30, 33, 34, 39, 41, 43-46, 51, 52, 57, 58, 60, 62, 65-67, 69-71, 74, 76, 79, 80, 84, 86, 89-92, 95, 97, 98, 101, 110, 111, 113-119, 121-128, 130-134, 136, 138, 139, 141, 143, 146-151, 153, 154, 157-160, 162-164, 167-178, 180, 181, 183, 186-190, 192, 193, 195-220, 224, 226-231, 234, 236, 237, 240, 241, 244-246, 248, 254, 255, 261, 262, 266, 270, 275, 280, 282, 283, 288, 289, 290, 292, 295, 301, 303, 304, 309, 311, 341-782, 784, 785, 790, 792, 794, 796, 800-804, 807, 808 and 810-826 under moderately stringent conditions; and

(c) complements of sequences of (i) or (ii);
in combination with an immunostimulant.

26. An immunogenic composition according to claim 25, wherein the immunostimulant is an adjuvant.

27. An immunogenic composition according to claim 25, wherein the immunostimulant induces a predominantly Type I response.

28. An immunogenic composition according to claim 25, wherein the antigen-presenting cell is a dendritic cell.

29. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of an antigen-presenting cell that expresses a polypeptide comprising at least an immunogenic portion of a lung tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(a) sequences recited in SEQ ID NOs: 1, 11-13, 15, 20, 23-27, 29, 30, 33, 34, 39, 41, 43-46, 51, 52, 57, 58, 60, 62, 65-67, 69-71, 74, 76, 79, 80, 84, 86, 89-92, 95, 97, 98, 101, 110, 111, 113-119, 121-128, 130-134, 136, 138, 139, 141, 143, 146-151, 153, 154, 157-160, 162-164, 167-178, 180, 181, 183, 186-190, 192, 193, 195-220, 224, 226-231, 234, 236, 237, 240, 241, 244-246, 248, 254, 255, 261, 262, 266, 270, 275, 280, 282, 283, 288, 289, 290, 292, 295, 301, 303, 304, 309, 311, 341-782, 784, 785, 790, 792, 794, 796, 800-804, 807, 808 and 810-826;

(b) sequences that hybridize to a sequence recited in any one of SEQ ID NOs: 1, 11-13, 15, 20, 23-27, 29, 30, 33, 34, 39, 41, 43-46, 51, 52, 57, 58, 60, 62, 65-67, 69-71, 74, 76, 79, 80, 84, 86, 89-92, 95, 97, 98, 101, 110, 111, 113-119, 121-128, 130-134, 136, 138, 139, 141, 143, 146-151, 153, 154, 157-160, 162-164, 167-178, 180, 181, 183, 186-190, 192, 193, 195-220, 224, 226-231, 234, 236, 237, 240, 241, 244-246, 248, 254, 255, 261, 262, 266, 270, 275, 280, 282, 283, 288, 289, 290, 292, 295, 301, 303, 304, 309, 311, 341-782, 784, 785, 790, 792, 794, 796, 800-804, 807, 808 and 810-826 under moderately stringent conditions; and

(c) complements of sequences of (i) or (ii) encoded by a polynucleotide recited in any one of SEQ ID NOs: 1, 11-13, 15, 20, 23-27, 29, 30, 33, 34, 39, 41, 43-46, 51, 52, 57, 58, 60, 62, 65-67, 69-71, 74, 76, 79, 80, 84, 86, 89-92, 95, 97, 98, 101, 110, 111, 113-119, 121-128, 130-134, 136, 138, 139, 141, 143, 146-151, 153, 154, 157-160, 162-164, 167-178, 180, 181, 183, 186-190, 192, 193, 195-220, 224, 226-231, 234, 236, 237, 240, 241, 244-246, 248, 254, 255, 261, 262, 266, 270, 275, 280, 282, 283, 288, 289, 290, 292, 295, 301, 303, 304, 309, 311, 341-782, 784, 785, 790, 792, 794, 796, 800-804, 807, 808 and 810-826;

and thereby inhibiting the development of a cancer in the patient.

30. A method according to claim 29, wherein the antigen-presenting cell is a dendritic cell.

31. A method according to any one of claims 21, 22 and 29, wherein the cancer is lung cancer.

32. A method for removing tumor cells from a biological sample, comprising contacting a biological sample with T cells that specifically react with a lung tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(i) polynucleotides recited in any one of SEQ ID NOs: 1, 11-13, 15, 20, 23-27, 29, 30, 33, 34, 39, 41, 43-46, 51, 52, 57, 58, 60, 62, 65-67, 69-71, 74, 76, 79, 80, 84, 86, 89-92, 95, 97, 98, 101, 110, 111, 113-119, 121-128, 130-134, 136, 138, 139, 141, 143, 146-151, 153, 154, 157-160, 162-164, 167-178, 180, 181, 183, 186-190, 192, 193, 195-220, 224, 226-231, 234, 236, 237, 240, 241, 244-246, 248, 254, 255, 261, 262, 266, 270, 275, 280, 282, 283, 288, 289, 290, 292, 295, 301, 303, 304, 309, 311, 341-782, 784, 785, 790, 792, 794, 796, 800-804, 807, 808 and 810-826; and

(ii) complements of the foregoing polynucleotides;

wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the antigen from the sample.

33. A method according to claim 32, wherein the biological sample is blood or a fraction thereof.

34. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient a biological sample treated according to the method of claim 32.

35. A method for stimulating and/or expanding T cells specific for a lung tumor protein, comprising contacting T cells with at least one component selected from the group consisting of:

(a) polypeptides comprising at least an immunogenic portion of a lung tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(i) sequences recited in SEQ ID NOs: 1, 11-13, 15, 20, 23-27, 29, 30, 33, 34, 39, 41, 43-46, 51, 52, 57, 58, 60, 62, 65-67, 69-71, 74, 76, 79, 80, 84, 86, 89-92, 95, 97, 98, 101, 110, 111, 113-119, 121-128, 130-134, 136, 138, 139, 141, 143, 146-151, 153, 154, 157-160, 162-164, 167-178, 180, 181, 183, 186-190, 192, 193, 195-220, 224, 226-231, 234, 236, 237, 240, 241, 244-246, 248, 254, 255, 261, 262, 266, 270, 275, 280, 282, 283, 288, 289, 290, 292, 295, 301, 303, 304, 309, 311, 341-782, 784, 785, 790, 792, 794, 796, 800-804, 807, 808 and 810-826;

(ii) sequences that hybridize to a sequence recited in any one of SEQ ID NOs: 1, 11-13, 15, 20, 23-27, 29, 30, 33, 34, 39, 41, 43-46, 51, 52, 57, 58, 60, 62, 65-67, 69-71, 74, 76, 79, 80, 84, 86, 89-92, 95, 97, 98, 101, 110, 111, 113-119, 121-128, 130-134, 136, 138, 139, 141, 143, 146-151, 153, 154, 157-160, 162-164, 167-178, 180, 181, 183, 186-190, 192, 193, 195-220, 224, 226-231, 234, 236, 237, 240, 241, 244-246, 248, 254, 255, 261, 262, 266, 270, 275, 280, 282, 283, 288, 289, 290, 292, 295, 301, 303, 304, 309, 311, 341-782, 784, 785, 790, 792, 794, 796, 800-804, 807, 808 and 810-826 under moderately stringent conditions; and

(iii) complements of sequences of (i) or (ii);

(b) polynucleotides encoding a polypeptide of (a); and

(c) antigen presenting cells that express a polypeptide of (a);

under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells.

36. An isolated T cell population, comprising T cells prepared according to the method of claim 35.

37. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a T cell population according to claim 36.

38. A method for inhibiting the development of a cancer in a patient, comprising the steps of:

(a) incubating CD4⁺ and/or CD8⁺ T cells isolated from a patient with at least one component selected from the group consisting of:

(i) polypeptides comprising at least an immunogenic portion of a lung tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(1) sequences recited in SEQ ID NOs: 1, 11-13, 15, 20, 23-27, 29, 30, 33, 34, 39, 41, 43-46, 51, 52, 57, 58, 60, 62, 65-67, 69-71, 74, 76, 79, 80, 84, 86, 89-92, 95, 97, 98, 101, 110, 111, 113-119, 121-128, 130-134, 136, 138, 139, 141, 143, 146-151, 153, 154, 157-160, 162-164, 167-178, 180, 181, 183, 186-190, 192, 193, 195-220, 224, 226-231, 234, 236, 237, 240, 241, 244-246, 248, 254, 255, 261, 262, 266, 270, 275, 280, 282, 283, 288, 289, 290, 292, 295, 301, 303, 304, 309, 311, 341-782, 784, 785, 790, 792, 794, 796, 800-804, 807, 808 and 810-826;

(2) sequences that hybridize to a sequence recited in any one of SEQ ID NOs: 1, 11-13, 15, 20, 23-27, 29, 30, 33, 34, 39, 41, 43-46, 51, 52, 57, 58, 60, 62, 65-67, 69-71, 74, 76, 79, 80, 84, 86, 89-92, 95, 97, 98, 101, 110, 111, 113-119, 121-128, 130-134, 136, 138, 139, 141, 143, 146-151, 153, 154, 157-160, 162-164, 167-178, 180, 181, 183, 186-190, 192, 193, 195-220, 224, 226-231, 234, 236, 237, 240, 241, 244-246, 248, 254, 255, 261, 262, 266, 270, 275, 280, 282, 283, 288, 289, 290, 292, 295, 301, 303, 304, 309, 311, 341-782, 784, 785, 790, 792, 794, 796, 800-804, 807, 808 and 810-826 under moderately stringent conditions; and

(3) complements of sequences of (1) or (2);

(ii) polynucleotides encoding a polypeptide of (i); and

(iii) antigen presenting cells that expresses a polypeptide of (i);

such that T cells proliferate; and

(b) administering to the patient an effective amount of the proliferated T cells, and thereby inhibiting the development of a cancer in the patient.

39. A method for inhibiting the development of a cancer in a patient, comprising the steps of:

(a) incubating CD4⁺ and/or CD8⁺ T cells isolated from a patient with at least one component selected from the group consisting of:

(i) polypeptides comprising at least an immunogenic portion of a lung tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(1) sequences recited in SEQ ID NOs: 1, 11-13, 15, 20, 23-27, 29, 30, 33, 34, 39, 41, 43-46, 51, 52, 57, 58, 60, 62, 65-67, 69-71, 74, 76, 79, 80, 84, 86, 89-92, 95, 97, 98, 101, 110, 111, 113-119, 121-128, 130-134, 136, 138, 139, 141, 143, 146-151, 153, 154, 157-160, 162-164, 167-178, 180, 181, 183, 186-190, 192, 193, 195-220, 224, 226-231, 234, 236, 237, 240, 241, 244-246, 248, 254, 255, 261, 262, 266, 270, 275, 280, 282, 283, 288, 289, 290, 292, 295, 301, 303, 304, 309, 311, 341-782, 784, 785, 790, 792, 794, 796, 800-804, 807, 808 and 810-826;

(2) sequences that hybridize to a sequence recited in any one of SEQ ID NOs: 1, 11-13, 15, 20, 23-27, 29, 30, 33, 34, 39, 41, 43-46, 51, 52, 57, 58, 60, 62, 65-67, 69-71, 74, 76, 79, 80, 84, 86, 89-92, 95, 97, 98, 101, 110, 111, 113-119, 121-128, 130-134, 136, 138, 139, 141, 143, 146-151, 153, 154, 157-160, 162-164, 167-178, 180, 181, 183, 186-190, 192, 193, 195-220, 224, 226-231, 234, 236, 237, 240, 241, 244-246, 248, 254, 255, 261, 262, 266, 270, 275, 280, 282, 283, 288, 289, 290, 292, 295, 301, 303, 304, 309, 311, 341-782, 784, 785, 790, 792, 794, 796, 800-804, 807, 808 and 810-826 under moderately stringent conditions; and

(3) complements of sequences of (1) or (2);

(ii) polynucleotides encoding a polypeptide of (i); and

(iii) antigen presenting cells that express a polypeptide of (i);

such that T cells proliferate;

(b) cloning at least one proliferated cell to provide cloned T cells; and

(c) administering to the patient an effective amount of the cloned T cells, and thereby inhibiting the development of a cancer in the patient.

40. A method for determining the presence or absence of a cancer in a patient, comprising the steps of:

(a) contacting a biological sample obtained from a patient with a binding agent that binds to a lung tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs: 1, 11-13, 15, 20, 23-27, 29, 30, 33, 34, 39, 41, 43-46, 51, 52, 57, 58, 60, 62, 65-67, 69-71, 74, 76, 79, 80, 84, 86, 89-92, 95, 97, 98, 101, 110, 111, 113-119, 121-128, 130-134, 136, 138, 139, 141, 143, 146-151, 153, 154, 157-160, 162-164, 167-178, 180, 181, 183, 186-190, 192, 193, 195-220, 224, 226-231, 234, 236, 237, 240, 241, 244-246, 248, 254, 255, 261, 262, 266, 270, 275, 280, 282, 283, 288, 289, 290, 292, 295, 301, 303, 304, 309, 311, 341-782, 784, 785, 790, 792, 794, 796, 800-804, 807, 808 and 810-826 or a complement of any of the foregoing polynucleotide sequences;

(b) detecting in the sample an amount of polypeptide that binds to the binding agent; and

(c) comparing the amount of polypeptide to a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient.

41. A method according to claim 40, wherein the binding agent is an antibody.

42. A method according to claim 43, wherein the antibody is a monoclonal antibody.

43. A method according to claim 40, wherein the cancer is lung cancer.

44. A method for monitoring the progression of a cancer in a patient, comprising the steps of:

(a) contacting a biological sample obtained from a patient at a first point in time with a binding agent that binds to a lung tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any

one of SEQ ID NOs: 1, 11-13, 15, 20, 23-27, 29, 30, 33, 34, 39, 41, 43-46, 51, 52, 57, 58, 60, 62, 65-67, 69-71, 74, 76, 79, 80, 84, 86, 89-92, 95, 97, 98, 101, 110, 111, 113-119, 121-128, 130-134, 136, 138, 139, 141, 143, 146-151, 153, 154, 157-160, 162-164, 167-178, 180, 181, 183, 186-190, 192, 193, 195-220, 224, 226-231, 234, 236, 237, 240, 241, 244-246, 248, 254, 255, 261, 262, 266, 270, 275, 280, 282, 283, 288, 289, 290, 292, 295, 301, 303, 304, 309, 311, 341-782, 784, 785, 790, 792, 794, 796, 800-804, 807, 808 and 810-826 or a complement of any of the foregoing polynucleotide sequences;

(b) detecting in the sample an amount of polypeptide that binds to the binding agent;

(c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and

(d) comparing the amount of polypeptide detected in step (c) to the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

45. A method according to claim 44, wherein the binding agent is an antibody.

46. A method according to claim 45, wherein the antibody is a monoclonal antibody.

47. A method according to claim 44, wherein the cancer is a lung cancer.

48. A method for determining the presence or absence of a cancer in a patient, comprising the steps of:

(a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a lung tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NO: 1, 11-13, 15, 20, 23-27, 29, 30, 33, 34, 39, 41, 43-46, 51, 52, 57, 58, 60, 62, 65-67, 69-71, 74, 76, 79, 80, 84, 86, 89-92, 95, 97, 98, 101, 110, 111, 113-119, 121-128, 130-134, 136, 138, 139, 141, 143, 146-151, 153, 154, 157-160, 162-164, 167-

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(b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; and

(c) comparing the amount of polynucleotide that hybridizes to the oligonucleotide to a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient.

49. A method according to claim 48, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a polymerase chain reaction.

50. A method according to claim 48, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a hybridization assay.

51. A method for monitoring the progression of a cancer in a patient, comprising the steps of:

(a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a lung tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NO: 1, 11-13, 15, 20, 23-27, 29, 30, 33, 34, 39, 41, 43-46, 51, 52, 57, 58, 60, 62, 65-67, 69-71, 74, 76, 79, 80, 84, 86, 89-92, 95, 97, 98, 101, 110, 111, 113-119, 121-128, 130-134, 136, 138, 139, 141, 143, 146-151, 153, 154, 157-160, 162-164, 167-178, 180, 181, 183, 186-190, 192, 193, 195-220, 224, 226-231, 234, 236, 237, 240, 241, 244-246, 248, 254, 255, 261, 262, 266, 270, 275, 280, 282, 283, 288, 289, 290, 292, 295, 301, 303, 304, 309, 311, 341-782, 784, 785, 790, 792, 794, 796, 800-804, 807, 808 and 810-826 or a complement of any of the foregoing polynucleotide sequences;

- (b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide;
- (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and
- (d) comparing the amount of polynucleotide detected in step (c) to the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

52. A method according to claim 51, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a polymerase chain reaction.

53. A method according to claim 51, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a hybridization assay.

54. A diagnostic kit, comprising:

- (a) one or more antibodies according to claim 11; and
- (b) a detection reagent comprising a reporter group.

55. A kit according to claim 54, wherein the antibodies are immobilized on a solid support.

56. A kit according to claim 54, wherein the detection reagent comprises an anti-immunoglobulin, protein G, protein A or lectin.

57. A kit according to claim 54, wherein the reporter group is selected from the group consisting of radioisotopes, fluorescent groups, luminescent groups, enzymes, biotin and dye particles.

58. An oligonucleotide comprising 10 to 40 contiguous nucleotides that hybridize under moderately stringent conditions to a polynucleotide that encodes a lung tumor

protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs: 1, 11-13, 15, 20, 23-27, 29, 30, 33, 34, 39, 41, 43-46, 51, 52, 57, 58, 60, 62, 65-67, 69-71, 74, 76, 79, 80, 84, 86, 89-92, 95, 97, 98, 101, 110, 111, 113-119, 121-128, 130-134, 136, 138, 139, 141, 143, 146-151, 153, 154, 157-160, 162-164, 167-178, 180, 181, 183, 186-190, 192, 193, 195-220, 224, 226-231, 234, 236, 237, 240, 241, 244-246, 248, 254, 255, 261, 262, 266, 270, 275, 280, 282, 283, 288, 289, 290, 292, 295, 301, 303, 304, 309, 311, 341-782, 784, 785, 790, 792, 794, 796, 800, 802, 804, 807, 808 and 811-826, or a complement of any of the foregoing polynucleotides.

59. A oligonucleotide according to claim 58, wherein the oligonucleotide comprises 10-40 contiguous nucleotides recited in any one of SEQ ID NO: 1, 11-13, 15, 20, 23-27, 29, 30, 33, 34, 39, 41, 43-46, 51, 52, 57, 58, 60, 62, 65-67, 69-71, 74, 76, 79, 80, 84, 86, 89-92, 95, 97, 98, 101, 110, 111, 113-119, 121-128, 130-134, 136, 138, 139, 141, 143, 146-151, 153, 154, 157-160, 162-164, 167-178, 180, 181, 183, 186-190, 192, 193, 195-220, 224, 226-231, 234, 236, 237, 240, 241, 244-246, 248, 254, 255, 261, 262, 266, 270, 275, 280, 282, 283, 288, 289, 290, 292, 295, 301, 303, 304, 309, 311, 341-782, 784, 785, 790, 792, 794, 796, 800, 802, 804, 807, 808 and 811-82.

60. A diagnostic kit, comprising:

- (a) an oligonucleotide according to claim 59; and
- (b) a diagnostic reagent for use in a polymerase chain reaction or hybridization assay.

SEQUENCE LISTING

<110> Corixa Corporation
 Wang, Tongtong
 Bangur, Chaitanya S.
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 Carter, Darrick
 Retter, Marc
 Mannion, Jane

<120> COMPOSITIONS AND METHODS FOR THERAPY AND
 DIAGNOSIS OF LUNG CANCER

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tcagggactt	ttctagctgt	atgactgtta	cttgaccttc	tttgaaaagc	attcccaaaa	300
tgctctattt	tagatagatt	aacattaacc	aacataattt	tttttagatc	gagtcagcat	360
aaatttctaa	gtcagcctct	agtcgtggtt	catctctttc	acctgcattt	tatttggtgt	420
ttgtctgaag	aaaggaaaga	ggaaagcaaa	tacgaattgt	actatttgta	ccaaatcttt	480
gggattcatt	ggcaaataat	ttcagtgtgg	tgtattatta	aatagaaaaa	aaaaattttg	540
tttcctaggt	tgaaggctta	attgatacgt	ttgacttatg	atgaccattt	atgcactttc	600
aaatgaattt	gctttcaaaa	taaatgaaga	gcag			634

<210> 24

<211> 512

<212> DNA

<213> Homo sapien

<400> 24

gcaaaacaag	cctaagcaag	cacaacgaag	agcagaagtc	agtgaatta	aaaagaggaa	60
aaagaaaaat	cataaaaaatc	ataaaaagtt	atttctttga	aaagatcaat	gaaatttagc	120
aagactgaca	cagataaaaa	ggaattagac	ccaaatcagt	gaacaggaat	gaaatagagg	180
atatcactac	agaggctgca	gccattgaaa	ggataattag	gaaatccac	agataacttt	240
gtgctcataa	atttgacaat	gtagaggaaa	tatctttagt	tttaattagc	tttttatttt	300
agttttttctc	aaaaactaaa	acttaataaa	actcaaccaa	gacaaaatag	acaatcagaa	360
tgtaggcata	cctcagagat	gtggcggatt	tggtttcaga	ctactgcaat	aaaccaata	420
tggcaataaa	aggagtcaca	gaaagtgggt	tcccagtgta	tatatataaa	agttacattt	480
actctatgaa	gtgcaataac	attttgtcta	aa			512

<210> 25

<211> 461

<212> DNA

<213> Homo sapien

<400> 25

ctctgtttca	gcacctcatt	gggattattg	aactcattaa	attctttaca	tgaacttgaa	60
ttgttcattg	aaatctctag	ccatttcctt	ggttaaacag	gataatcttt	ttttttcact	120
aaagaacatt	cggtgtggtt	tagtgatgag	gttaatatct	ccctcttgtc	cacctccaca	180
ttggaaaaac	caggttgagc	tgagttttga	ggagcaaaga	actaatcact	tgaccaaaag	240
ggccctgtat	ccccacaagc	cctgggtatt	tttctctcat	agagagaaga	gggtctgtat	300
ggatacctga	aaatgtgatt	ttatatattc	ttggcatcca	ggggagaaaa	atcaaaaagc	360
aaggaagtta	cagttatctc	cccagaaatt	aatgggtcat	gtcaagacta	taggttttca	420

tttccttctg ttgcttggtta gaatgatgtt cttgtgggaa a 461

<210> 26
 <211> 317
 <212> DNA
 <213> Homo sapien

<400> 26
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 taggatttat taaactaaaa aaaaattagt ttttgaaaag aaataggaga atacagaaac 120
 atgaatttca cgaggctatc atctaacagt gggggccttc tacacacgtg gtgccaaaat 180
 gtgtcattct gagtcaattg caattcctct ctaggagtga aaagagataa aagataagcc 240
 aagaacctg gacagattct tgggtttggt gacaaagagg aaaggacctg agaatggggc 300
 tgggtggggag agggggg 317

<210> 27
 <211> 250
 <212> DNA
 <213> Homo sapien

<400> 27
 taattgctgt gattattaga attctatcat gactgtattg tagtttttgc tctatttcag 60
 ataagcmaga tctaagaagt tatcaaaact attcttttaa atgctaaagc aggttaacttt 120
 ttcttccatt attttttctt cctaccactg agttttgtta tgaattcctt gtgtatacaa 180
 gcaatacagg tgaataactaa actgttattt ttagcttctt caaaagctat tttagaaagc 240
 ttctggaaa 250

<210> 28
 <211> 532
 <212> DNA
 <213> Homo sapien

<400> 28
 cctatatcat tcatttatatc agaagctgct tgctgcttag caagttgggtg ggtttgattt 60
 tccttggttg ctttgcagac ctcccttgag aggatccctt ctggatggag atttctttgt 120
 tgctgtctcc cttgccacaa ctctgaccaa gattgcattg cgctatgtag ctttggttca 180
 ggagaagaaa aagcaaaatt cttttgttgc tgaggctatg ttgctcatgg ctactatcct 240
 gcatttggga aaatcctctc ttctaagaa gccaatctat gatgatgatg tggatcgaat 300
 ttccctgtgc ctcaagggtc tgtctgaatg ttcaccttta atgaatgaca ttttcaataa 360
 ggaatgcaga cagtcctctt ctacatgtt atctgctaaa ctagaagaag agaaattatc 420
 ccaaaagaaa gaatctgaaa agaggaatgt gacagtacag cctgatgacc ccatttcctt 480
 catgcaacta actgctaaga atgaaatgaa ctgcaaggaa gatcagtttc ag 532

<210> 29
 <211> 486
 <212> DNA
 <213> Homo sapien

<400> 29
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 ctctctattg tcatgttgct tctttctgca aatatatctt acaagttaga ctttaaaccct 120
 ttgatctccc acaccaaaag agaaaataat atttatatgg aagtaatttt attttagtgt 180
 ttgtgattta ttgtggagag caggbgttta aaaatttttag aatttccttt taacaaaatc 240
 aaatacattg ttaaggtaac aaagaataat tcactatttc agcatttcaa agcaacatat 300
 tctacaactt caaagatatt tgcaaaaata atacaactgt tgaagttcaa atgttatgga 360

aagaaacatt agaagtatga aaagtggtag aaaaacatgt ttctttttat tctcttggat 420
 atatatctat atatttagga aaatacatat atgtatgtgt atgtatatat atgtatgaaa 480
 atatac 486

<210> 30
 <211> 240
 <212> DNA
 <213> Homo sapien

<400> 30
 aagacctgag gaaggaac aaattggctt cctgctgaag aakcaaaata gacatttttt 60
 aatgtctctt gacccagtt ccaagttcac cctgttgctt gttcttctc ccaccttttg 120
 gggttctata actgcatccc ccacacatct ttcaccacca cccatacat accagctctc 180
 ctgttggtggg attcaggaca taggaagagt tgctgaaggc acgggtgctt ttgggattcg 240

<210> 31
 <211> 233
 <212> DNA
 <213> Homo sapien

<400> 31
 ccattgatgc aggatatcgg cacattgact gtgcctatgt ctatcagaat gaacatgaag 60
 tgggggaagc catccaagag aagatccaag agaaggctgt gaagcgggag gacctgttca 120
 tcgtcagcaa gttgtggccc actttctttg agagaccctt tgtgaggaaa gcctttgaga 180
 agaccctcaa ggacctgaag ctgagctatc tggacgtcta tcttattcac tgg 233

<210> 32
 <211> 233
 <212> DNA
 <213> Homo sapien

<400> 32
 gaggaatgct ggactggagg cccctggagc cagatggcaa gagggtgaca gcttcctttc 60
 ctgtgtgtac tctgtccagt tccttttagaa aaaatggatg cccagaggac tcccaaccct 120
 ggcttggggg caagaaacag ccagcaagag ttaggggcct tagggcactg ggctgttgtt 180
 ccattgaagc cgactctggc cctggccctt acttgcttct ctagtctctt agg 233

<210> 33
 <211> 319
 <212> DNA
 <213> Homo sapien

<400> 33
 ctgggccttg atggtctagg atagccttac tcaattgcct ggcaggtgac aggctgttgg 60
 ctggaattgc ttggttctcc tccatgtggc ctctccagta ggctagctca ggcttattca 120
 catgatggct tcaggattcc aaagagagt agagtagaag ctgaaagact tcttgagttc 180
 ttggcctgga actgggacta ggacagtgtc acttctgcta agttcttttg gtcagagcaa 240
 atcacaaggc tttaccaga ttcaagggat gagaaacaga ctacatgtct tgatgagggg 300
 aaccacaaag agcttgtgg 319

<210> 34
 <211> 340
 <212> DNA
 <213> Homo sapien

<400> 34

tacagattta	attcatgtta	ttaaactcct	gccttttacc	tcttccctcc	tcccttgga	60
caactgccag	atggatgtgg	ctggaagtca	gaggacattc	tctgtgggttc	gtgggcctag	120
ggtacaaatg	acctcagcgt	gacagcaaac	aggacagaga	agaccaggct	cttactcagg	180
aatccaccag	ccaggagaat	gacaatgttg	aacaccggaa	ccctgatgat	atctgtcaca	240
tttghtaagg	tgatttcaga	gtcaggagtg	gagacatcgg	cagttgactt	gggtggagct	300
tgggtcacag	ttctggggct	ggtatagagt	gggcacaagg			340

<210> 35

<211> 170

<212> DNA

<213> Homo sapien

<400> 35

acatgggtcc	ttactcctc	gctgagatgt	tgccgcagcc	ttttcttcca	atgcggttgt	60
ggcaggagaa	tccacggatg	taatgttttc	acctttttcc	ctgaggggtgc	tttctgagga	120
accagycctt	aagaggtggg	gtcttggatt	cctgaccag	gcgtccggca		170

<210> 36

<211> 475

<212> DNA

<213> Homo sapien

<400> 36

ctgttttttg	acttaattaa	ccattgcaag	tggaaaccaa	gaaataattg	tagcataact	60
ctctctattg	kcatgttgct	tctttctgca	aatatatctt	agaagttaga	ctttaaacct	120
ttgatctccc	acaccaaag	agaaaataat	atttatatgg	aagtaatttt	attttagtgt	180
ttgtgattta	ttgtggagag	caggtgttta	aaaattttag	aatttcttta	acaaaattct	240
aaagagaaaa	taaaaaagaa	atcacagtat	ttacagagat	aacagaatgg	cttagccatg	300
caaaacaaat	aacttttggt	tttccctttt	tactttgggt	taaatgttga	ccaagattca	360
attttttttc	ctgccaaata	aaacttcaat	aaaagtttag	aggcaaaata	acgtattttc	420
tttttttccc	ataataat	atacagcatc	gagtctaaga	atattttatg	cattt	475

<210> 37

<211> 246

<212> DNA

<213> Homo sapien

<400> 37

ccttgagctt	gggccgggca	ctgaggcgcc	ccacatatgc	tgagagcagg	gggaacgcat	60
ccaggcagcc	aggggctagg	acctcatgga	tcagcagcaa	gtccagcagg	ttgtagtcag	120
cgaaggagat	ctggtctccc	acaatgaagg	tcttgccctc	ctggttctgg	gacagcaggg	180
tctcaaaagg	cttcagttgc	ccgggcagtg	ccttcacata	gtcatccttg	cccacctcat	240
agttgg						246

<210> 38

<211> 512

<212> DNA

<213> Homo sapien

<400> 38

gctggaagtg	aaatgcagat	cagacccatt	gtgatgtcac	agaaagatgg	ggacaggcca	60
aagaaaaaag	tgactttcaa	ctcttcttcc	atcattttta	tcatcaccag	tgatgaatca	120
ctgtcagttg	acgacagcga	caaaaccaat	gggtccaaag	ttgatgtaat	ccaagtctcg	180
cctttgtagg	aatgaagaat	ggcaacgaaa	gatggggcct	taaattggat	gccacttttg	240

gactttcatc	ataagaagtg	tctggaatac	ccgttctatg	taatatcaac	agaaccttgt	300
gggccagcag	gaaatccgaa	ttgcccatac	gctcttgggc	ctcaggaaga	ggttgaacaa	360
aaacaaattc	ttttaattca	acgggtgctt	tacataatga	aaaaaccact	tgtggcacac	420
gatgggcatc	taacatcatc	atcttctaat	gtgttgga	ttttcatttc	aaatatatct	480
tttaaattac	tctattttcc	aaaacacgta	at			512

<210> 39

<211> 370

<212> DNA

<213> Homo sapien

<400> 39

ttttatgaac	aagatataag	gatcaaaaaa	aagggtgttg	atatgttttt	ccaagcagag	60
atgtactega	ctctgtccta	tttagccttc	ccatacctga	cttctaatac	cttttcctgg	120
tgccttycca	tctccctaac	ccccctcac	agggatgcct	cctccaagg	ctccagaaac	180
tctgaccctc	gcactgctgg	aggagacca	tgaattgctg	gtcaatatcg	ctcatcctct	240
akactccatc	ctgcgtgtgc	ttcttcctac	aagagctaga	gaggcactga	ctgataaata	300
cctgtcacct	gcccctttcc	cagaggggtga	aactccaccc	actcccactg	cagaaatgaa	360
tcttaaatgg						370

<210> 40

<211> 204

<212> DNA

<213> Homo sapien

<400> 40

cctgaggggt	ttccctttaa	attttcattg	agttgtccat	ctccagcata	tagggcttca	60
ggagcagagc	agacctgtt	tttagtggtt	ccatgggata	aaatgggatt	ggaggagcta	120
gaagaattca	gggtctggtc	caatctgcca	gtcttcttga	aatatcgaaa	atacaccagg	180
gctgtatat	cagagccacc	ctgg				204

<210> 41

<211> 447

<212> DNA

<213> Homo sapien

<400> 41

caggcagcaa	ttcgtaaaga	attaaatgag	tacaaaagta	atgaaatgga	ggtacatgca	60
tcaagcaagc	acttgacaag	attccacagg	ccatagagat	tttcttctga	gaagaatttg	120
tgtttaattt	tttgatacca	acactgaaca	ttcatcaggg	aactttcctg	aagttcagct	180
caagactacc	ctacctgctg	tgtttgtag	aagagtagga	tcacacacac	aggtgcaatc	240
ttgaccacac	ttacctgcaa	gaggagtaac	cagaggacac	acttccttcc	ttctttgggtg	300
tctgaggagt	gtgaactggt	gggtcagtt	aagacccaac	ataactctat	cagaagaaaa	360
ctgttggttg	cctttcaacc	ttgttttaca	gttctgcagt	gtagtggagg	acgggcaacg	420
tgcattgtgca	ggctcaccac	tcccagg				447

<210> 42

<211> 498

<212> DNA

<213> Homo sapien

<400> 42

ctgggtttgt	aaaaacagtc	tctttattct	actgtgctga	aaccctcacc	aatatagaaa	60
attagattct	cattgcactg	aactatattt	atatgcctaa	gtatgtagaa	gtaaaattat	120
ataccccaaa	aggattttat	cttggtgtat	atattaaaatg	ttatttctgc	atatagggtc	180

ttttatggag aaactgatga tgataagctt aatactcact tgtttagcag catctgaatg	240
cacaaatgct ttatatatct cttctgcttt acagggcaaa agatcagact ctgttttctt	300
atagtcttca caagccagcc agaactcaat attctcctca ctgaattcag actttaggaa	360
acttccaaa acattttgac cagtttggtt ggcaagaagt tttccagag attgagacca	420
ttgcattact tcagcagcag aaagtacatc cttggacttg gaagatttca ttccagattc	480
cagatgtggg atcataga	498

<210> 43

<211> 312

<212> DNA

<213> Homo sapien

<400> 43

caggaaggcg gccaaagaatg tgagtgc aaa gattggttcc tgagagcccc gagaagaaaa	60
ttcatgacag tgtctgggct gccaaagaag cagtgcctt gtgatcattt caagggcaat	120
gtgaagaaaa caagacacca aaggcaccac agaaagccaa acaagcattc cagagcctgc	180
cagcaatttc tcaacaatg tcagctaaga agctttgctc tgcctttgta ggagctctga	240
gcgcccactc ttccaattaa acattctcag ccaagaagac agtgagcaca cctaccagac	300
actcttcttc tc	312

<210> 44

<211> 417

<212> DNA

<213> Homo sapien

<400> 44

ctaacacatt tactctccac tattcgtact ctggtagcca tgtaacccc atcagagatt	60
ccttctcaag ccatgtctca gagctgagag gcatcccagc aagttttgca gctcacagtt	120
ttttccgtaa attacttatt ctataaaatt ggagtaggcc ataaactttg gagggcccta	180
gaccaatttt ttggattatt tttcgtcttc tatcattecg ctgatcttag atattctctg	240
cattaaatat taaatatcac ttctaggctg aaaaatcccc ctaaaaatat ttctagctca	300
gatttttctt ccaaatcttg caatagaaga tcacaatgtg aactctgcat ctccatgtta	360
aagtctaattg gacattcaca cttagcatgt ctcaaagaaa tctcatgtaa accatgg	417

<210> 45

<211> 494

<212> DNA

<213> Homo sapien

<400> 45

cgcggtgctg tggtatgtgt acacgtgcat gttctgcatg tctgtaggtc acacatgctt	60
tggtgcatgt acacgtgtgt gtgtgtatgc gtgtaggagc tcacacttgt gtacacgttt	120
gtgtgcatgc atgtgtgcag gagcttgac gtttgtggtg ggtacatgta catatgtgag	180
tgatcctgtg tgcaagcccc catgtggaca tggtatgag tgagcgtgga gccaaaagcc	240
aggtaacacg catgcagcag gccactgtg cgtgtctgag acggtctgtg gcagggactg	300
ggtgtgaatc atgcagcagg cccactgtg gtgtctgaga cggctctgtg cagggactgg	360
gtgtgaatca gtgaccgtgt ctctgaccaa catgctgaat taaaaattga taatttatta	420
acctgtgcag caacaaataa gatttttcaa aactcaacaa agtgctcaaa gttgacatta	480
cttgcttcaa agtt	494

<210> 46

<211> 516

<212> DNA

<213> Homo sapien

<400> 46

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cttctattgc	taattttgtg	acctccaaag	ctttacttct	cggaacctcc	tcctttggcc	120
gtcatttgat	cattcaactc	tttgtcagtg	gcaactcccg	ctattttggg	gtgttggttt	180
gttactacac	agtgcagaca	aacatgggtg	tccaatacag	aggctcttcc	tgtaggtgtg	240
caaccagaaa	gttcatctaa	cactgtgata	tttgcatact	tcttgaacag	ttgttggtctg	300
aagattcatt	tgatgaatcg	atTTTTcaaa	agagatgatt	cttggttctt	ccgagcgctc	360
agctctcccg	ccgagcttct	ttgagacgtc	ctcaggtgtc	ctttgacgat	gcgtcctcca	420
ctttcacaca	ctctagcatt	ccttcactgg	ggtcttcatt	gccccacatt	gggcagccag	480
gaatgttggg	gtgatcagac	acaacaccag	gtcatg			516

<210> 47

<211> 459

<212> DNA

<213> Homo sapien

<400> 47

ccaattcaga	gtggcattct	gcatttctgt	ggcttccaag	tcttagaacc	tcaactgaca	60
tatagcattg	ggcacactcc	agcagacgcc	cgaattcaaa	tcctggaagg	atggaagaaa	120
cgccctggaga	atatttgga	tgagacacca	ctgtattttg	ctccaagcag	cctctttgac	180
ctaaacttcc	aggcaggatt	cttaattgaa	aaagaggtac	aggatgagga	gaaaaacaag	240
aaatttgcc	tttctgtggg	ccatcacttg	ggcaagtcca	tcccaactga	caaccagatc	300
aaagctagaa	aatgagattc	cttagcctgg	atttcttctt	aacatgttat	caaactctggg	360
tatctttcca	ggcttccctg	acttgcttta	gtttttaaga	tttgtgtttt	tctttttcca	420
caaggaataa	atgagaggga	atcgaksaaa	aaaaaaaaa			459

<210> 48

<211> 430

<212> DNA

<213> Homo sapien

<400> 48

cctatatcca	gccacagcct	ctgggagtg	tgctgataat	cggagcttgg	aattaccctt	60
tcgtttctac	cattcagcca	ctgataggag	ccatcgctgc	aggaaatgct	gtgattataa	120
agccttctga	actgagtga	aatacagcca	agatcttggc	aaagcttctc	cctcagtatt	180
tagaccagga	tctctatatt	gttattaatg	gtgggtgtga	ggaaaccacg	gagctcctga	240
agcagcgatt	tgaccacatt	ttctatacgg	gaaacactgc	gggtggcaaa	attgtcatgg	300
aaagtgtctg	caagcatctg	accctgtga	ctcttgaact	gggagggaaa	agtccatgtt	360
atattgataa	agattgtgac	ctggacattg	tttgcagacg	cataacctgg	ggaaaatata	420
tgaattgtgg						430

<210> 49

<211> 288

<212> DNA

<213> Homo sapien

<400> 49

ccatccgaag	caagattkca	gatggcagtg	tgaagagaga	agacatattc	tacacttcaa	60
agctttggwg	caattcccat	cgaccagagt	tggtccgacc	agccttgga	aggctactga	120
aaaatcttca	attggattat	gttgacctct	accttattca	ttttccagt	tctgtaaagc	180
caggtgagga	agtgatccca	aaagatgaaa	atggaaaaat	actatttgac	acagtggatc	240
tctgtgccac	gtgggaggcc	rtggagaagt	gtaaagatgc	aggattgg		288

<210> 50

<211> 411

<212> DNA

<213> Homo sapien

<400> 50

ccagagaatg	acattcatgt	ccccgtggat	cccttgcaga	gagtacatgg	agccactgcc	60
accagtgggtg	atggaaagca	ctgtcttctt	actccggaag	ggtcctttgt	catacatggc	120
agcgttaagt	taagcaaact	ctcctatgaa	cactcgctca	aaccagcctt	tcagaatggc	180
agggactcca	aaccactgca	gggggaactg	gaatatcaca	aggtctgcgg	cttccagctt	240
cttttgttca	gccacaatat	ctgggctcag	atggccttct	ttataagcca	gaacagactc	300
ggcaggatac	tgaaagtctg	cagggtcctt	cagtttacct	gtgatgtcct	ttctggaaat	360
gatgggattg	aagttcatgg	catagaggtc	cgactccacc	acctcccatc	c	411

<210> 51

<211> 503

<212> DNA

<213> Homo sapien

<400> 51

gatatcttat	gattaaaaac	aaattaaatt	ttaaaacacc	tgaagatata	ttagaagaaa	60
ttgtgcaccc	tccacaaaac	atacaaagtt	taaaagtttg	gatctttttc	tcagcaggta	120
tcagttgtaa	ataatgaatt	aggggccaaa	atgcaaaacg	aaaaatgaag	cagctacatg	180
tagttagtaa	tttctagttt	gaactgtaat	tgaatattgt	ggcttcatat	gtattatttt	240
atattgtact	tttttcatta	ttgatggttt	ggactttaat	aagagaaaatt	ccatagtttt	300
taatatccca	gaagtgaagc	aatttgaaca	gtgtattcta	gaaaacaata	cactaactga	360
acagaagtga	atgcttatat	atattatgat	agccttaaac	ctttttcctc	taatgcctta	420
actgtcaaat	aattataacc	ttttaaagca	taggactata	gtcagcatgc	tagactgaga	480
ggtaaacact	gatgcaatta	aga				503

<210> 52

<211> 503

<212> DNA

<213> Homo sapien

<400> 52

gatatcttat	gattaaaaac	aaattaaatt	ttaaaacacc	tgaagatata	ttagaagaaa	60
ttgtgcaccc	tccacaaaac	atacaaagtt	taaaagtttg	gatctttttc	tcagcaggta	120
tcagttgtaa	ataatgaatt	aggggccaaa	atgcaaaacg	aaaaatgaag	cagctacatg	180
tagttagtaa	tttctagttt	gaactgtaat	tgaatattgt	ggcttcatat	gtattatttt	240
atattgtact	tttttcatta	ttgatggttt	ggactttaat	aagagaaaatt	ccatagtttt	300
taatatccca	gaagtgaagc	aatttgaaca	gtgtattcta	gaaaacaata	cactaactga	360
acagaagtga	atgcttatat	atattatgat	agccttaaac	ctttttcctc	taatgcctta	420
actgtcaaat	aattataacc	ttttaaagca	taggactata	gtcagcatgc	tagactgaga	480
ggtaaacact	gatgcaatta	aga				503

<210> 53

<211> 531

<212> DNA

<213> Homo sapien

<400> 53

tttttttttt	tttttaaaat	gaggatattt	tattatttca	ggtaattttc	ccagaggkga	60
gaatagtaca	tgggaaattc	tctttaggcc	aggtctagta	ttacagkgtg	gkgctcaagg	120
ccgcccatac	gaacagtgat	actctcccaa	cagatttcat	ccaccccgtc	tccactaact	180
tttgccataa	aaattcctct	gaattgtatc	ttcttggaag	aagtaaatat	ctgttcgact	240
atacaaagaa	acagagaaac	cactcccatc	gcaatcaatc	ttcaagagag	ggagcaggga	300

agccgtgttc	tttctgctga	gttttataga	ctctgacaag	ctgtgaaata	aacataaaca	360
gaagacaaaa	cagtgccaca	aataagcagt	agatgaccct	gtgacaagac	ggcattgcag	420
aacaaagact	gacgtttaa	ggggagtcac	gcagagtaac	atgggaacac	aagcctgaca	480
acctggtcag	cttccactta	ctctagctcc	tttgaactct	caacactaaa	a	531

<210> 54

<211> 450

<212> DNA

<213> Homo sapien

<400> 54

ccatgggtgt	ctggagwcc	ctgaaactgt	atcaaagttg	tacatatattc	caaacatttt	60
taaaatgaaa	aggcactctc	gtgttctcct	cactctgtgc	actttgctgt	tgggtgtgaca	120
aggcatttraa	agatgtttct	ggcattttct	ttttatttgt	aagggtggtg	taactatggt	180
tattggctag	aaatcctgag	ttttcaactg	tatatatcta	tagtttgtaa	aaagaacaaa	240
acaaccgaga	caaacccttg	atgtcccttg	ctcggcggtg	aggctgtggg	gaagatgcct	300
tttgggagag	gctgtagctc	agggcggtgca	ctgtgaggct	ggacctgttg	actctgcagg	360
gggcatccat	ttagcttcag	gttgtcttgt	ttctgtatat	agtgacatag	cattctgctg	420
ccatcttagc	tgtggacaaa	ggggggtcag				450

<210> 55

<211> 648

<212> DNA

<213> Homo sapien

<400> 55

caacttcaac	cacaggctgc	tggasatgat	cctcarcaag	ccagggtctca	agtacaagcc	60
tgtctgcaac	caggtggaat	gtcatcctta	cttcaaccag	agaaaactgc	tggatttctg	120
caagtcaaaa	gacattgttc	tggttgccta	tagtgctctg	ggatcccacc	gagaagaacc	180
atgggtggac	ccgaactccc	cggtgtctct	ggaggaccca	gtcctttgtg	ccttggcaaa	240
aaagcacaa	cgaaccccag	ccctgattgc	cctgcgctac	cagctrcagc	gtggggttgt	300
ggctctggcc	aagagctaca	atgagcagcg	catcagacag	aacgtgcagg	tgtttgaatt	360
ccagttgact	tcagaggaga	tgaagccat	agatggccta	aacagaaatg	tgcgatattt	420
gacccttgat	atthttgtctg	gccccctaa	ttatccattt	tctgatgaat	attaacatgg	480
agggcattgc	atgaggtctg	ccagaaggcc	ctgcgtgtgg	atggtgacac	agaggatggc	540
tctatgctgg	tgactggaca	catcgccctc	ggttaaatct	ctcctgcttg	gygayttcag	600
caagctacag	caaagcccat	tggccggaaa	aaatatcaag	gggtcaaat		648

<210> 56

<211> 536

<212> DNA

<213> Homo sapien

<400> 56

ctggcatgag	aatatthttt	tttttaagt	cggtagttht	taaactgttt	gttttttaac	60
aaactataga	actcttcatt	gtcagcaaa	caaagagtca	ctgcatcaat	gaaagttcaa	120
gaacctctg	tacttaaa	cgattcgcaa	cgttctgtta	ttttttttgt	atgtttagaa	180
tgttgaaatg	tttttgaagt	taaataaaca	gtattacatt	tttaaaactc	ttctctatta	240
taacagtcaa	tttttgactc	acagcagtga	acaaaccccc	actccattgt	atgtggagac	300
tggcctccct	ataaatgtgg	tagcttcttt	tattactcag	tggacctgcc	cgggcggccg	360
ctcgaagccg	aattccagca	cactggcggc	cgttactagt	ggatccgagc	tcggtaccaa	420
gcttgcccg	aatcatgggc	atagctgttt	cctgtgtgaa	attgttatcc	gctcacaatt	480
ccacacaaca	tacgagccgg	aagcataaag	tgtaaagcct	ggggtgccta	atgagt	536

<210> 57

<211> 391

<212> DNA

<213> Homo sapien

<400> 57

aggaactact	gtcccagagc	tgaggcaagg	ggattttctca	ggtcatttgg	agaacaagtg	60
cttttagtagt	agtttaaagt	agtaactgct	actgtattta	gtgggggtgga	attcagaaga	120
aatttgaaga	ccagatcatg	ggtggtctgc	atgtgaatga	acaggaatga	gccggacagc	180
ctggctgtca	ttgctttctt	cctccccatt	tggacccttc	tctgccctta	catttttgtt	240
tctccatcta	ccaccatcca	ccagtctatt	tatttgtcta	gttgatttc	atttcttctg	300
gaaaatttat	tgtttattgg	catgtgaccc	ttgactgatg	gcttcattag	cattytgttt	360
ttcttttttg	atccttaata	gaaaactcaa	t			391

<210> 58

<211> 455

<212> DNA

<213> Homo sapien

<400> 58

gaagacatgc	ttacttcccc	ttcaccttcc	ttcatgatgt	gggaagagtg	ctgcaaccca	60
gccctagcca	acgccgcatg	agagggagtg	tgccgagggc	ttctgagaag	gtttctctca	120
catctagaaa	gaagcgctta	agatgtggca	gcccctcttc	ttcaagtggc	tcttgtcctg	180
ttgccctggg	agttctcaaa	ttgctgcagc	agcctccacc	cagcctgagg	atgacatcaa	240
tacacagagg	aagaagagtc	aggaaaagat	gagagaagtt	acagactctc	ctgggcgacc	300
ccgagagctt	accattcctc	agacttcttc	acatggtgct	aacagatttg	ttcctaaaag	360
taaagctcta	gaggccgtca	aattggcaat	agaagccggg	ttccaccata	ttgattctgc	420
acatgtttac	aataatgagg	agcagggttg	actgg			455

<210> 59

<211> 398

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(398)

<223> n = A,T,C or G

<400> 59

ctcagaggca	gcgtgcgggt	gtgctctttg	tgaaattcca	ccatggcgta	ccgtggccag	60
ggtcagaaa	gagagaagg	tatggtgcag	cccatcaacc	tcactctcag	atacttataa	120
aatagatcgc	ggattcagg	gtggctctat	gagcaagtga	atatgcggat	agaaggctgt	180
atcattggtt	ttgatgagta	tatgaacctt	gtattagatg	atgcagaaga	gattcattct	240
aaaacaaagt	caagaaaaca	actngntcgg	atcatgctaa	aaggagataa	tattactctg	300
ctacaaagt	tctccaacta	gaaatgatca	atgaagttag	aaattgttga	gaaggatata	360
gtttgttttt	agatgtcctt	tgtccaatgt	gaacattt			398

<210> 60

<211> 532

<212> DNA

<213> Homo sapien

<400> 60

gacttctgag	acctggggca	cccgggcctt	tgccgcagct	actggcagg	cctggccacc	60
tcataggact	cagttccctt	ctgaacactc	gggggacatg	ggcctctaac	tgcccactct	120
gatatgcctg	ggtgagccta	ggaggggaagg	ctctgatttg	gatttctcca	gtcaaagctc	180

acagaaaaaa	acctggcact	ttgattttca	tgggatggtc	ctaacagggc	cagtcacctc	240
cgagcagttt	gggaaccag	tttcttgctc	tgggccctca	ggtcagcctg	gctgaattag	300
gaccttcct	tggcacagg	gtgagaaaga	gcttggggaa	cgcttggcat	tatggagggc	360
tggaaagggc	tcaacccga	tttgagagaga	agtttgggat	ggagtgggcg	agagattgag	420
agagcgagca	ggaaaagagg	tcttggagcc	tgggactgat	ggtggataag	gcctggaaag	480
aasatgacsa	ggaggaggag	agaggggaagt	gggtggatga	ggagcaggct	ga	532

<210> 61

<211> 466

<212> DNA

<213> Homo sapien

<400> 61

gcgacggcga	cgtctctttt	gactaaaaga	cagtgtccag	tgctccagcc	taggagtcta	60
cggggaccgc	ctcccgcgcc	gccaccatgc	ccaacttctc	tggcaactgg	aaaatcatcc	120
gacggaaaaa	cttcgaggaa	ttgctcaaag	tgctgggggt	gaatgtgatg	ctgaggaaga	180
ttgctgtggc	tgcagcgtcc	aagccagcag	tggagatcaa	acaggaggga	gacactttct	240
acatcaaaac	ctccaccacc	gtgcgcacca	cagagattaa	cttcaagggt	ggggaggaggt	300
ttgaggagca	gactgtggat	gggaggccct	gtaagagcct	ggtgaaatgg	gagagtgaga	360
ataaaatggt	ctgtgagcag	aagctcctga	agggagaggg	ccccaaagacc	tcgtggacca	420
gagaactgac	caacgatggg	gaactgatcc	tgaccatgac	ggcgga		466

<210> 62

<211> 548

<212> DNA

<213> Homo sapien

<400> 62

ttttgaattt	acaccaagaa	cttctcaata	aaagaaaatc	atgaatgctc	cacaatttca	60
acataccaca	agagaagtta	atttcttaac	attgtgttct	atgattattt	gtaagacctt	120
caccaagttc	tgatatcttt	taaagacata	gttcaaaatt	gcttttgaaa	atctgtattc	180
ttgaaaatat	ccttggtgtg	tattagggtt	ttaaatacca	gctaaaggat	tacctcactg	240
agtcattcagt	accctcctat	tcagctcccc	aagatgatgt	gtttttgctt	accctaagag	300
aggttttctt	cttattttta	gataattcaa	gtgcttagat	aaattatgtt	ttctttcaagt	360
gtttatggta	aactctttta	aagaaaattt	aatatgttat	agctgaatct	ttttggtaac	420
tttaaatctt	tatcatagac	tctgtacata	tgttcaaatt	agctgcttgc	ctgatgtgtg	480
tatcatcggt	gggatgacag	aacaaacata	tttatgatca	tgaataatgt	gctttgtaaa	540
aagatttc						548

<210> 63

<211> 547

<212> DNA

<213> Homo sapien

<400> 63

tttccaaagc	ggagacttcc	gacttcctta	caggatgagg	ctgggcattg	cctgggacag	60
cctatgtaag	gccatgtgcc	ccttgcccta	acaactcact	gcagtgtctt	tcatagacac	120
atcttgcagc	atctttctta	aggctatgct	tcagtttttc	tttgtaagcc	atcacaagcc	180
atagtggtag	gtttgccctt	tggtagagaa	ggtaggttaa	agctgggtgga	aaaggcttat	240
tgcattgcat	tcagagtaac	ctgtgtgcat	actctagaag	agtagggaaa	ataatgcttg	300
ttacaattcg	acctaatatg	tgcattgtaa	aataaatgcc	atatttcaaa	caaaaacacgt	360
aattttttta	cagtatgttt	tattaccttt	tgatatctgt	tggtgcaatg	ttagtgtatg	420
tttaaaatgt	gatcgaaaat	ataatgcttc	taagaaggaa	cagtagtgga	atgaatgtct	480
aaaagatctt	tatgtgttta	tggtctgcag	aaggattttt	gtgatgaaag	gggatttttt	540
gaaaaat						547

<210> 64
 <211> 528
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1) ... (528)
 <223> n = A,T,C or G

<400> 64
 cacctmctcc cscwggcgc ttwctcsgac gccttgccca scgggcccgc cgaccccctg 60
 srccatggac cccgctcgcc csctggggmt gtygatktcg ctgcttttcc tgrckgaggc 120
 tgcactgggc gatgctgac argagccaac aggaaataac rcggagatct gkctcctgcc 180
 cctagactac kgaccctgcc kggccctact tytccgytac tactacgaca ggyacacgca 240
 gagctgccgc cwgttcctgk rckggggctg crasggcaac rccaacwatt yctacacckg 300
 kgaggmttrc gackatgctw gstggargat agaaaaagtt cccaaasttt gccggctgma 360
 agtgaatgag gacnaccagg gtgaggggta cacagataag tatttcttta atctaakkwc 420
 catgacatgw gaaaaattct ttncgggtgg gngtcaccgg accggattga gaacangttt 480
 gcagatgang ctactgggat gggctcctgc rcacnaaaga aantatca 528

<210> 65
 <211> 547
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1) ... (547)
 <223> n = A,T,C or G

<400> 65
 kgaatgaasa acgaacgctg gaagtagaaa tagagcctgg ggtgagagac ggcattggagt 60
 acccctttat tggagaaggt gaggctcacg tggatgggga gcctggagat ttacggttcc 120
 gaatcaaagt tgtcaagcac ccaatatctg aaaggagagg agatgatttg tacacaaatg 180
 tgacagtctc attagttgag tcaactgggtg gctttgagat ggatattact cacttggatg 240
 gtcacaaggt acatatctcc cgggataaga tcaccaggcc aggagcgaag ctatggaaga 300
 aagggggaagg gctccccaac ttgacaaca acaatatcaa gggctctttg ataatacactt 360
 ttgatgtgga ttttccaaaa gaacagttaa cagaggaagc gagagaangt atcaaacagc 420
 tactgaaaca agggtcagtg cagaagggtat acaatggact gcaaggatat tgagagtga 480
 taaaattgga ctttgtttta aataaagtga ataagcgata tttattatct gcaagggtttt 540
 ttttgtg 547

<210> 66
 <211> 535
 <212> DNA
 <213> Homo sapien

<400> 66
 ggggaggtct acgcttctag agcttgagcc agcggggcga ccctgcagtg gcaggactcg 60
 gcaccgcgcc ctccaccgcc gggttggtggc ctgcgtgaca gtttctctcc gtcgacatcg 120
 aaaggaagcc ggacgtgggc gggcagagag cttcatcgca gtaggaatgg cagccccatc 180
 tatgaaggaa agacaggtct gctggggggc ccgggtagag tactggaagt gtttagatga 240
 gaacttagag gatgcttctc aatgcaagaa gttaagaagc tctttcgaat caagtgtgcc 300

ccaacagtgg	ataaaatatt	ttgataaaaag	aagagactac	ttaaaattca	aagaaaaatt	360
tgaagcagga	caatttgagc	cttcagaaaac	aactgcaaaa	tcctaggctg	ttcataaaga	420
ttgaaagtat	tctttctgga	cattgaaaaa	gctccactga	ctatggaaca	gtaatagttt	480
gaatcatagt	gaacatcaat	acttgttccc	tatatacgac	acttgataat	taaga	535

<210> 67
 <211> 527
 <212> DNA
 <213> Homo sapien

<400> 67						
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ttcatcttct	acaaggccct	cttagctcta	aaacttgaca	gtggaataag	gaaatgtttt	120
tccaaatctg	cattgccggt	gagatcctca	acatcagcat	gttgagatgg	acctcaaccc	180
cacctctaac	cctgaaacac	actactcgat	attatcttag	gtatgtttta	gggttttagtt	240
tgtaaaataa	taatttattt	ttgaaggaaa	tataaaatat	taaagagtaa	taatagctat	300
cattttttta	gattcaatct	aaaacaatgg	actctttttt	ttccatttg	tgatgtagat	360
aagcaagaca	attttgatca	tgagtgggtga	aaagaggatc	aaacttgact	attcttgcaa	420
tggcagtgcca	gcaacaagcc	tttcattttac	attaaattat	aacttttcat	tcatttcctaa	480
accaaactta	aaattctgct	ttcctttgag	tagaagggtat	ttaactt		527

<210> 68
 <211> 431
 <212> DNA
 <213> Homo sapien

<400> 68						
gggaaacttc	atgggtttcc	tcatctgtca	tgctgatgat	tatatatgga	tacatttaca	60
aaaataaaaa	gcgggaattt	tcccttcgct	tgaatattat	ccctgtatat	tgcatgaatg	120
agagatttcc	cataattcca	tcagagtaat	aaatataact	gctttaattc	ttaagcataa	180
gtaaacatga	tataaaaaata	tatgctgaat	tacttggtga	gaatgcattt	aaagctattt	240
taaatgtgtt	tttatttgta	agacattact	tattaagaaa	ttggttatta	tgcttactgt	300
tctaactctg	tggtaaagg	attcttaaga	atttgcagg	actacagatt	ttcaaaactg	360
aatgagagaa	aattgtataa	ccatcctgct	gwtcctttag	tgcaatacaa	taaaactctg	420
aaattaaaac	t					431

<210> 69
 <211> 399
 <212> DNA
 <213> Homo sapien

<400> 69						
gacacggcgg	acacacacaa	acacagaacc	acacagccag	tcccaggagc	ccagtaatgg	60
agagccccaa	aaagaagaac	cagcagctga	aagtcgggat	cctacacctg	ggcagcagac	120
agaagaagat	caggatacag	ctgagatccc	agtgcgcgac	atggaagggtg	atctgcaaga	180
gctgcatcag	tcaaaccacc	gggataaatc	tggttttggg	ttccggcgtc	aagggtgaaga	240
taatacctaa	agaggaacac	tgtaaaatgc	cagaagcagg	tgaagagcaa	ccacaagttt	300
aaatgaagac	aagctgaaac	aacgcaagct	ggtttttat	tagatatattg	acttaaaacta	360
tctcaataaa	gttttgcagc	tttcaccaar	aaaaaaaaa			399

<210> 70
 <211> 479
 <212> DNA
 <213> Homo sapien

<400> 70

cgcgggcgag	ctgtgagccg	gcgactcggg	tccctgaggt	ctggattctt	tctccgctac	60
tgagacacgg	cggacacaca	caaacacaga	accacacagc	cagtcccagg	agcccagtaa	120
tggagagccc	caaaaagaag	aaccagcagc	tgaaaagtcg	gatcctacac	ctgggcagca	180
gacagaagaa	gatcaggata	cagctgagat	cccagggtgt	gggaagggaa	atgcgcgaca	240
tggaaaggtg	tctgcaagag	ctgcatcagt	caaacaccgg	ggataaatct	ggatttgggt	300
tccggcgctc	aggtgaagat	aatacctaaa	gaggaacact	gtaaaatgcc	agaagcaggt	360
gaagagcaac	cacaagttta	aatgaagaca	agctgaaaca	acgcaagctg	gttttatatt	420
aggatatttg	acttaaaacta	tctcaataaaa	gttttgcagc	tttcaccaa	aaaaaaaaa	479

<210> 71

<211> 437

<212> DNA

<213> Homo sapien

<400> 71

ctcagcggct	gccaacagat	catgagccat	cagctcctct	ggggccagct	ataggacaac	60
agaactctca	caaaggacc	agacacagt	rgcaccatgg	gacagtgtcg	gtcagccaac	120
gcagaggatg	ctcaggaatt	cagtgtatgt	gagagggcca	ttgagaccct	catcaagaac	180
tttcaccagt	actccgtgga	gggtgggaag	gagacgctga	ccccttctga	gctacgggac	240
ctgggtcacc	agcagctgcc	ccatctcatg	ccgagcaact	gtggcctgga	agagaaaatt	300
gccaaccttg	gcagctgcaa	tgactctaaa	ctggagtcca	ggagtctctg	ggagctgatt	360
ggagaagcgg	ccaagagtgt	gaagctggag	aggcctgtcc	gggggcactg	agaactccct	420
ctggaattct	tggggggg					437

<210> 72

<211> 561

<212> DNA

<213> Homo sapien

<400> 72

ggatgggtata	ctgtaaattc	agcatatgga	gataaccatta	tcataccttg	ccgacttgac	60
gtacctcaga	atctcatgtt	tggcaaatgg	aaatatgaaa	agcccgatgg	ctcccagta	120
tttattgcct	tcagatcctc	tacaaaagaa	agtgtgcagt	acgacgatgt	accagaatac	180
aaagacagat	tgaacctctc	agaaaactac	actttgtcta	tcagtaatgc	aaggatcagt	240
gatgaaaaag	gatttgtgtg	catgctagta	actgaggaca	acgtgtttga	ggcacctaca	300
atagtcaagg	tgttcaagca	accatctaaa	cctgaaattg	taagcaaaag	actgtttctc	360
gaaacagagc	agctaaaaaa	gttgggtgac	tgcatttcag	aagacagtta	tccagatggc	420
aatatcacat	ggtacaggaa	tggaaaagtg	ctacatcccc	ttgaaggagc	ggtggtcata	480
atttttaaaa	aggaaatgga	cccagtgact	cagctctata	ccatgacttc	caccctggag	540
tacaagacaa	ccaaggctga	c				561

<210> 73

<211> 916

<212> DNA

<213> Homo sapien

<400> 73

ggagaaaata	aggtggagtc	ctacttgttt	aaaaaatatg	tatctaagaa	tgttctaggg	60
cactctggga	acctataaag	gcaggatatt	cgggccctcc	tcttcaggaa	tcttcctgaa	120
gacatggccc	agtcgaaggc	ccaggatggc	ttttgtctgc	gccccgtggg	gtaggagggg	180
cagagagaca	gggagagtca	gcctccacat	tcagaggcat	cacaagtaat	ggcacaattc	240
ttcggatgac	tcagaaaaat	agtgttttgt	agtccaacaa	ctcaagacga	agcttatctc	300
tgaggataag	ctctttaaag	gcaaagcttt	atcttcatct	ctcatctttt	gtcctcctta	360
gcacaatgta	aaaaagaata	gtaatatcag	aacagggaag	aggaaatggc	tgctggggag	420

cccatccagg	acactgggag	cacatagaga	ttcacccatg	tttggtgaac	ttagagtcac	480
tctcatgctt	ttctttataa	ttcacacata	tatgcagaga	agatatgttc	ttgtaacat	540
tgtatacaac	atagccccaa	atatagtaag	atctatacta	gataatccta	gatgaaatgt	600
tagagatgct	atatgataca	actgtggcca	tgactgagga	aaggagctca	cgcccagaga	660
ctgggctgct	ctcccgagg	ccaaacccaa	gaaggctctg	caaagtcagg	ctcagggaga	720
ctctgccctg	ctgcagacct	cggtgtggac	acacgctgca	tagagctctc	cttgaaaaca	780
gaggggtctc	aagacattct	gcctacctat	tagcttttct	ttattttttt	aactttttgg	840
ggggaaaagt	atttttgaga	agtttgtctt	gcaatgtatt	tataaatagt	aaataaagtt	900
tttaccatta	aaaaaa					916

<210> 74

<211> 547

<212> DNA

<213> Homo sapien

<400> 74

agtggcatta	acttttagaa	tttgggctgg	tgagattaat	tttttttaat	atcccagcta	60
gagatatggc	ctttaactga	cctaaagagg	tgtgttggtga	tttaattttt	tcccgttccct	120
ttttcttcag	taaacccaac	aatagtctaa	ccttaaaaaat	tgagttgatg	tccttatagg	180
tactacccc	taaataaacc	tgaagcagg	gttttctctt	ggacatacta	aaaaataacct	240
aaaaggaagc	ttagatgggc	tgtgacacaa	aaaattcaat	tactgtcatc	taatgccagc	300
tgttaaaagt	gtggccactg	agcatttgat	tttataggaa	aaaatagtat	ttttgagaat	360
aacatagctg	tgctattgca	catctgttgg	aggacatccc	agatttgctt	atactcagtg	420
cctgtgatat	tgagtttaag	gatttgaggc	aggggtaatt	attaaacata	ttgcttctat	480
tcttggaata	atagaagkgt	aaaatgttaa	taatacaaat	gtcactgtga	cctcctccac	540
tgagagg						547

<210> 75

<211> 793

<212> DNA

<213> Homo sapien

<400> 75

tgaggaagtt	gcaagccaac	aaaaaagttc	aaggatctag	aagacgatta	aggggaaggtc	60
gttctcagtg	aaaatccaaa	aaccagaaaa	aatgttttat	acaaccctaa	gtcaataaac	120
tgaccttaga	aaattgtgag	agccaagttg	acttcaggaa	ctgaaacatc	agcaciaaaga	180
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gagggaaatt	gtggagttag	cctcctgtgg	agttagcctc	ctgtggtaaa	ggaattgaag	300
aaaatataac	accttacacc	ctttttcatc	ttgacattaa	aagttctggc	taactttgga	360
atccattaga	gaaaaatcct	tgtcaccaga	ttcattacaa	ttcaaatacga	agagtgtgga	420
actgttatcc	cattgaaaag	accgagcctt	gtatgtatgt	tatggatata	taaaatgcac	480
gcaagccatt	atctctccat	gggaagctaa	gttataaaaa	taggtgcttg	gtgtacaaaa	540
ctttttatat	caaaaggctt	tgacacattc	tatatgagtg	ggtttactgg	taaattatgt	600
tattttttac	aactaatttt	gtactctcag	aatgtttgtc	atatgcttct	tgcaatgcac	660
attttttaat	ctcaaacgtt	tcaataaaac	catttttccag	atataaagag	aattacttca	720
rattgagtaa	ttcagaaaaa	ctcaagattt	aagttaaaaa	gtgggtttgga	cttggggaaca	780
ggactttata	cct					793

<210> 76

<211> 461

<212> DNA

<213> Homo sapien

<400> 76

accttgcact	attcccctca	gtccatctat	cgaggctctt	gcaggaagca	tactgggaat	60
------------	------------	------------	------------	------------	------------	----

tgaacgaga	gcctaaatga	catctaagaa	aggcagtgtt	caataccagg	tattaggtga	120
ggatgggatt	ctaaggacat	cagtgggagg	caggagacca	ccttcagacc	tcagcatgga	180
agcttccaag	atccagagga	agaggcaaca	gcactgagag	tcataggtag	aagaatcatc	240
acagccctgc	taaccaggca	gctgatgccc	ctctcccctg	gctccctgtg	tccaaatcct	300
acaggggcat	ctgttggtg	aactcaacct	gaagccaaag	agaagatgag	tggagagagg	360
caacatttat	agagctcagg	tttctagggc	tggagagggg	tctggagggg	cacacaggag	420
acacctggca	taaccaaaaa	atgattaaaa	aaaaaaaaaa	a		461

<210> 77

<211> 642 <212> DNA

<213> Homo sapien

<400> 77

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gctgtgagac	tacctattgt	agatattgca	ccctatgaca	ttggtggtcc	tgatcaagaa	120
tttgggtggtg	acgttggccc	tggttgcttt	ttataaacca	aactctatct	gaaatcccaa	180
caaaaaaat	ttaactccat	atgtgttctt	cttggtctaa	tcttgtcaac	cagtgcgaag	240
gaccgacaaa	attccagtta	tttatttcca	aatgttttg	aaacagtata	atttgacaaa	300
gaaaaatgat	acttctcttt	ttttgctgtt	ccaccaaata	caattcaa	gctttttgtt	360
ttattttttt	accaattcca	atttcaaat	gtctcaatgg	tgctataata	aataaacttc	420
aacactcttt	atgataacaa	aaaaaarawa	wattctttga	atcctagccc	atctgcagag	480
caatgactgt	gctcaccagt	aaaagataac	ctttctttct	gaaatagtca	aatacgaaat	540
tagaaaagcc	ctccctattt	taactacctc	aactggtcag	aaacacagat	tgtattctat	600
gagtcccaga	agatgaaaaa	aattttatac	gttgataaaa	ct		642

<210> 78

<211> 519

<212> DNA

<213> Homo sapien

<400> 78

gcagaagaag	aagcggacct	tccgcaagtt	cacctaccgc	ggcgtggacc	tcgaccagct	60
gctggacatg	tcctacgagc	agctgatgca	gctgtacagt	gcgcgccagc	ggcggcggtc	120
gaaccggggc	ctgcggcgga	agcagcactc	cctgctgaag	cgcctgcgca	aggccaagaa	180
ggaggcgccg	cccattggaga	agccggaagt	ggtgaagacg	cacctgcggg	acatgatcat	240
cctacccgag	atggtgggca	gcatgggtgg	cgtctacaac	ggcaagacct	tcaaccaggt	300
ggagatcaag	cccagatga	tcggccacta	cctgggcgag	ttctccatca	cctacaagcc	360
cgtaaaagcat	ggccggcccc	gcctcggggc	cacctactcc	tcccgttca	tccctctcaa	420
gtaatggctc	agctaataaa	aggcgcacat	gactccaaaa	aaaaaaaaaa	aaggcgggcc	480
gccaccgcgg	gggagctcca	ctttgtttcc	ctttaatga			519

<210> 79

<211> 526

<212> DNA

<213> Homo sapien

<400> 79

gtctggaggc	ggtgtcctct	ccgccctgtc	gggtcctgga	tgagtacgag	ttatggtcac	60
ggtcacagcc	tgatctctta	tgtgttcata	gccattcgct	ctcccatcag	aactgtttgt	120
cctgaatgtg	ttcctctagt	tctagaaaat	gaccactaat	ttaaaaaact	cggttgtag	180
gtttgccag	aggcacttgt	tccagaat	cccctcctgc	ttcagccatg	tccttgtcac	240
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tttgttaagt	ggtgcgcgtc	tatctcataa	ctagatgtac	caaccagggg	agggccaagg	420
atggaaaagg	gtaacttttg	tgcttccaaa	gtagctaagc	agaagtgggg	gagcagttta	480

gccagatgat ctttgattag gcaaacattg agttttaaaaggaggctg 526

<210> 80
 <211> 281
 <212> DNA
 <213> Homo sapien

<400> 80
 gttatattag tgggtagtgt aacattttat ccagggtggg gtgaggggag atggccacag 60
 tagcaagtgg tgacactaaa taccattttg aaggctgatg tgtatataca tcattactgt 120
 ccgtagcaat gaaggataga gtactgtgtt gtgggtgagt gttgctattg cccagcatta 180
 atatttgggt gtgtatgttt gaggctatga aacacgcagg agtggttttg tgctattaat 240
 tttaagagaa agcagctttt tcttaaaatt cactgttgag a 281

<210> 81
 <211> 405
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (405)
 <223> n = A,T,C or G

<400> 81
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 aggagtttga statcgacat gtcagtctgc ccaaggacat akccaasctg gtccttaaaa 180
 cccatctgat gtctgaatct gaatggagga atcttggcng ttcagmagan tcagggatgg 240
 gtccattata tgatccatga nccagaacct cdcactctgc tgttccggcg scccacttac 300
 cccaanaaac caamgaaatg aaccttggct actacttttc aatcctcaaa kcttttcaca 360
 vhtgaccttc cttcctaaca ttctttmtga taaacattta ttaag 405

<210> 82
 <211> 547
 <212> DNA
 <213> Homo sapien

<400> 82
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 gttaatcata taataatgat tcttaaatgc tgtatggttt attattttaa tgggtaaagc 120
 catttacata atatagaaag atatgcatat atctagaagg tatgtggcat ttatttggat 180
 aaaattctca attcagagaa atcatctgat gtttctatag tcactttgcc agctcaaaag 240
 aaaacaatac cctatgtagt tgtggaagtt tatgctaata ttgtgtaact gatattaaac 300
 ctaaatgttc tgcctaccct gttggtataa agatattttg agcagactgt aaacaagaaa 360
 aaaaaaatca tgcattctta gcaaaattgc ctagtatgtt aatttgctca aaatacaatg 420
 tttgatttta tgcactttgt cgctattaac atcctttttt tcatgtagat ttcaataatt 480
 gagtaatttt agaagcatta ttttaggaat atatagtkgt cacagtaaat atcttgtttt 540
 ttctatg 547

<210> 83
 <211> 529
 <212> DNA
 <213> Homo sapien

<400> 83

ctatttctaag	agatgctctt	agtgatcttg	cattacactt	tctgaataaa	atgaagatca	60
tggtgattaa	ggatattgaa	agagaagaca	ttgaattcat	ttgtaagaca	attggaacca	120
agccagttgc	tcatattgac	caatttactg	ctgacatgct	gggttctgct	gagttagctg	180
aggaggtcaa	tttaaattgt	tctggcaaac	tgctcaagat	tacaggctgt	gccagccctg	240
gaaaaacagt	tacaattggt	gttcgtgggt	ctaacaaact	ggtgattgaa	gaagctgagc	300
gtccatttca	tgatgcccta	tgtgttattc	gttgtttagt	gaagaagagg	gctcttattg	360
caggaggtgg	tgctccagaa	atagagttgg	ccctacgatt	aactgaatat	tcacgaacac	420
tgagtgggtat	ggaatccctac	tgctgttcgtg	cttttgcaga	tgctatggag	gtcattccat	480
ctacactagc	tgaaaatgcc	cggcctgaat	cccatttcta	cagtaacag		529

<210> 84

<211> 527

<212> DNA

<213> Homo sapien

<400> 84

cccattcacca	gaatcccttc	atgggagggga	tggtatgcctg	ttgaaactca	ctgacctatt	60
ggactgacgc	tgggggtggta	tcttcatcag	agctatttga	agtcattccaa	aaggcttctg	120
acgaaaagaac	aattttttaa	aagtcctctc	tttcaatcaa	gccaatgtcc	tatttttattt	180
ctaaaagtgtt	tgggactcgt	gctgttatca	agtacaatga	aaatggcttt	ataaatagct	240
gttttgacat	tgtgatagaa	ggcttgaata	cggaggaaaag	atgtcgtctgg	agctagtctt	300
gagttccgac	tgtccctgtg	gtgggaatcc	agctctgggaa	agcaggactg	tttttagcaaa	360
cgtgtactcg	ttctataaaa	atggaatctg	ttctgcaggt	taccgtccct	ccccgcccaa	420
gcatccccctc	tgtcctgtct	ctctgctgct	gggacccagg	gcttttttcag	ctgcagaacc	480
cactggactt	ccaggaatca	aggaaaaagt	ggaaatgtcc	aactgtg		527

<210> 85

<211> 401

<212> DNA

<213> Homo sapien

<400> 85

cagtgtggtg	gaattcccaa	gatagaaatg	aaaaactctt	ttatagagtg	ctgacatctg	60
acattgagaa	attcatgcct	attgtttata	ctcccactgt	gggtctggct	tgccaacaat	120
atagtttgggt	gtttcgggaag	ccaagagggtc	tctttattac	tatccacgat	cgagggcata	180
ttgcttcagt	tctcaatgca	tggccagaag	atgtcatcaa	ggccattgtg	gtgactgatg	240
gagagcgtat	tcttggcttg	ggagaccctg	gctgtaatgg	aatgggcac	cctgtgggta	300
aattggctct	atatacagct	tgcggaggga	tgaatcctca	agaatgtctg	cctgtcattc	360
tggatgtggg	aaccgaaaaat	gaggagttac	ttaaagatcc	a		401

<210> 86

<211> 547

<212> DNA

<213> Homo sapien

<400> 86

gaagcctctt	gtgtttgtgt	gcagagaagt	atatgatcca	ccatgctaata	gacacttgcc	60
tttttttcca	ccattaaggc	tttaagaaca	tgtggaataa	gttttttagc	tgctaataac	120
aaaacaaatc	ctgtaactac	ccagccagca	agtatatagc	acagaacact	gtgttacttt	180
acaagggtct	atgtgactgg	aataagggtg	tcccacttga	ctgttccaaa	gagcagcttc	240
tcagatcttc	agtgttcact	ggtaaatttc	taacagtgtg	tttgtgtaaa	gtttgtcatt	300
tcatactcca	tacactacag	ttgctgtcac	tgatccctgt	tttgtctggc	tttaagctac	360
tcggtcaaaa	atcctgcttc	cttaaaacat	agagaattaa	tgagcatctc	aagctttttc	420
ttttcctttt	taatgatgcc	tgcactatca	agagtattct	agtgttctct	ctttgttttg	480

catataatca tgcaccaaac tttttatttc ttttaagggtgg gagtatatatt ttatttccta 540
aatgcca 547

<210> 87
<211> 530
<212> DNA
<213> Homo sapien

<400> 87
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tttggcacct atgcgcctgc agaggttcct aaaagtaaag ctctagaggc cgtcaaattg 120
gcaatagaag ccgggttcca ccatattgat tctgcacatg tttacaataa tgaggagcag 180
gttggactgg ccatccgaag caagattgca gatggcagtg tgaagagaga agacatattc 240
tacacttcaa agctttggag caattcccat cgaccagagt tgggtccgacc agccttggaa 300
aggtcactga aaaatcttca attggactat gttgacctct atcttattca ttttccagtg 360
tctgtaaagc cagggtgagga agtgatccca aaagatgaaa atggaaaaat actatttgac 420
acagtggatc tctgtgccac rtgggaggcc atggagaagt gtaaagatgc aggattggcc 480
aagtcacatcg ggggtgtccaa cttcaaccac aggtgctggtg agatgatcct 530

<210> 88
<211> 529
<212> DNA
<213> Homo sapien

<400> 88
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atcttttcta taagtttaca gcctttttct tatatataca gttattgcca cctttgtgaa 180
catggcaagg gactttttta caatttttat tttattttct agtaccagcc taggaattcg 240
gttagtactc atttgtattc actgtcactt tttctcatgt tctaattata aatgaccaaa 300
atcaagattg ctcaaaaggg taaatgatag ccacagtatt gctccctaaa atatgcataa 360
agtagaaatt cactgccttc ccctcctgtc catgaccttg ggcacagggg agttctgggtg 420
tcatagatat cccgttttgt gaggtagagc tgtgcattaa acttgcacat gactggaacg 480
aagtatgagt gcaactcaaa tgtgttgaag atactgcagt catttttgt 529

<210> 89
<211> 547
<212> DNA
<213> Homo sapien

<400> 89
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cacacaagggt tatgattttt ttaattactg gcttctgatt tctttcactt ctgacccctt 120
tcctttttct cagatgtagc tgagtcttga tcattttaag acaacgatgg gtagaatttt 180
gagattaatg ttaattttcc ctttttggtt atttcagtc cctctcacta tgcttttgct 240
cagaaggatc aagaattcta ccatcccttg ggtctttgtg tataaacaat gttaaataaa 300
ggtagactca gtctttaaga tattagacag tttttttagt ccatgggatt gtaaataata 360
acattaactt tcctataaga atattttggc tttgtaatct atagcctcaa attggtattt 420
attatggatt cactagacaa acagctgttt ccttattgtc ttttttcttt agtgtttctg 480
atttgctatc agtagctgtt tttaaagcca tccaaggaaa ataattattt acagtttttg 540
aagtcac 547

<210> 90
<211> 528
<212> DNA

<213> Homo sapien

<400> 90

gagcagcaga	agctgtacag	caagatgac	gtggggaacc	acaaggacag	gagccgctcc	60
tgagcctgcc	tccagctggc	tggggccacc	gtgcgggggtg	ccaacgggct	cagagctgga	120
gttgccgccc	ccgccccac	tgctgtgtcc	ttccagact	ccagggtcc	ccgggtgct	180
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cgtgtgctg	gctgagtgg	tggggagatg	tggccatgg	cttgtgctag	agatggcgg	420
acaagagtct	gttatgcaag	ccggtgtgcc	agggatgtgc	tgggggcggc	caccgcctct	480
ccaggaaagg	cacagctgag	gcactgtggc	tggcttcggc	ctcaacat		528

<210> 91

<211> 547

<212> DNA

<213> Homo sapien

<400> 91

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acaatctcat	catcctgaag	cctataatga	agaaaaagat	ctagaaactg	agttgtggag	180
ctgactctaa	tcaaatgtga	tgattggaat	taraccmttt	ggscyttgra	ccttymtwrg	240
raaaawgrmc	cmaccttityt	taacmtgrac	cwccytmatc	tctagaagct	gggatggact	300
tactatyctk	gttwatat	ttaaatackga	aagggtgctat	gcttctgtta	ttattccaag	360
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aactgttaga	cttcccgttt	ctgaaagaaa	gagcatcggt	ccaatgcttg	ttcactgttc	540
ctctgtc						547

<210> 92

<211> 527

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(527)

<223> n = A,T,C or G

<400> 92

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ttggggtaac	aggatgggta	cctgtcacgg	cctgtgcaaa	cataacatgt	gtcaccacac	120
tgaaggatag	gtggaacaag	tggcctcacc	aaggctcgac	cccaatggac	tttttgcttc	180
ttgggagctt	atgggtctat	gaggacacag	tagcctttcc	tatcagcaaa	ctggagtgga	240
tggtgtatct	gggggtggcc	ttatgtacct	gctactgttc	tccccacatt	gccagatgc	300
ctgtataact	gggaggcact	gkgctctcag	tttttgcgaa	tgtgatgagc	cccctgggtg	360
ttctaccctt	ttggcaatga	ctatccctgg	agnatgtgt	caaaactgta	aagcacaatt	420
tactgctctt	tgcggagcac	accgctcatg	ctctgaatta	cacctgaktg	ttcctcctcc	480
wgktawtgaa	tgaggttgat	cnvatcagaa	adgtggkgtt	ggcmata		527

<210> 93

<211> 531

<212> DNA

<213> Homo sapien

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<400> 93
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ttacacaatg aagggtttcaa gctgtttgcc acggaagcca catcagactg gctcaacgcc      180
aacaatgtcc ctgccacccc agtggcatgg ccgtctcaag aaggacagaa tcccagcctc      240
tcttccatca gaaaattgat tagagatggc agcattgacc tagtgattaa ccttcccaac      300
aacaacacta aatttgtcca tgataattat gtgattcgga ggacagctgt tgatagtggg      360
atccctctcc tactaatttt tcaggtgacc aaactttttg ctgaagctgt gcagaaatct      420
cgcaagggtg actccaagag tcttttccac tacaggcagt acagtgtctg aaaagcagca      480
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<210> 94

<211> 547

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (547)

<223> n = A,T,C or G

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<400> 94
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gatgtgtctc cattcctgga aggtcttgaa gaaagaccac agagaaaggc acagcctgct      180
caacctgctg atgaacctgc agaaaaggct gatgaaccaa tggaaacatta agtgataagc      240
cagtctatat atgtattatc aaatatgtaa gaatacaggc accacatact gatgacaata      300
atctatactt tgaaccacaaa gttgcagagt ggtggaatgc tatgttttag gaatcagtcc      360
agatgtgagt tttttccaag caacctcact gaaacctata taatggaata ctttttctt      420
tgaaagggtc tgtataatca ttttctagaa agtatgggta tctatactaa tgtttttata      480
tgaagaacat aggtgtcttt gtggttttaa agacaactgt gaaataaaat tgtttcaccg      540
cctggtn                                547

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<210> 95

<211> 1265

<212> DNA

<213> Homo sapien

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<400> 95
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ctaactggga aagacccagg gagactggga tgggctcatg attctacata cagaactcat      120
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<210> 97
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 <212> DNA
 <213> Homo sapien

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aactgc						546

<210> 98
 <211> 547
 <212> DNA
 <213> Homo sapien

<400> 98						
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<210> 99
 <211> 122
 <212> DNA
 <213> Homo sapien

<400> 99
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 aa 122

<210> 100
 <211> 449
 <212> DNA
 <213> Homo sapien

<400> 100
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 aaattgaggt ctttttctta gttgtatgg 449

<210> 101
 <211> 131
 <212> DNA
 <213> Homo sapien

<400> 101
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<210> 102
 <211> 199
 <212> DNA
 <213> Homo sapien

<400> 102
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<210> 103
 <211> 321
 <212> DNA
 <213> Homo sapien

<400> 103

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ccttgggcca	gcttggtttt	actctagatt	tcactgtcgt	cccaccccca	cttctttcac	180
cccacttttt	ccttcaccaa	catgcaaagt	ctttccttcc	ctgccaccca	gataatatag	240
acagatggga	aaggcaggcg	cggccttcgt	tgtcagtagt	tctttgatgt	gaaaggggca	300
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<210> 104

<211> 309

<212> DNA

<213> Homo sapien

<400> 104

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cctattactt	tgcaaggggc	ccttcaaaag	tctctgggct	tctatttcaa	ccgcgatgat	180
gtggctcttg	aaggcgtgag	ccactttttc	cgggaactgg	ccaaggaaaa	gcccagaggc	240
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<210> 105

<211> 591

<212> DNA

<213> Homo sapien

<400> 105

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tgtggtaaca	tttgttgcat	gaatggaccg	ttgaaatagg	gcctggcagg	gagaaattca	480
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<210> 106

<211> 450

<212> DNA

<213> Homo sapien

<400> 106

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ccactctgta	cattaatact	ttggtgatta	atgtttgggg	agaggcagga	ttctcaccca	420
cctttttgac	ttcaaacact	ctcactcaag				450

<210> 107

<211> 116

<212> DNA

<213> Homo sapien

<400> 107

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tgcaaaatat acatgttctc ctccctgttt caattcttcc atcttttttc ttgagg	116

<210> 108

<211> 291

<212> DNA

<213> Homo sapien

<400> 108

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ctccttctact ttggttgtgt tagtagacag ggcaacaaag tgcttcgcca ctgcagtagg	180
atccttggcc gcctggagaa accactcctt cgccgtctct gcattcgtga tggctcctcg	240
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<210> 109

<211> 662

<212> DNA

<213> Homo sapien

<400> 109

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gtgcaggaag ggggcaagga ctctgccag ggtgactccg ggggccctct ggtctgtaac	180
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<210> 110

<211> 323

<212> DNA

<213> Homo sapien

<400> 110

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ctaacaaaaa actatatttt ccaaagtcac tatcatttgg gccaatataag tgatcttttc	240
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<210> 111

<211> 336

<212> DNA

<213> Homo sapien

<400> 111
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 tgcttctagt gctctcattt ggaaatgagg caggcttctt ctatgaaatg taaagaaaga 300
 aaccactttg tatattttgt aataccacct ctgtgg 336

<210> 112
 <211> 218
 <212> DNA
 <213> Homo sapien

<400> 112
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 caccocgtgc cacagacctt cctcggttgc agagattctg ggcaaagcat ccgtgctctc 180
 atgagattat cctggggaga tttagaagaa ttttgggg 218

<210> 113
 <211> 533
 <212> DNA
 <213> Homo sapien

<400> 113
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 gggttcctgag agccccgaga agaaaattca tgacagtgtc tgggctgcca aagaagcagt 240
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 gaagacagt agcacaccta ccagacactc ttcttctccc acctcactct cccactgtac 480
 ccaccctaa atcattccag tgctctcaaa aagcatgttt ttcaagatct aaa 533

<210> 114
 <211> 261
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(261)
 <223> n = A,T,C or G

<400> 114
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 ggggacaaac tgaagttaaa caggtcgaaa ctagaggagc tgctgacctt ggagctgacc 180
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 accaacatag gacaacaacg t 261

<210> 115
 <211> 267

<212> DNA

<213> Homo sapien

<400> 115

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acacagcagg ctccctaagc aatgtgacgc accagagggg tgggtgtaca cgttcccctt	180
gaagtcacct gaaaattaga gaacagattt gcctcatagc tgaagagaga ccctattcca	240
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<210> 116

<211> 239

<212> DNA

<213> Homo sapien

<400> 116

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aaagtcctag actaggaggt ctcaaccttg gctgcacaga attatctggg gagtttttaa	180
atttccagtg gcccaggctg cattcatatc atagtagaga cagggttttg ccattgctgg	239

<210> 117

<211> 168

<212> DNA

<213> Homo sapien

<400> 117

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ttgtaggagt tgtagactac ctaaaatttt aagttatgga tttgttcata ggtgtaggg	120
gtaggtaaag aaggaaacag acaagaaaat ggcttcttga ggtggcag	168

<210> 118

<211> 150

<212> DNA

<213> Homo sapien

<400> 118

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gttgtgcttc tctaggaggt tgggtttttt	150

<210> 119

<211> 154

<212> DNA

<213> Homo sapien

<400> 119

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<210> 120

<211> 314

<212> DNA

<213> Homo sapien

<400> 120

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taaaaaatca	atttgagctc	atttcgaata	cagaacaagt	atggcacaga	tggaaagtcct	180
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<210> 121

<211> 601

<212> DNA

<213> Homo sapien

<400> 121

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ccagggtgtc	catgagctct	gtgatctgga	ggagactcca	gtgagctgga	aggatgacac	540
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<210> 122

<211> 486

<212> DNA

<213> Homo sapien

<400> 122

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ctacaagggt	ggcaacagcg	cctgaggatc	taattttatg	catattactc	ccaagtattt	180
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<210> 123

<211> 239

<212> DNA

<213> Homo sapien

<400> 123

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ttaggaaaca	gtgtgggaga	ataggagtcc	agccgtaaga	taaactggaa	atatttgggc	180
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<210> 124

<211> 610
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(610)
 <223> n = A,T,C or G

<400> 124
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<210> 125
 <211> 196
 <212> DNA
 <213> Homo sapien

<400> 125
 ctatagggt cgagcgccg cccgggcagg taaaaaatca gcccctaatt tctccatgtt 60
 tacacttcaa tctgcaggct tcttaaagt acagtatcct taacctgcca ccagtgtcca 120
 ccctccggcc cccgtcttgt aaaaagggga ggagaattag ccaaactg taagctttta 180
 agaagaacaa agtttt 196

<210> 126
 <211> 247
 <212> DNA
 <213> Homo sapien

<400> 126
 aaattagtta aaaaaatgca ttcctcattt gatatagcca cattccaaat gcttaaaagc 60
 cgcattgtatc tagtgactac catactggag agtacaaata tagaacttta cccgtcactg 120
 cagacagttc tggttgattg tgcagcattg gacaatatat acagtttgcc tgtatatgag 180
 aaagagagag agagagagag tgtgtgtgtg tgtgtgtgtg tgaagtgcaa taaggctgac 240
 aggcac 247

<210> 127
 <211> 590
 <212> DNA
 <213> Homo sapien

<400> 127
 cctccacggc atggcgcaat tggtgttcag gggccgccag gttgctgccc atgccgatgt 60
 agatacgttc cagtgctta ctgccagac gcactcgaag cgtcgccagc gctacgtttg 120
 cgcttgctgc cactgctgcg gcgacgctt ttcgggcat cgcgggtggc ttcgcctttg 180
 ctgctgagct ctttgatcat ctgcggcgc tggctgtcgt tggcgtcctg gtagtcggtc 240

```

caccactcgc caaggccgctc ggtctgttcg ccggcgcttt cacgcagcag caggaagtca      300
tagcccgcca cggaagcgcg ggttgtccag caacaggctcg gcacgtttgc cgctgcggcg      360
tggcaggcgc tcctgcatgt cccagatttc acggatcggc atggtgaagc gtttcgggat      420
ggcgatgcgc tggcattgct cggcgatcag ctctgtagca gcttcctgca tggctggaat      480
tgccggcatg ccacgggtctt gcaggcgcat gacgcgtttc gaaagcgcg gccacaacag      540
ggcggcaaaag aggaacgccg gggtgaccgg tttgttctgc ttgatgcgca      590

```

<210> 128

<211> 361

<212> DNA

<213> Homo sapien

<400> 128

```

ctgccatgg aaacctcca ggagctgctg gacctgcaca ggaccagtga gaggagggcc      60
attgaagtct tcatgaaaaa ctctttcaag gatgtaacca aagtttccag aaagaattgg      120
agactctact agatgcaaaa cagaatgaca ttgtaaacg gaacctggaa gcatcctcgg      180
attattgctc ggctttactt aaggatattt ttggtcccct agaagaagca gtgaagcagg      240
gaatttattc taagccagga ggccataatc tcttcattca gaaaacagaa gaactgaagg      300
caaagtacta tcgggagcct cggaaaggaa tacaggctga agaagttctg cagaaatatt      360
t                                     361

```

<210> 129

<211> 546

<212> DNA

<213> Homo sapien

<400> 129

```

aaaaatatac attcagtaag acttttctc taacaacaat ttttcaaac gaatcaacaa      60
caaaaaagta tccagtgttt cttttcttat gaagatataa taaaacacag tattggtaag      120
cacattttta cagtatgctt ttcttttgta gggaaaggag atatggctat gtctaaccatc      180
gtgggatcca atgtgtttga tatgttgtgc cttggtattc catggtttat taaaactgca      240
tttataaatg gatcagctcc tgcagaagta aacagcagag gactaactta cataaccatc      300
tctctcaaca tttcaattat ttttctttt ttagcagttc acttcaatgg ctggaaacta      360
gacagaaagt tgggaatagt ctgcctatta tcatacttgg ggcttgctac attatcagtt      420
ctatatgaac ttggaattat tggaaataat aaaataaggg gctgtggagg ttgatattat      480
taatagtgtt atgcagaaaa tatgaatggc agggaggggc agagagaaaa atccatttct      540
tcattt                                     546

```

<210> 130

<211> 733

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(733)

<223> n = A,T,C or G

<400> 130

```

ggggcctctt cctaaaggca ctaatcccat ccaatagggc ttaacctcat gacttaatca      60
actttcaaag acaccacatc ctaatgccat cacatcagaa tttaggcttc aacatatgaa      120
ttttgggggg acacaaacat tcacctcata gcattcattg tttcttgta ttggcaaagc      180
caagactcac attgtctaag ttatttgact tttagtccg cagatgtgaa aacagtgcta      240
aacagtccag ctcatgagt ggagaacagc atttgtgaca accaccaaag tacctctgtg      300
gtcagtgtcc tcaaccaggg cacagcatca tggaccagag cctctgcagg gcacagagga      360

```

```

gtggtgagga acaggggctc tggagcaacc ccacttccct ctgctttgta tatgggggggt      420
tctgcacatg actgcatttg aaaagggctt cactgcgctt gctgaaggag tgcacttgag      480
ctagcggaga gttcccagag ggtgtctgga agaagcaaag gctattcttt gtttcaactca      540
gttatagatg gaagtcagac acttctgcct gaagtacttt cacacactcc acagtcttaa      600
gaaggatgga naaagcatgc caactactca naaaaccaca ggtgttcaag caatgggtatc      660
cttttatncc tacaactagt ggacaaagng gggcctctgt aatttgggaa agctaggaaa      720
actttttctg ggg                                     733

```

```

<210> 131
<211> 305
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(305)
<223> n = A,T,C or G

```

```

<400> 131
aaacacatac gaatanntna actgtgatta tgaagtgaca gccggctaaa tatgtcttgt      60
attttctctc ttcctttttt tgctaactca tcctttattc cattcctgct tccatggtaa      120
tgcaggctca aataaattac taggatacaa gattacttca agcctctttt ctgtggaaact      180
cataatatga taagcatttg ttacaagatt gcctgtagtt gtttagggga caaattatat      240
tagggaaaga aagtctttct ttagttgggt aaattttcta ttataattgg gtactaaatt      300
tattt                                     305

```

```

<210> 132
<211> 545
<212> DNA
<213> Homo sapien

```

```

<400> 132
aaacaatgct acactcattt ttggcaaagt gctgtattgt tcagtctgtg tacaaaaactg      60
accatctatg aaccaatcag tataaaaaat ttctataaaa acaaaattta gacagcggct      120
caagaaaaca agctgccatt tatgcataga ttgatgtaca gtaacctaac caaatgtccc      180
ttttgaattt tcaagttact gaaaaaaaat gtgtcgagaa acacattaag aaggcacatg      240
tacagtctac aatactcttc agtctcccta actcatgccc tgcccctata aaggaaatat      300
gttcacaatt ttacttgaga aaaaaaaaaca aagccactta aaaaaaaaaa aacacacacg      360
caattattaa agttcaaaaat ctctggagga aaatacaagc aaaaccactc atacactcca      420
agcctgaaac acacatctaa cctccccagg tactggtttg gttttcagag gtccacctag      480
aaaacaaatc taaaacttca ggcaaaacag agcaaaactg gacatttaac aattacacaa      540
ttttt                                     545

```

```

<210> 133
<211> 330
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(330)
<223> n = A,T,C or G

```

```

<400> 133
aatatttatt actaatatct tataatgttt tgtggnacca tggcatacct tgggtactat      60

```

```

tgtaacanat agttcaggaa accctactat aagggtttatc aaatgggtctc ataaacagtt      120
acttattcaa gcacgccaaa gctcagtgaa aagtattttt cacccttact ctttctcgtg      180
tcattcaaag agaagttttg atgtagtgta tttatttgta gggagtaatg aacagatcca      240
tttcacagta gactttgtgc tctagggtgat gcagctaatt gccccagttt ggaaaacatg      300
gacttggtatg aattgtcttt tgtttgggac                                     330

```

```

<210> 134
<211> 627
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(627)
<223> n = A,T,C or G

```

```

<400> 134
aaatattact tcaaatacat tttaaagctc aacaaacttg tgttgaactg aattgcagat      60
cctgaactct atttgaatat acatcatgaa acagaaaanc ccattccaaa tgaaaatgat      120
agtgccttgt tgggggtggg aatgaggcgg ggagactaaa tcactattaa cagacttctt      180
ttcccaatgc aatttgtcaa aagttcaaaa gttctgaaat gtactaaatc ttaagcaaat      240
taaattcatg atattactaa aactttttta atagtgaat gacttatcaa gttatagtgg      300
ctgcattaaag aacaaattat tgtgtgaaat acctgtataa acacaaaata caattaata      360
tttctttaca aaaagctgag cattacgcat aatagtggaa tgtctttcat taggtgtatt      420
ttttaagat taacaaaagt aacatttcct aaaatgtata catgtgccat atttttgcaa      480
acatgcctga gaatgtattt aaaacatttc tgtagtaaga gtttgcaaga acttcacaaa      540
cctgcaataa aaatgcatct ttttaaaaag gtgaaaatgg catctccaca ctgcaacaat      600
tcaaaaagtg cagcatccct aatcttt                                     627

```

```

<210> 135
<211> 277
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(277)
<223> n = A,T,C or G

```

```

<400> 135
aaaatcaaat atattatttg ttaaaaatca gcttggttca ttacnggaaa ttacaccagt      60
ccgttctatt tactttcaaa ccatattcaa ctcttcaact ttcaaacatg taatcaacta      120
atttcaaaaag ggaaaaggta ccctttataa aggagagatc tgttaagaca ccaagaaatc      180
aaaattaata tcacttaata attaatgga taacacatgc ctccaatac agtgacgtga      240
gaaacacaaa acatcaattc ccgcgtactc tgcgttg                                     277

```

```

<210> 136
<211> 486
<212> DNA
<213> Homo sapien

```

```

<400> 136
aaaacagaat gaattcattg ttacagttac agaagtcaga agcccaaata cagtctgcct      60
gaaccaaagc cagggtcagc aagggttcctt tccactgttt tgccaacttc tagaggccac      120
ctgtattcct tgggtcatgg cccctctctt catcatcaaa taatcagcat agctttatga      180

```

```

cattggcagc tctgattttg ctcttttgcc ttctctcttat gtagaccctt gtaattacat 240
tgggtacacc cagataaacc caaataatct ccctatctca agattcttaa tgtaattata 300
ttgggaaagt cccttttgtc atataagata acatagcaat ggattccaag gattagtatg 360
tgagtttctt ttgaggggct ataattaacc ctaccacaat atggaaatgt ctattgtttt 420
tctatgtacc agaaataaga cattaggatg tgaaattaat aacataacac cacttacggc 480
atcacc 486

```

<210> 137

<211> 552

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(552)

<223> n = A,T,C or G

<400> 137

```

ccatcttgca tcaaatgttc ttaaggcagt gactggctat caaccacagt ttctgtctcc 60
ccagttgcaa acacaggatc catgcaacag ttctgagacc atacacttag aaaccacagg 120
ggatgcggat caaatgcaga actcccaaat tataaaacag tcaggctaca ctcaaaacaa 180
aacatagaac atcaacaaca cacatctccc aaaaaagaag tgcaacgcat gcttgataaa 240
accaacaata acaaaaaaac cacaataaaa aatgcagagt ctcccaacaa agttttcaaa 300
tgtattgcan aaagaaaaaa aatgtatata tatataaaat taaaaagtct gaaatactag 360
tgcatagtca attacctaac accaagtttc ttttctttct gtccaagctc tactgcccct 420
ctgatactag cagcatgtct acaggctaag accatagcag caaaaaacgt ttttcatttg 480
gcatttacaa aattaaatta ctgaataaaa atataatttt ttaaaaaact atttcttaca 540
gtaataattt tt 552

```

<210> 138

<211> 231

<212> DNA

<213> Homo sapien

<400> 138

```

aaattttact agtgttactt aatgtatatt ctaaaaagag aatgcagtaa ctaatgccct 60
aaatgtttga tctctgtttg tcattacttt ttcaaaatat tttttctgt aaagtataat 120
atataaaact tcttgcttaa attgaatttc tatattagtg gttaattgca gtttattaaa 180
gggatcatta tcagtaattt catagcaact gttctagtgt tttgtgtttt t 231

```

<210> 139

<211> 535

<212> DNA

<213> Homo sapien

<400> 139

```

cagttgcaa ccctctgaac cgtttaggcc ggttcatcgc tgcctttgaa tctgggccgg 60
tggtgatccg gcaaggggtg aaaccaaaga gcgggggctg tgaggccctt cgcagtcctt 120
cgtaagtcgc tgcgatggag tgaactatca cgcctcgtgt ttatttcgtc aacacgaaat 180
gtgatttatt tttgcgaatt aacacggcag ttctcgggta cgttttcgga aagcgtggga 240
tatgattctg tctatcctgt acggatatac agtaattacc gggaggggat tccatggcga 300
agaagcaggc ggcaccggca gcacggcagg aaatgagcgg tatggcgcgc ctccgggttc 360
cgtctctatc gatgattaat caccgggtcg ccagacgca gcgctgggtt acgattcctc 420
gcctggacac ggatggggat cgggagtggg aagaggttct gagcgtgatc gctgataccg 480
acgagctcga gctgacgctc aatgacgatg gcagtgtgac ggtgaggtgg gagca 535

```

<210> 140
 <211> 640
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(640)
 <223> n = A,T,C or G

<400> 140
 acattggtgg cacttgaact gagtgcaaac cacaacattc ttcagattgt ggatgtgtgt 60
 catgacgtag aaaaggatga aaaacttatt cgtctaattg aagagatcat gagtgagaag 120
 gagaataaaa ccattgtttt tgtggaaacc aaaagaagat gtgatgagct taccagaaaa 180
 atgaggagag atgggtggcc tgccatgggt atccatgggt acaagagtca acaagagcgt 240
 gactgggttc taaatgaatt caaacatgga aaagctccta ttctgattgc tacagatgtg 300
 gcctccagag ggctaggtta gtacaaactc gcattcatgg cttgggtttcc cagaagatct 360
 ccatttaact tttttaaaga aagtttattg ctttctttaa cctgcatttt ttctaagttt 420
 tttttcgcac aaaggtgctg tctttgtggc aaggcctagg catgacaatc ggaggactcg 480
 agggggatgg aggactagtg atccggctgg ctgcttccag tcgattagag aggtgaaaaa 540
 gctgaacgtg tgcccantna atcttcaaaa aggcagaaac atatcacctt ntgccccnt 600
 aaacttgctc tttttccgaa ggggaaaaaa aaaatggaaa 640

<210> 141
 <211> 127
 <212> DNA
 <213> Homo sapien

<400> 141
 aaaaatcaca cactgacaac acagaaatac gaaatgctag gaaaagtcta gcatatgaag 60
 gaaaaacatg tcttatgcac tctaataata ttttttcaat tagtataaag gcaaatgcgg 120
 ttttttt 127

<210> 142
 <211> 126
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(126)
 <223> n = A,T,C or G

<400> 142
 aaatatcctc tggatgcntt caagtaatac taatcatttc atgngnaaaa gtcttttaat 60
 aaacaaattc agagtataat taattgaaat atttataata catttggttac acagttattc 120
 ccaata 126

<210> 143
 <211> 730
 <212> DNA
 <213> Homo sapien

<220>

<221> misc_feature
 <222> (1)...(730)
 <223> n = A,T,C or G

<400> 143
 gcaagttctg gagtgttcac ttctgagcct gaattccctc ccctgcaaaa tgggggaata 60
 ccctcctcag aggggtccctg cgagggtgag gggagatcag catggcaggt gtgctgggca 120
 cggcagggcc tgggaagggc agatcctttc cccatccctg ccacaaacaa cccaaacctt 180
 taaaggagag caatggcctt gtgtcaaaaa caaaaacaaa acaaaacctt gtccataggag 240
 actggggccc taatttctaa tagcaagcct ttatgagtcc ctaacactct actgggctga 300
 gtatctcaca cgccagagga taacctgcct tctgctcacc accaccccggt agtagttgtc 360
 attgtgtcca ttccacagat gaggcaaagg ctgagaagag tcatgtgtta aaccagcttc 420
 tagagcccat gcaggagctg cagggtgggga gaatcacctc taggtgctct tcccatggaa 480
 tctcaccctt ccttgagtgg tcaactcactc anctttccaa tgggtgtgtg acctttgacc 540
 agctttcttt ccttntctgg gcctcagttt cccaccttgg acaaagtaag aggtctcttg 600
 ggnttcangg tagttcttcc taactttctt tcttttcat ttgagcatcc ttcttcattt 660
 tttgccacct ctcttgtcat tacangcttt taccttcggc cgcgaaccac gcttaagggc 720
 naaatttcca 730

<210> 144
 <211> 485
 <212> DNA
 <213> Homo sapien

<400> 144
 ctggtcagaa atgattctct tgtgacacca tcgccacaac aggctcgggt ctgtcctccc 60
 catatgttac ctgaagatgg agctaccttt cctctgtgtg gcattttgtc gcttatccag 120
 tcttctactc gtagggcata ccagcagatc ttggatgtgc tggatgaaaa tcacctgtgt 180
 tgcgtggtgg gtctgctgcc gccacttcta atcctcatca tgacaacgtc aggtatggca 240
 tttcaaatat agatacaacc attgaaggaa cgtcagatga cctgactgtt gtagatgcag 300
 cttcactaag acgacagata atcaaaactaa atagacgtct gcaacttctg gaagaggaga 360
 acaagaacg tgctaaaaga gaaatggtca tgtattcaat tactgtagct ttctggctgc 420
 ttaatagctg gctctggttt cgccgctaga ggtaacatca gccctcaaaa atattgtctc 480
 aacag 485

<210> 145
 <211> 465
 <212> DNA
 <213> Homo sapien

<400> 145
 ccaagacagc tcgtttcttg agagtatgag ggtgtgtttt cttattgtga aaggaactac 60
 cttctcttag agggtaggaa gaatgtggtg tgtgtgtgtc tcataaagca accggacatt 120
 atagggtccc aggtcatcta taaaaacgat ccttgggctg tgtaaaaatg aagtggcttt 180
 tcagtatcct ctttcacact tgctgcttcg ggagactatg caatgatggg aagggtgattg 240
 cccctttatt tcattcagtg ccatgggtccc tgttgttcta gtaatttatt tgtttagttc 300
 attttttttt tcttaacagt caaggggaag agtgattcct cactactgctt tcaagctgga 360
 ctgagccagt ctcatctctg gaaagaaatg ctgtgtccag aactcagcag ctccatctat 420
 tttttccagt cgaaagaaac tgatctttta gcagttttta cttgg 465

<210> 146
 <211> 351
 <212> DNA
 <213> Homo sapien

<400> 146

ccagccgggg	taatctgtat	gtggcggact	tgagctacga	cgtgggcggc	aagtgcctgt	60
ttgaccagat	cagcggcgtg	aagcttatgc	caactcatcg	tttgataaat	ccgaggatca	120
gttcaagacg	tcgcagcggg	tgatttttggg	aacgtcgttt	tcggtcagta	aattgtgggt	180
agcgcaggag	tggttgatcg	gcaagaatga	tccgtatatatt	ggcgggagca	gctataccga	240
gagcctgggg	gctgggggga	gtaaccagtg	ggagaatcag	ttatatatga	acattgggta	300
ctactttctga	cttaagatct	ccagcgtttt	aactggcctt	atcgcaggca	a	351

<210> 147

<211> 654

<212> DNA

<213> Homo sapien

<400> 147

acttatTTTT	aattactgaa	tatttcttag	acgttttggg	acagatttta	tgtaatcttt	60
ataagtatga	tttctgaaga	aaagcaaatg	cattagtagt	tttgccttaa	acttgtagac	120
taaaccaagt	attgtaaaat	aaacagcgat	aacagtgata	gtttttaact	ctatggctcat	180
tgtatcactc	tggaaaatgt	ggagtagctg	taataaatct	actcctgtat	tatgctttac	240
agtgcaggtc	ttagtttttc	ttttttctca	tttcttttga	aatggcatct	cgaacaaagt	300
ccaccaatcc	ctttacaaaa	gaatgaactg	ctcctctgtg	tgtacttcac	agaagggtga	360
atcggacaga	ggcagggttag	tgacagttag	tccctgaaata	caggagcaga	gtacagctctg	420
ttgtggtttc	ccggattccg	cgcctagctc	agccaattaa	gcatgagaca	taggccattg	480
agccacttag	tagttatgcg	agtggataga	ttggtatgta	agagggaaag	aggtctgctg	540
taaagaacaa	cacttgtttg	tctgtgggga	aagaaaagca	gaatcttgag	atgaaagtgtg	600
gcatacaaat	aggatactat	cgccagtagg	ttatattaca	aaacatttat	cggg	654

<210> 148

<211> 539

<212> DNA

<213> Homo sapien

<400> 148

tgaatatcat	gagggtgatt	ttcacctgat	tgcaaaactg	ccatagtttg	aaacactttt	60
tcaatttacc	agacacactc	tgtcaagact	tcatatactt	ccaacttgca	agcctgtgtt	120
ttgccttctc	caacctaaaa	aggaaaagct	ttaaacgatg	aacttacatt	ctattaaacc	180
atcagacttg	agcttatcca	tctgttttagc	gtgaatgtac	aaaccaggta	catttccacc	240
aaacacatag	aaaaatcttg	tgcatacacag	ttcagctaag	ggtagtagga	caatccttac	300
aatcctcctt	ggatttcttt	tttaagatgt	caaagaagca	ggtaagcaac	attgttcatt	360
tgttactggg	tgttctagat	caaaccttca	caagctatat	atatagcttc	atatgctata	420
gcttacaaat	ggggtacaa	agtaaaagaa	aagaacaaat	tatactttga	cactttatag	480
tcaaagtata	attaaaaaag	aaatcctaca	gtgggtaatg	gagaaataga	taatttttc	539

<210> 149

<211> 273

<212> DNA

<213> Homo sapien

<400> 149

tttttggtea	tttctctcaa	ggagccgctg	gatagtagtc	ttgattgact	tccaccttgc	60
ccctcataca	gtccggtact	aaggccaccg	acatcccagag	gaacctccgg	aaccacgacc	120
gccaaagcaac	tcgaccacag	ataggtgggg	cctacgctct	cgaagttgat	tggatgctcc	180
cgcctacagg	gcggggtaca	gaagggacgt	catttgtgac	tggacgcgca	agagctatac	240
tcagcagctt	tcctctgtcc	cagcccttag	aac			273

<210> 150

<211> 200
 <212> DNA
 <213> Homo sapien

<400> 150
 gtttttacta ccgtatggcc cattttaaag ggatgtgtac gccttacact ataaccctta 60
 aaccacctag aaatatgaaa ctcaaactgc cactgacctc cctcaccaag ctccataaaa 120
 gtaaaaaatt ataacaaacc ttattaacca aactgaacga acatatgggc gattgattca 180
 ttgccccac aatcctaggg 200

<210> 151
 <211> 515
 <212> DNA
 <213> Homo sapien

<400> 151
 ctgtagcgat cttaagaat attttatata tgaaatctgg atttagggtt cccatggctc 60
 ggcaccactg ggtacagtag ttctacatgg cagtaattca ttggagttga agcagtgagg 120
 aaagagtcaa gtactagtct tttatcctca gtgtccagtg actgtcaaga gaaatgggac 180
 tgccttctgc attgggatat gtgggttaaa gtagtagcca atatagaaga gtgagaaagt 240
 gmacctctgc aggcatagta atgttttatt kraaaacatc tcacatgtat tgaatactta 300
 sataggatgt attctgtatt actgaatatt ccagattatt gaagcaatca cctttctgtg 360
 tttaaagttt tagaaagaat gcttttaaaa atgcttaaca taagataagc ctgttttcat 420
 ggtgcaaggc cctttctatg aacatgaatc actggactct gaggggttga ctaagatcac 480
 atctacatcc cttttaaatg actagtgtgc tcaga 515

<210> 152
 <211> 243
 <212> DNA
 <213> Homo sapien

<400> 152
 atttcaacaa catacttgtc gaggtagtta taaatcttct tagggggagg tgggtggttc 60
 tgttggaatg ccaattttac agcttctgct gctgattcag gttctttaat tatgcttttc 120
 tttgagtcctg cttcagatag cacaacaaaa aaatgatgac acttttcaca cttgacaaaa 180
 cggttggtg atacaaaagg tctctacatg tgtgcacaa tgcgccacatt taggacagcg 240
 cag 243

<210> 153
 <211> 620
 <212> DNA
 <213> Homo sapien

<400> 153
 ttgtcttctc taccttacca tagccagttg ctttcatttt aaaccagagc aagtaacata 60
 ttagtgactt gaatcttcat aagttaaagt aaaaaacagc aaaaaaccta gatctttgtc 120
 ttttagaaca cagaccattt tcaggaaagc agttagctaa gtgtttaatt catgaatatt 180
 gtatactgca tcccctacca caatttacac aatcctgtgg atagtcctac ctccacctgg 240
 tcaacctaca tgatccttaa gctaattggc gatcacgatg accttgtaga catgcacaca 300
 actatacctt tgtccaacag atcataatat atctgtctac caactgggtt tacctgccta 360
 atcctactga tttgggcact gcttgtatag tctctcaagt tcacaggaag tgttgatttt 420
 ctaaggctct catttttaca gagtatacag gcaaaagtgc aggggaaaag gaattagtct 480
 aagagtaagg ggtgattat tatattgagg ctaaaaccac aaagtggctc aggcctttaa 540
 aaaaaacact gtggataatg acaaaaagca taagtaaaaa tatttttgaga aaaataaagt 600
 acaagttttg aacaccccc 620

<210> 154
 <211> 843
 <212> DNA
 <213> Homo sapien

<400> 154
 cattgttagt gacccaagta aatttatagt ttttaagttc agaggaaaaa taaagcctat 60
 tttttgttaa cagtcttaat aaataataaa atggaataaa gaaacaaaa aaaaaagaaa 120
 aagtttgtat gaaaattcat ccctatttct ttattttgga ctaagtagtc aaatttctac 180
 tatattaata ttatgtaagc gacacccatt taaattcact ctctttgata gaaaggtgag 240
 ttgattatca cactgctat tttttcactg ccaaaragac tgcaataacc tccctccatc 300
 accctcaaaa aacaaacaga aacctctga ggcatagcca ttgtttacat attgtgtttg 360
 tgtgcaccta tctacaacgt tctttcttct aaggagttta tctgccaata ttttcggctt 420
 cagcagcagc gctcttcttg acagactaag agaaggatct acagaaaagt catctgatta 480
 aggttttggg tcaaattaaa actctctgga cagaatcttc tttccttcac ttggatttct 540
 gcaaacagaa agcagattat tctcctggca caatagcgac tctagaaacg cttatgtttt 600
 tcagactttg gcagaacttg ttaagaacag catcatcata atacatttgt acaaactcga 660
 atttcagtgg ctcttttgtc ccacatgatg catgatgaaa tttataaagg tctgttttac 720
 ccccacaggg tcatttcttt tgtgttccta cagagccaat aggcctcatt taagtccaag 780
 ttatttatatt aacctccct ttcactagac tagagaactt ctttttcatg gtccatatcg 840
 tga 843

<210> 155
 <211> 674
 <212> DNA
 <213> Homo sapien

<400> 155
 tttcgtgtca gccccaggtt tgctccagct attcacaagc agaataatac acaagaaaaa 60
 caattcatat ccttaggga aaaaagagga tcaattcatc actcaatatt taatacagcc 120
 aaaatgagct gccaaaacaa gcacacacac aaatactgtg aacagaaaaa tacaagaaaa 180
 tgactaagct gggagtcttg acggggtatg gacattgctt aaagcactta tcagtcccca 240
 gaaaaaccaa accaaaaaca ttttttacga tggcatggcc tcatggcccc ctttaaaact 300
 gttgatggta acaaagggca gggggtgggg agagaaaaca caatcactgc tccctttttg 360
 ctcgccagtg tgactgcacc cctcacggca cggcatgta cacaactacc acacaaggag 420
 gaccaagtcc ctctgctggg ggcctcctaa aaggcaaggc ttgagttttg gctgatgagc 480
 aagttctctc cgttaccaat cctgccaac cagcactacc atggctgaat tgatctaccg 540
 ttttcttgag taaactgtaa ctggctacag tttcggtaac atggaaaaga actcagctac 600
 tacageccaac tgcaatactt caggaacccc ctccatccct ggggctcttc actcctagtg 660
 catcttgatt ggat 674

<210> 156
 <211> 671
 <212> DNA
 <213> Homo sapien

<400> 156
 ccttttagtga acacctttat ctccatgtcc ctcttagagc ccagagagct gcccataggc 60
 attttccaga attcctcatg tcacctagt tcaatttccat taactcagat cagccattgt 120
 gattcaccat ttgtcaggct cttaggttta acaaaacctt ctatcaccat catccttcaa 180
 cagccacagt ctgaattgag ccaacatttt tttttctttg agaaagaagt gggctggggc 240
 acaactttta gtctgagggg agctagtagt cggcttgaca attaaagcca tccataacaa 300
 cttttcctca aatgtgttga ctctcaggg gctaaactgc tcttagctta gaattatgct 360
 ttactagaga tctaccatat aagtgggtta atcactacca tctgttaact agttatatag 420

cttccagaca	tgagggagac	atcaaacagg	gatggaagca	accccaagga	tatgcaagaa	480
gggcatgatg	aacccccctc	cctctggcag	gagaacaagg	ccaaccaagg	gacagactgg	540
aaagcactta	gatgtttaag	gaggagaaaag	gggaagcttt	gaccagtcct	tgccttttgc	600
caagttcagc	cagttctccg	ctgcttgcaa	cctctagcgc	agtaacattt	tgcagaattg	660
cagattttcc	c					671

<210> 157

<211> 474

<212> DNA

<213> Homo sapien

<400> 157

cgcgttcttt	aattctttaa	gcctagaaaag	tccttttacac	tacttaccta	aagggtcccaa	60
agtaaaacac	acactagtag	taaggctagt	gcatttcctt	tctagcactc	aaagaaagct	120
taacattttt	gacagtttgc	aaataccgcc	ttgtatttct	gattcagcct	tattcaaagt	180
atcataataa	aatattttatt	aaatstatgt	tgatctgcgt	gcattttatga	tctccagatt	240
aacgttaggc	ttctctgttg	ggccctaact	tggaggtgct	tttttggatc	cctcctcccg	300
tgattcattg	taatttcatt	tcccttgtea	tggctctgac	cagagaagat	tctaaatata	360
tgcccccaaa	gcaaaaatta	tatcttttga	aaagtgaat	gaagagttga	gtcastaatt	420
tatttttagat	attactgcct	aaaacaattc	cccaaaattt	atggaagttg	gagg	474

<210> 158

<211> 584

<212> DNA

<213> Homo sapien

<400> 158

ttggattctg	cagttccaca	tcattcactc	cggcaaagga	gagaacttgt	aacaaagatg	60
agtgccaaagt	ttagtcaatt	tacctacct	ggaatactat	atacaactct	gggtctcatg	120
tgtgttaaaa	tacatacagt	gaagctgagg	aagagccact	gaagtaaaaa	gtattgttta	180
caagttggaa	aggatgtaaa	aataatctaa	agtatactaa	gtcaggaata	aaaggcagag	240
ttaataaaaat	tgtggctggt	actgatagac	gaaacagata	tattttctaa	atcctggaat	300
aattattaaa	aaattttaca	tgtatcaatg	gattccagac	tccatatttt	aagtttcaca	360
actactgtca	tttaaaaacta	taccttattg	aacgtctccc	actctcaata	aattacccca	420
aatcactctt	ctccaaaacg	taaatttgga	acacactgac	ttacaaaattt	tgggcttaat	480
ttataggatg	ttgtggccct	caaaaatata	attgtgggct	aaacaaaata	aattcttgaa	540
acaattctaa	aaatcaatca	ttgtccaaaa	tgaacttttt	ctaa		584

<210> 159

<211> 671

<212> DNA

<213> Homo sapien

<400> 159

cctaatttta	ttacttttct	tgccactgct	attattgata	gaaatacaat	taaataatta	60
agatgaacca	atccattgga	agattactaa	aattgtatct	tcccaatgcc	tcctacagta	120
agattttctt	ataattataa	cccttgga	caatttgaac	tttatttaaa	tgttctgctc	180
aaatctaaat	ttccttctcc	taggctgaag	cctgatctaa	ataaggaagt	agttgggata	240
tatccacagg	ctgtcgaaca	tggagctgca	tctgagagac	aggtggcagc	aacccaaaagc	300
aaagcaggga	ctgagaacag	gcagggtcca	agagcaaaaat	ggaacttgaa	agccaagtat	360
ggttcactgt	aaaggagaaa	atatagaaat	acggaactag	aacacctggt	ctgggatgtg	420
gtaagcacc	aaaatatagg	aaaactgtat	gaattcttgt	gaagcagtaa	actatgatag	480
taatcatgtg	acacatatga	taacaaactc	aaaacaggga	aaagaggggc	tttatttcaat	540
gctggagata	agtgaaaaaa	aaagtgaagt	gtctcaagga	cagaagttat	catctcaaaa	600
aggcatatca	gctagatctc	gcggaaacca	tatgattatc	ataattctag	actctgttcg	660

gtattacaaa g 671

<210> 160
 <211> 315
 <212> DNA
 <213> Homo sapien

<400> 160
 ccagagaggg agggctctgc ttcaccacag ggcaccagaa gaggactggt gcgcgggaag 60
 accaggtaat cataatgcta ttaaaaatag cagtaatcat actgttttat acattgtata 120
 atgtcataag gattttaact ttcatgtaac ataattgctg taaaagtttc cccagtttgt 180
 tttgtgctat ttaccctggg gttaaaatgt gtaagaattt acattttagg tatgttaggt 240
 ttattccttt ttatatgggt tctgtttgaa attttgattt tagaagacat tcattctcaa 300
 ggtcataaaa cacac 315

<210> 161
 <211> 607
 <212> DNA
 <213> Homo sapien

<400> 161
 ttttgtgtgc accttggata attgcttaac ttttaaaatt tacgttccct catttccaaa 60
 aagggattat aactcactgt tattttgata attgagataa atgtacgtac aagtgttttg 120
 aaactgtaaa gtgcattata aacagagggg tttaccatag aggttctacc ttgatgtatc 180
 aagagaagcc ttttctggaa tctgggtgcag cttgttgaga tgctgttagg taaggggact 240
 ccttggtaga atttcttaca tttgtgtaaa aagttctggt tcctgagtaa ttccaaagaa 300
 gatgctatga ggagttcact gtgcctttga tttgatccca atgggtcaga atatgttttc 360
 tcattcagta ggctactaca ggatttgaag tagaaaaaac aggggtccagt gaccttcacg 420
 ggatcctaga tgttcatgaa tttcaatcat ttgagattgt ggggtgtggt ccaatgctgc 480
 tctcaaaaag atgttgccct tcttcasaga gcattaataa ctaaaaaatc ccctgggtccc 540
 aaattttattg tgtgtmtctg aaggctttta ctgaagaaat gaaawgcaca ctcatggaac 600
 aaactaa 607

<210> 162
 <211> 443
 <212> DNA
 <213> Homo sapien

<400> 162
 tgagttttga aaaagtgaat aatcaaaagg aaaataattc cttgttggtc ataaattaag 60
 catcactaaa gtctcttgaa aggcatttct gtattgggca agatttataa tactaaagcc 120
 ttaggtccta ttcatattta aagtagcatg tttgtaacct gttactattt ggagagagaa 180
 gcagttgcct gccacaattg aagactacct ttcaaatagc aaaagagaga gagaaggctg 240
 atatttcggg ctttttaata aagatttgtg tgggtctgct tttactgtaa ctgtcacttt 300
 cccagtgaat atgatttcat atacatttga gggctttaca sgtatgggta aagttctata 360
 aattgcaaca aaatgatacc caatttcatt ttatcctttt tgtattgtga aactggaaac 420
 tttatgacat tgtaaatat cag 443

<210> 163
 <211> 686
 <212> DNA
 <213> Homo sapien

<400> 163
 caggcaaat atagtcaa atcatcacc cctcaggcat ctgtggcaag gcacccctct 60

agagaacaac taattgatta cttgatgctg aaagtggccc accagcctcc atatacacag	120
ccccattggt ctcctagaca aggccatgaa ctggcaaaac aagagattcg agtgagggtt	180
gaaaaggatc ccagaacttg gatttagcat atcagggtgt gtcgggggta gaggaaccc	240
attcagacct gatgatgatg taagttagct ttgtatatc ttgaaacacc tataaagttt	300
tatttaccga ttgaatactt aaatgtaagt gaaaatctaa tagatgttta tgtaaactta	360
ggtagacatc acctggattc cccactctat tgcttacctt tttgtttgt aatttgatca	420
gttcaagtta aaacaattta accaaaaact atgaatgttt atgatataat gaaatgattg	480
ttaactttct tattgctttt tcacacacct ataaaagtaa ttttattact cccaagagaa	540
atcactaaag gcagaattac tagaggtaaa aataactagg gttggtacag tattactcag	600
gagaagtcaa ggggagaaaa cttgtcccaa tgattcaaaa taattttggc atgggggggg	660
ggagggaaaa aaatttggtc tccttt	686

<210> 164

<211> 706

<212> DNA

<213> Homo sapien

<400> 164

ttttttttgt ttcatttgct gcttaaaata aaaattataa attagattta aatggagcac	60
taattataaa acagattgca agtaccacca tttgaaaaaa aaaaaaaaaa tcagtggatt	120
tccataacac agaaaaatgca tggacatgca tctacagtag agttaaaaaat ttcctgtgac	180
taaaaaatta aaactggaa tcaccagtag caaatgtata gtcaatggct atgacaagaa	240
cagatcctgc cgagctcata aatgcaatta ttggcttttt tgctttataa aaaagacatt	300
acatatttta ttgcattatt ctcttaataa aaacatact accacgtagc tctccccatc	360
cccattcttt gcttcagat ttttatagaa aataactgtt ttagtctggc cttggaaagt	420
gaaccaccca gcaccacct cactactca ctcttcaatt caatatgcac atagcaaaag	480
ccaacacttc aaatctcttg cccacatcaa aaaaagtagt ttcaggagaa aaacattaat	540
accagtggaa taaaaataag ggcataaaag ctatgagaga gatagctctg ccatctgtct	600
ctgggctaaa aatcaaggct aactattgcc ttggcacca caaggttcaa ggtccatggt	660
tttattagaa aagtccccac aaaaaaatta aacccccctc acccca	706

<210> 165

<211> 427

<212> DNA

<213> Homo sapien

<400> 165

tyywgggcaa ttaggcagga gaaggaaata aagggtattc aattaggaaa agaggaagtc	60
aaattgtccc tgtttgcaga cgacatgatt gtatatctag aaaaccccat tgtctcagcc	120
caaaatctcc ttaagctgat aagcaacttc agcaamgtct caggatacaa aatcaatgta	180
caaaaatcac aagcattctt atacaccaat aacagacaaa cagagagcca aatcatgag	240
tgaactccca ttcacaactg cttcaaagag aataaaatac ctagggaatcc aacttacaag	300
ggatgtgaag gacctcttca aggagaacta caaacactg ctcaaggaaa taaaagagga	360
tacaaacaaa tggaagaaca ttccatgctc atgggttagga agaatacaata tggatgaaat	420
ggaaaaa	427

<210> 166

<211> 124

<212> DNA

<213> Homo sapien

<400> 166

accatgtttt cgttgtgtgt gagcagggaa gggaactttc ctgccttatt taaacctggg	60
ccgaggattc gtggaatctg cttgatcaga gactctgagg ccaaaaacgc atcatacttc	120
ttgg	124

<210> 167
<211> 232
<212> DNA
<213> Homo sapien

<400> 167

tctgcatagc	aaatatgatt	taagaattta	acatcattat	ttgatcacia	gcgtaaatat	60
gtcaccataa	ataaatgtaa	attcattgta	caaaaattcc	caacaactct	taatacaaat	120
atggtacatt	tgacagtttc	tgaacagat	tattttttaa	acttttttaa	acctaagctt	180
tatttttttc	ctggttatta	gacacacaca	aaaaaataa	aaagaggctg	gg	232

<210> 168
<211> 677
<212> DNA
<213> Homo sapien

<400> 168

tttcacaatt	aaccaacatg	caaaaattct	cagactaaac	actgagaaat	tcttcataca	60
atgcatttgc	caccttattg	cattttttaa	atctttatct	tatagtgaat	tggtattccc	120
aatctgccta	agcaaaggca	tgcccttcta	acaagatttg	cttagagcag	aggtgataga	180
aggaagaatc	cgaagaccct	ctggcatggc	aatctgggag	cagcacattg	ttgatggagt	240
ccaagtgagc	acatttcaca	caattcattt	agtgacaagt	gggcttgctc	ccttttcata	300
caggaaaaaa	actactcaca	gaccactgcc	cagaatctgg	aataagaacc	ctcattttta	360
ggtattcttc	ccaacaaata	aatatctaaa	tattgaaagg	gggcataatc	gaaaacttaa	420
aagacacaat	aacaaaaacc	aaaaccctct	tcaaaacaag	taagcaatgt	ctgtatttag	480
ttcactctaa	aacattctta	gcttttcttg	cagtttggtc	ctaaaagatt	tgattgggca	540
caagaggaac	gaaattatta	ataaaaataa	agcttatttt	tgtttttgct	gtggataatc	600
ggtacaaaac	gtttccagat	ctgagactta	aatggatctt	ttaaggtgaa	aaggagaatg	660
ccaggttcta	ctgaaat					677

<210> 169
<211> 635
<212> DNA
<213> Homo sapien

<400> 169

ttaagaagac	tggtgattta	tactctctct	tgctagtcag	cctggagcaa	gcttgagca	60
gacgcacatt	tttgtactgg	cacatattct	tagacgacca	attatagttt	atggagtaaa	120
atattacaag	agtttccggg	gagaaaacttt	aggatatact	cggtttcaag	gtgtttatct	180
gcctttgttg	tggaacaga	gtttttgttg	gaaaagtccg	attgctctgg	gttatacgag	240
gggccacttc	tctgcttttg	ttgccatgga	aatgatggc	tatggcaacc	gaggtgctgg	300
tgctaattct	aataccgatg	atgatgtcac	catcacattt	ttgcctctgg	ttgacagtga	360
aaggaagcta	ctccatgtgc	acttcctttc	tgctcaggag	ctaggtaatg	aggaacagca	420
agaaaaactg	ctcagggagt	ggctggactg	ctgtgtgacg	gaggggggag	ttctggttgc	480
catgcagaaa	gagttctcgg	cgggcgaaat	cacccctgg	tcactcacat	ggtacaaaaa	540
tggttttgac	ccgctaccga	cagatccggc	cgggtacatc	cctgtctgat	ggagaggaag	600
atgaggatga	tgaagatgaa	tgaaaaaaaa	aaaaa			635

<210> 170
<211> 533
<212> DNA
<213> Homo sapien

<400> 170

ctgtgatctc	acaagtgtga	aaaatcttat	gaatgtaaaa	tgtgtggaga	ttcttctttg	60
tttttagctt	ccactttggg	aacatgtcaa	agcacacatt	gagaagtccc	atgagtga	120
gagatgttgg	aaagcccttg	aacttggtcg	ttaggaaaca	tccacactga	agaggaacct	180
gactgtatgg	aaggtcaaaa	aggctgtatt	aatttacatg	caaaaagtca	cactagagga	240
atgccatata	agaatgcttt	tggtaaata	acatgtttta	aagaggttat	atatcattaa	300
taaaaatata	tagctgggtc	gaagaccctg	agttatctca	attgttcacg	gttacagatg	360
gaactcttta	ttattgagga	gttccactct	ttccccatt	tgtcactact	acacttccct	420
agtctttaa	acaatttttag	gctgggtgca	gtggctcatt	cctgtaatcc	cagcactttg	480
aaaggccgaa	gcgagtggat	catttgaggt	caggagttcg	agaccagcct	gga	533

<210> 171

<211> 568

<212> DNA

<213> Homo sapien

<400> 171

cccttgsc	aa	actttccctt	aagtattgca	ctacaagtct	aagacacttt	tcactcaaag	60
ttcttccctt	ccttacctct	cttttaactt	ggagtcagac	tttcatcagt	ctgacaactt		120
ctcccctgtc	cttccctttt	cccccttca	caagcatttc	acctaacaaa	tttcttatgt		180
gcttaatacc	ctcttagaag	cagatgcaa	gatgggatta	agcacataag	aggctcctgga		240
ctaatacaat	gacaaaggct	ccccttgaag	catcacacta	aaaggaaaaa	aaaaaaaaaa		300
acctagccat	tttacattaa	ctattttctaa	aatatagtat	ttgcttccct	atttgctaaa		360
acaaaatata	ctaaacatga	ctattccaaa	aatctgtagg	gtactaagaa	tatgaagaga		420
ttcactctac	ttcaggggat	ggagttgtag	tagaaaaggc	tttgtggagg	gaggggtggtg		480
tttgaaatgt	actttaaaag	ccatcctcaa	agcctcgagg	gctatacctg	gcctggtgat		540
tatccaagga	cagtccattc	aaacaggg					568

<210> 172

<211> 167

<212> DNA

<213> Homo sapien

<400> 172

ccattttacag	gaatcagcca	cttcagttca	gacagcttta	ttaaaccgcc	tggagcgaat	60
tttcgaagca	tgttttcctt	ccatacttgt	ccctgatgct	gaagaggaag	ttacttccct	120
gaggcacttg	ctggaaacaa	gcactttgcc	aataaaaacg	agagagg		167

<210> 173

<211> 391

<212> DNA

<213> Homo sapien

<400> 173

cctcccaaag	tgctgggatt	acaggcatga	mccmccmcgc	cctgatgata	gacacgtttt	60
taactttctaa	aaatatatga	tcattgattgt	gtctgtggag	acttgacacat	ataactaaatt	120
ttaaamcaatt	agagatattt	gttcattacc	acattttggg	agtcattatt	tcctctatga	180
agagagaaaag	gaatttgata	caagttcaca	ggggcttcca	gtagattgag	actttttattt	240
ctagctgagc	tgctgatgta	tgaatttttt	ttgktattat	gactttcata	tgtattaaaa	300
ataaaaatgaa	aaaacaaggg	attaggtgag	gaacctatac	gtctctaata	tgcaaaatac	360
cacagaaata	atgactgktg	ggaaaattag	g			391

<210> 174

<211> 474

<212> DNA

<213> Homo sapien

<400> 174

gaactcagag	agaggattgt	cacccttggc	atctgagctg	acactataag	gacaatgagg	60
agtctccttg	gggatatagatg	gggagatgga	aggacgatgc	ctgtcctacg	gggtcttggg	120
aggttagggg	tacacactgt	gagctgccac	aggctcaaca	gtacggatag	ggggtgctgg	180
aaccagccag	ggctctgatac	accaagctat	gtgccccatg	cagagggaagg	ggtagtgcca	240
caactgaacca	cccagccaca	aggctatctc	cccatacagg	gcacctttaa	aaaaattatc	300
cttacagggg	aagacgggga	ggaaggatga	actgtgtgcg	gtgatgttgc	agtgagtgtg	360
agtttgtgtc	cgtccgcttg	tatgagggcc	taccttttac	taactagccc	ccaactttca	420
ttatctcccc	tttttctgtc	tacccttctg	ccttttttaa	gtggcttgca	atcc	474

<210> 175

<211> 655

<212> DNA

<213> Homo sapien

<400> 175

ccttgccagg	gtggggatgt	gtgggcttgt	tcactgttac	agcccatgta	tacctgaagg	60
gcaacatgta	cccacaaatg	ttccaggagg	tacataaaaa	atacaattca	gcctcttcta	120
aaccatcctt	gttgatatct	ctgtacttcc	cgaaagttaa	ttcgttattt	ggactccata	180
atttttccta	ttaattcacc	ctatgtccaa	ctccaacagt	gaaaaaaatt	tatttaattc	240
ttgcaataag	cctataggca	ggcagcatta	tcctcagctc	gcagataaag	taaggctcag	300
agaagcttgt	atactgtcac	ttaggtagta	attgcaagag	ctggcattca	gaccagact	360
gtgggactcc	tcactccatt	ctctttcccc	ccactaggct	gtcctttaa	atacaatgga	420
tgcttgatga	acgcttgtgg	gaatcctggg	tggacacagt	tccttttcgg	ccaaaagcac	480
cttgacgact	tgtgaagaat	taatctggaa	aacttaacct	atttataaaa	acgtgttatt	540
aagggcaggt	tattcccacc	ccctttacca	aagaaaccgg	ccctgacctt	tttttactgg	600
gggttggctc	tgggcatttt	caacaagggg	ggaacagttt	aaaaattccc	ccctt	655

<210> 176

<211> 660

<212> DNA

<213> Homo sapien

<400> 176

cctgggtcaaa	gtgggcatta	ccattcaagc	attactagac	atcaccgtaa	cgaaggctct	60
gttcacatga	aactaccocct	tctccattgg	gggctcagac	tctgtctctca	tccaggatcc	120
tgaactctgc	tccaggcacc	tgttcaaccc	tctctcccac	ccactgcctg	tcacttcaact	180
gactccagtt	acattgaaac	aattttcagt	ctaaggagg	attttctacc	tttcagagct	240
gacctccgac	tttaagactt	gacaggtatt	tatcttgaaa	ccagagaggg	agctggaggga	300
aaaaaaaaact	gagcaagcac	atcaatgcct	tttccaccct	tcttcaccc	ttccacactc	360
accgactgcc	attaccaaaa	cgccaagcac	aaccggtttg	gaacaagacg	cattccgttt	420
taattaaaaac	caactcatta	tgtatttttag	tgggggggaa	gggggggcaca	atcagggttt	480
tcaccaccaa	attttccaca	cggtttctga	acaccattgc	cttttaaaaa	actatttttc	540
cacctccaaa	atattttatt	aaattttatt	tattacggag	gtgggtattct	tcctttggga	600
gccaaattgg	gaaatttagg	gaaccttttt	tattaccggg	ttttttgggc	gggtaaacct	660

<210> 177

<211> 459

<212> DNA

<213> Homo sapien

<400> 177

ctttttctct	tcctctgtgg	aatgggtgaa	gagagatgcc	gtgktttgaa	gagtaagatg	60
atgaaatgaw	tttttaattc	aagaamcatt	cagaamcata	ggaattaaaa	cttagagaaa	120

tgatctaatt	tccctggtca	cacaaacttt	actctttaat	ctgatgattg	gatattttat	180
tttagtgaaa	catcatcttg	ttagctaact	ttaaaaaatg	gatgtagaat	gattaaaggt	240
tggtatgatt	ttttttta	gtatcagytt	gaacctagaa	tattgaatta	aatgctgkc	300
tcagtatttt	aaaagcaaaa	aaggggaatg	aggaaaattg	catcttagac	catttttata	360
tgcagtgtac	aatttgctgg	gctagaaatg	agataaagat	tattttattt	tgktcatgyc	420
ttgkactttt	ctattaaaa	cattttacga	aaaaaaaa			459

<210> 178

<211> 720

<212> DNA

<213> Homo sapien

<400> 178

ctgcaagctc	ccactccttc	catttatctt	aacgcccagg	ctgacttcta	agctgctttt	60
cacttttcta	cctccactgc	attttcgccc	ctgataattt	ttgtaagctt	acctaagcct	120
cccttctttt	gagatccctt	tcttaaaagg	gtccattcta	ttaaccctac	cccatatcca	180
gttactttta	ctacctgctg	atctatcgct	accttgcca	attcatggga	attacagggg	240
gcactgggac	aagagtaaaa	tgatccaaca	aacataatgt	tgcattttaa	aaaataagct	300
aaaagatact	gatgactttt	tataactaca	acatattcgt	ttgtgaataa	gaacatatat	360
agtaaaaaga	tgaaaatgtg	aacaggttga	ctatttctta	aatttatggc	agaaggttgt	420
tctggagagg	atgggaagaa	aaaatgaagg	ctggcagtg	tgggtgggga	aatgcaacct	480
ccaaaattat	ctatctatat	atttttatta	aaaacacca	cagtaattat	ggcaaatggt	540
aatggtttgt	ttgttctaag	gttttgata	catttaagat	ctcttgcttt	ctgggtacca	600
tttcttttct	tttcttttct	ttttttttca	aattaattcc	aaaagactta	tatctgctac	660
atgaagaacg	aagcaagttc	agctctcttg	gctgaaatgt	tcaaagctt	gagggcaagg	720

<210> 179

<211> 427

<212> DNA

<213> Homo sapien

<400> 179

ctgtgaatct	gtctggttct	gaacttattt	tttagttatt	ggcaatcttt	gtattactat	60
ttcaatctct	tcttggttta	atctaggagg	gttgatatatt	tccaggaatt	tatccatctc	120
ttgtaagttt	tctagtttat	gcacataaac	gtgttcata	tagccttgaa	taatcttttg	180
tatttctgtg	atatcagttg	taatatctcc	catttcattt	ctaattgagc	ttatttgaaa	240
cttctctctt	cttggtta	cttgcta	gtctatcagt	tttatttate	ttttcaaaga	300
accagctttt	tgtttcattt	atcttttgta	ttgtttttgt	ttgtctcaat	ttcatttagt	360
tctgctctga	tcttcgttat	ttcttttctt	ctcctgggtt	tgggtttaga	ttgttcttgg	420
tttctct						427

<210> 180

<211> 728

<212> DNA

<213> Homo sapien

<400> 180

caaacacaaa	agtcactgtg	tgtgtgatgc	ttctccaatt	ccactcatcc	tggtgccat	60
tcatgcacta	gtgcatgtat	gcattttttac	atttttttaa	ttacaaaaat	caacctatta	120
taactgctta	gatatatatg	aagtaaaaa	gaaagttctc	cctttacatg	acccatcccc	180
catcatttcc	ctctttatct	tatactgtca	gcattcccag	cttgtagcac	agtgtctggc	240
aatagtaaat	cctcaaaaa	tgatcaatga	ataattta	aatgattaat	aaataaatta	300
atgatgatgg	tgaagataaa	ttttagcatt	tattgaacgc	taactacaaa	ccagggagtg	360
tggtaaatat	tttataaaaa	tcaatgaatg	agctaaaaatg	ccattctatt	atttttttgg	420
atacgggtta	atattttact	cataaatatg	cttaagaat	attataatta	tatgacttag	480

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aatggtaaaa caatatgtac agcagtatcc tatttttttag aataaaaaata taaatatgtg   540
ctcacatatg tgggtggggc atgcctagaa acccgattag aacgggattt tttcttacca   600
ccattttttt tacctgggaa aaatatggga aaattttatt tcccttcttt ttggttctaa   660
aatttatata caggagccta tttggctttg gataaatcat tttaaaaaag gtggtttaaa   720
aaaaaaaa                                         728

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<210> 181
<211> 546
<212> DNA
<213> Homo sapien

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<400> 181
acaatccttt ggaagacact actgggcttt gggtgctgct ttttaataat tgagttattt   60
tgagcttgcc aagtaggata tattgcctgg actaaaaattt atttcctaatt ctctctgatga   120
ccaagaaagg aaaaattaag tttgcagatg ggagatgaaa tatagccagc gaatatgcat   180
actggttctg aatgaaagga attaactttt cagtcaagaa acagtctgca tgccgtaaat   240
tgaatttttc ctgcaactgg aatgattggg taattctttt tgaacactgg cctttctccc   300
caagaacact aatgaattgc taatatattt taaagaaaac tggtttttta attaggtaag   360
ctccacttcc tcttattttt taatccctaa agaaaactgt taaaaggga tggatctatc   420
acgccttttc ttttaaaacc acctttttta aaaaggattt ttccaacccc caatttgctc   480
ttatttttaa attttgaacg ccaaaagaag ggaataaaa atttttccct taattttacc   540
ccctta                                         546

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<210> 182
<211> 333
<212> DNA
<213> Homo sapien

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<400> 182
ggccactctg actgggtctg ctaattcaca tgctctttgt gacatacggc tctaagaggc   60
agaggctgga agagaagtat gtgggttggt ggatcaagat acccaagttt cagtcttgac   120
actgctatta cttagtacag tgaccactgt aacttcatct tgattgagcc tcagatgtct   180
cacctgcaaa atggagtttg aaatttgcta tgggtgggtg tcacacggat taaatgaat   240
aatgctgtgt aagcgcctat ccagcactta ataagatggc cactgcatca taatgctttg   300
ggcacaaagta acacaacatc caacccaaag ggg                                         333

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<210> 183
<211> 393
<212> DNA
<213> Homo sapien

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<400> 183
ctgaatttct tgggctttat gtggcagtgt ggtaaaaaata tatgatcaga tttcactgtt   60
aagaaaattc tttcagcaat acatgtagag tcaagtttct tgcattggata actgaacatg   120
tgggttatga gattttaaaa aatgtctcgt gacaaaacttt acggaaatgc aacaatctgg   180
acatctagtt ttgtctgaga gtggcgtgga tatgaagaac tgtgctgttg gtgctgatgc   240
cacactaagt tttggcagtc acactcttgg ttcttcatat ttgaggagat gggatggtga   300
ggaggcctgt tggctttatt ttattacgtg ccaccatcta gaatacagat tcttggatat   360
ttcatcttca caaagggtgaa gctgcaaact cag                                         393

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<210> 184
<211> 700
<212> DNA
<213> Homo sapien

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<220>
 <221> misc_feature
 <222> (1)...(700)
 <223> n = A,T,C or G

<400> 184

ccaggscawt	gaggaaaagr	gaaagaatwt	arrggstwt	caaataaggaa	aaraggaagt	60
ccaaattggt	cccntgttkg	ccagataacc	atgattgkkg	athtagaaam	ccccatgwty	120
tcagcccaaa	atctccttaa	gctgattaag	camcttcagt	aaaktctcag	gataaaaaat	180
caatgtgcaa	aawtcacaag	crttcctatm	cgamcaatam	cagmcaaaca	gagccaawtc	240
atgagtgrac	tcttattcac	aattgctagt	aagagaagaa	aatmcctagg	aatacaactt	300
mcaagggatg	tgaaggwtct	cttcaaagaa	gaactacaar	ccrctgctca	aggaaataag	360
agaggmcmca	agtaaatggg	aaaagcattc	tatgctcatg	gataggaaga	atcaatcccc	420
tgaaatggk	gatactgccc	aaaataattt	atagattcaa	tgctatcccc	atcaagctac	480
cattgacttt	cttcmcgga	ttnggaaaaa	tctactttac	acttyatagg	graccaaaaa	540
agaagcccwt	gtagccaaga	caatcctagg	caaaaaagac	caamcctgga	ggcatcacag	600
tmcytgactt	cmaactatwc	taccaaggny	tmcrkgmcc	aaaacagcac	ggkacntggt	660
mccaaaccrg	acwtwtwgac	cmmcagacac	agaacmgagg			700

<210> 185
 <211> 192
 <212> DNA
 <213> Homo sapien

<400> 185

ccagyccttc	ttttaagtaa	gcgctttttc	aagctcattg	tagctacaaa	gtcaataaat	60
tggctcttgt	tatttttacc	tgaaaaggct	gttaaagggt	aaaatgacaa	actcaaatc	120
aaagggattg	gaggatttgg	tgtttatgat	ttctcagaac	aacaatctag	agaccaccag	180
ggtgggtttc	ag					192

<210> 186
 <211> 688
 <212> DNA
 <213> Homo sapien

<400> 186

gtgctggaat	tcgcccttag	cgtgggtcgcg	gccgaggtgg	gatatttctt	ctggatagat	60
ttcagatagg	tagttccctc	aaataagatt	atatgggttt	gcattttcaa	ggcagagttg	120
tatacttcct	gctctttatt	taaataaaaa	aacttgaaaa	tctgttctgc	ccagtattgt	180
aagcgctcag	gtacaaatat	gaatgaaaca	atctctgcct	aagtaacaca	agtatagggg	240
caagattctc	agtaaaatc	tcacgtgaaa	tttgtaactc	actagacact	atcaggagat	300
caataattat	gtaattaaaa	aaaataatta	cctgccaaac	tgggttcttc	tttggcactt	360
ctgcttggtt	ttaagacaat	tctcacatag	aagcttatta	ttccccatta	gtcattccat	420
agatgtaaaa	ctggtagaaa	caggacttga	attgaacatt	ctttacaagt	aagttatata	480
gcttctgaaa	aaagggcttg	aaaaagcatt	tttggggact	ataagaacct	tcaaatgctt	540
tccccctcta	acaaacctta	aaattatttt	gaaaataatt	taaggggggt	gatttttctt	600
tgtaaaaatc	ttgaacccca	cttaccaggt	ggttgggtcaa	accaaagttc	aaaaaaaagc	660
ttctggcctt	tcctttatcc	cacttgca				688

<210> 187
 <211> 779
 <212> DNA
 <213> Homo sapien

<400> 187

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gcaaaaaaca gatacatttt cagtgtttta aaatgaacaa gtatggaaag gcttatacag      60
taactgaaaa gtctcctttg ggaagccaag gtgggaggat tgcttgaggt caggagttca      120
agaccagccc aagcaacatg gcgagacccc atctctacaa aaaattaaaa aatcagccag      180
gcatggcgga catacttgta gtagtaacta catgggaggc tgaggcggga ggatcacttg      240
agtccgagag tttgaggctg cagtgcgccc caacgcgccc tgtactccag cctgggcaac      300
agagcaagat gctgctctaa aagaaatttt cttttaaaga aaaaagtctc cctcatagcc      360
tgttctacaa aagtccattt tcttcccaca aaaagcctct ggtacctggt gttagttctt      420
ggggtggaag attactttta aaaatagaac tattttttta gtatatcttt tagggaactt      480
tagttcccga agcttttaga aatgggatct tgaatacaaa agggatttca atacctatga      540
caatgcttaa agaattattg gggcatttat ttttcaatgg aggggtccaca aatctttgga      600
aacccttggc caattaccag aagccacttt aatttttgac cgaaaatggt tttaaaaatt      660
ggcttttgga aaaactgtct ctttcccaaa aaatgaaac cttgaaaaaa aggggaattt      720
ttaagggtgc cccctcatta aattttaacc cctctgaaag aaaaccctct tgtgacagg      779

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<210> 188

<211> 394

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(394)

<223> n = A,T,C or G

<400> 188

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ggcgamgtct ggycaccatc atgcccttta atcaactcac acctgtttaa agagtgtttc      60
tgatttgacc ttcacccctt agtttactgg cgtaaaaaaa agtctcagca attttcatta      120
tttctcgtgg gtctcattat caaaccttta cttatttcgg catatttcct ctgggcttct      180
tctagtttct gccttacaag caatgctggt ctgtaaatatt attgaaacct ctggaacatt      240
tcacctttag agatggagga tggaaggatt ggyaccagaa gagggctaag atacgttytc      300
tgtcttngag ctgaaagcac agyctactct ccttcgtttt gycgatgaga aaagttgagg      360
ccagaagggga ggtgacatgt ttagagtcac ccag                                     394

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<210> 189

<211> 681

<212> DNA

<213> Homo sapien

<400> 189

```

aagttctgac tttggtctat aaaacagggt tattggctgt ggctgcactc aatatctaaa      60
aagttattag gaagtgcctc gttattgtca ttaaagatat ctaaatatgg tagaccaaag      120
gttggtgaga aacacatatt atggactgag ttctgtttct tctgctgtgg cgcacctaaag      180
ctcaagcctt ccttctctcc ctccccttct ggccggcatg gtatctgagc tcacagacag      240
acaaggcatg ttagaatcat cagatcatga gcaccgtgct gggatttagc cctctccaaa      300
gtcaattctt acagtccata ctttgcttaa atcctcagtt gttgaggtct gctctgctgt      360
cagtaatccc agctataaat tcccccaaaa tgtggggcct agataaagta gaagggtgat      420
ggactcagct tattttcatg ggatgacagg aactggaaaag agaaaaggga ttgaaaataa      480
aaagttattc cagaatagca ttaaccctct tactgttcaa gaattaagaa agcctactta      540
gaaatgaggg ccttgagaat gatacccaaa tattggtctt tctacaaaaa aatggccttt      600
ccaaatatct gcttctctgt tcccccaattg gctttttaag tagaattaag ttacctaaaa      660
ctttacctga aggggtggtt t                                     681

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<210> 190

<211> 839

<212> DNA

<213> Homo sapien

<400> 190

caaatacatg	atttccattg	gcatagactc	ttctatagtc	tctcaggcac	accttatgac	60
taataagaac	actgtcttct	agatataagc	caagttttag	gagttatctt	tgtagtttct	120
gtgttgagac	tatgggtctt	ccctgtgcaa	agacttgatt	agcaaatact	atttgaaacg	180
atcccaaatt	catagtgcag	ttgaccaccc	ttctgatcaa	ggggatctct	gtatatccca	240
tgaaagcttc	ataggtctca	ccctagatta	agtgtctcac	ttctcaagac	agtgaacaga	300
tggaagactt	ttgtagttat	cattatacaa	ctgtgccctg	tgtgttttat	tatacaacca	360
gagaactgag	gcactggctt	tacctgtcag	ctacgccagg	ggtgtgacgt	catctttctg	420
acttgatcac	acatgccaca	ttgcttaata	tttcaagctt	agactgaaat	aatcctgtgg	480
taaaaaattt	ttggggggct	ggggaggtaa	agaacaagg	ggggaacttt	ggaatatttt	540
tattcattaa	tcatatttcc	cgaattgtat	tttattttga	aatgaccata	agggacttaa	600
atacgtattg	tgggttaaatt	aaatggaccc	aaatggaggt	aagtaaacct	aatgggacaa	660
atgaataaaa	ggtttatgac	tgggagcatt	tacccatgaa	cctccttaga	agctatttaa	720
cctttctttt	ggaaagccct	gaaggctggg	aacttaaatt	ttaaagacag	tacctatttc	780
cagaatcgct	tccaaatggc	catgttttaa	agggccaaca	ttttgggatg	gccctgccc	839

<210> 191

<211> 697

<212> DNA

<213> Homo sapien

<400> 191

ccatcctgaa	tactgatttt	ctaattggaac	tctattcaat	ggcgattgta	aaaccctgag	60
gctccgttac	tattatggag	catactttca	tctcattctc	ggctattggg	caatatgtat	120
ctcataagat	tttatcacat	ttcacagatg	aactgttaat	tgattccatg	ggtacgatta	180
ggcgagatcc	aagctggagc	tgcagctctg	agtcccataa	attcctttgtg	cttctgtaaa	240
gaataaatct	gtttttaatg	caaattaaaa	ctactggcag	ggaatttttg	ctcccagtta	300
ttaaaagact	ggaatgtgt	aagtggagaa	aggcaataac	tgcagtaate	tcttaccgga	360
ctctattata	attccaaaca	tacataatgg	tgagaaaaac	cgggaaggga	agaatgtggc	420
aatgtccact	ctttgcccga	aacataaccc	ttaatttcca	tggcggggcc	aaacactggt	480
aaaaacaaaa	atgggtaccct	ctatagcatg	caacttttat	ttcactccaa	acgaaaaatt	540
attttgacta	tggcttgga	aatccattag	tagaagaagt	tttataacct	ataggaaccc	600
ggccatttca	tttctaccaa	atcacaggaa	ttttagaatg	ggcaagggaat	ttacaggaag	660
acttgcccaa	ttatcttttt	ttgggggact	aaaccaa			697

<210> 192

<211> 687

<212> DNA

<213> Homo sapien

<400> 192

ctggttacta	tagctttgta	gtataattta	aagtcaggtg	atgtgattct	tccagttttg	60
ttatttctgc	ttaggatagc	tttggctatt	ctggatcggt	tgtggttcca	tataaatttt	120
aggatagttt	tttgctattt	ctgtgaagag	tgtcattggg	actttgatag	ggattgcatt	180
gaatctgaag	attgcttttg	gtagtatgaa	cattttaaca	atattgattc	ttccgattaa	240
tgaacatgga	atgtttttcc	tttatttggc	gctctcttta	atttccttca	tcagtgggtt	300
ataggtttca	ttatagagat	ctttccttct	tttgggtaat	tcctacgtat	ttaatttatg	360
tatcgctatt	gctaaatgga	atgacttttt	aaatttcttt	ttcacattgc	tcctgggtggc	420
atattaaaag	ctactgatgg	atggtgattt	tggattctgc	cactttactg	gaattgggtg	480
atcagttcta	atcgttttct	tatgcacccc	tttacgggtt	ctacatgtaa	gaatatatca	540
ccttcaaaaca	cggataattt	gactttcttc	ccatccaatt	gggaggccct	ttatatcttc	600
tcttggcctg	aaggctctac	ttaaaacttc	ttatcccttt	gttggataaa	cagtggggac	660
aaatggacat	cccttgtcat	ggtccca				687

<210> 193
 <211> 493
 <212> DNA
 <213> Homo sapien

<400> 193
 ctgctaaaat gatgttgcta aagcattcct ttttcttttg attaaacttc atgtttacaa 60
 aaaaattaat tctagcagaa taacgaatgg ttttggtttc tagttctctg ctgaatgaac 120
 agttttgcca attatcttca tagagtagtg atataatgaa tgcaacctca aatgcaaacc 180
 aaccaattca cagtccatac cccaatcact tccttcatca gcctcaaaaa tcgctaagtg 240
 aaccagtaga atggttttgg agcagtaata ggaaagcaaa tagaaagtca aggggggactt 300
 tcaacgccaa caagaccaat tcagatcctg atctgactgg tttctaatac aatctctttc 360
 cagagtaatg gagcatgagt ctgccacaca gaactttaga gagagtcctt tatttcaaag 420
 actgtaaagt tggaagaatt cattcatctg caaagtcaaa tgtcaaaagt tgtgcttccc 480
 actcctcatc agg 493

<210> 194
 <211> 424
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(424)
 <223> n = A,T,C or G

<400> 194
 cyagggcant tnagcangas aaggaaatan mggggattca attagggaaac wraggakarw 60
 caagttgtcc stgtmtgcag atgmsgtgat tgtatatcta gamcacccca ttgtctcagc 120
 ccaaaatctc cytaagttga taagcawctt cagcarmgtc tcasgatser acmtcwatns 180
 gcraaantca cmwgcattct tatacaccaa tawcagacaa acagagagcc aaatcatgag 240
 tgaactccca ttcacaattg ctacnmaaga gaataaaata cctaggaatc caacatacaa 300
 gggatgtgaa ggacctcttc aaggagaact acmaaccact gctcaaggaa ataaaagagg 360
 atmcaamcaa atggaagaac attccatgct catgggtagg aagaatcaat atccgkgaag 420
 atgg 424

<210> 195
 <211> 229
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(229)
 <223> n = A,T,C or G

<400> 195
 tgaacaccct tnngaaggaa cctgctcgna tgtannanaa anggaccgga cagtctgcta 60
 aaatcgccct ctttagacgc ggcgcgccgg ggcagagttt ttctctgggtg ctttgacctg 120
 tatttggttt aatgggttttgc tcctaattctc ttcaatcaat aaaattgtgc gtattttaact 180
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 229

<210> 196
 <211> 557

<212> DNA

<213> Homo sapien

<400> 196

gcgggtggctc atgcctgtaa tcccaccact ttgggaggct gaggtgggca gatcacttca	60
agttgagagt ttgagaccag cctgggcaac ataacaaagt gagatcttat ctctacaaaa	120
aaattaaaca aacaaaaaaa caaatcaaca ttcatcttga gggctctttg gtcttcttaa	180
agaacaaaca tatgaaataa ataagctgat tcttaaagat aacaaatata atgagctttc	240
tcaactgtaa aagcatctct aagtgtgtct atcaatgcat atccactcca tgaactaacc	300
tgaagaaagt gttgaccatt ctacccaatt aactgtaaac taagattgct ttaatgggtt	360
gcctaaattt gagtaccttt aaatttttgc tttttatcca aattcattct cccttcttca	420
aattaaatag tttgttaga aatcggataa gcaagatgta ctttttagaa agggcaatag	480
aatcctacaa catgctagaa ttgaaatgt ttttttaaat cagtmmttc tctatgctag	540
taactaagaa aattata	557

<210> 197

<211> 624

<212> DNA

<213> Homo sapien

<400> 197

ttttactacc tatatttaaa atgatccctg acgcccctca agacaaatat attaatTTTT	60
ttactttgtg ggatagagat cagaaaaaga gtagagatga aaatactgga gaaacaatgc	120
aggagatatt tatgagggtga gaatgtcaag aaacttgtaa agggagaata ctataatgac	180
ccctgaagag agagcttttag accagttgag tattagaggt tgccacgtgg ctattcatcc	240
actaataaat acaagaaatt actaaaatgg aagccactgg aaatatgttt tgaggaaggt	300
gagaatgtgg acctattata aatgggtgaa tatgatttct ttctcattaa gttcataaat	360
aactttcaga catgtaacag tttatgaagt gtgccgtagt catttagtat aagttttata	420
cacaaaagtg tttttactaa gactgtcaca ggttcttttg tgaatcttgt ttgtttttcc	480
tcattgtaaa tactgcaata gaacatttgt gtcttaacat aaggcaataa atgaccttaa	540
gaaccttcac ttttatatag aaagtggagg aaaagttggc agagtaattt gttgattata	600
gataaaaagt cttgtagaaa ttgg	624

<210> 198

<211> 175

<212> DNA

<213> Homo sapien

<400> 198

tttttttttt tttttttttt ctaacactta tgcatttatt ttcattgtga agaagaaaaa	60
cgtaactagc acgtgaacat gactgcatgg atacacggct cagcacgagg cttaagttag	120
aagttagtga aagcaaaacc gcatgttgat ttaagtgaat taacagaaca gaaaa	175

<210> 199

<211> 871

<212> DNA

<213> Homo sapien

<400> 199

ctgttgatca atgatgagct cccaagagta accagcctct atatagtcag catcactggg	60
ttctcaggaa aagcatcacc attgttcac ttgctgcaaa atgtatgcac aagtatcttt	120
ttatttttaa aaaagccctg acattttatg actgctgctt ttctaagata ttttcaata	180
tacagtccat acggttcaga cacaatggac tggggataga gacggctata gtgccgataa	240
tggagaaact agccagagct tcagatattt gttttccagg acatctcaat aattgggtac	300
acctcacaat atgtgagact tgacgtcgag tggcacggca tactctggcg caggcacttg	360

ataaagactg	tgtttgcaaa	tacttagcct	gcacttcaag	ataccaggca	tctaagcacg	420
tcccagatgg	tgacagttaa	tcttcaaaaa	accctatgtg	gaagtattat	cattgtcctc	480
attttacaga	tgaggaaaaa	gagacacagg	gatgtcaata	tcttcctcaa	ggtcacacag	540
caagtaagtg	atggaacagt	ggctcagcca	tgaagctatt	gctgttaacc	actaggttga	600
tttgccctca	tttaatttctt	cctaaaaactg	cacatttccc	gttagtccct	ctttttggtc	660
tgtcgtttga	ctcttggtta	ctgcttagag	gaagattcat	tctattatct	tctaacttag	720
taaatatgtg	caactccttg	gggacatgac	caggcaaaaag	ctggatacag	aaatgtatgc	780
ccaaacacca	tcccaagtta	cccctaacag	gtcttttctg	gaccctgttt	gtaagggggg	840
tatatttgga	aaaatttttta	aaattttctg	g			871

<210> 200

<211> 737

<212> DNA

<213> Homo sapien

<400> 200

gacattttga	aggtaacagc	aatatctgtg	tatagatggg	gttgtgggtt	tgttatttat	60
ctgctattgc	tgaactatcc	tttgtcttga	gcgataaaaag	agaagtaaaa	tactaaagaa	120
ctgaactgtc	catttcttga	ccatgagtaa	agatgctggc	tgtcaaactt	cctgttcata	180
cattagttta	tttatagagt	gtactctcta	tgaagggtat	tgactgataa	tgttactttg	240
acttcagata	gcttgcagtt	taatggaggga	agaagacaaa	catgcaaata	actaggtcaa	300
tgaggcatcc	tttgtgttcc	attggaagct	aggctgcttt	gtaaccttgt	taatttctgt	360
ggttttggag	tgcattcatt	agcaaataca	cccctgttcc	ttatccattc	tctgcttttt	420
tctttatttg	gcatttgatg	acattttttc	atgtggggaa	attgagtcag	gtgaggtgga	480
aagaaaataa	ggacacgaca	ctaaattctt	tgatgttttt	ccttaaaaaa	ttgtttttca	540
agtgtcccat	aaaggggttg	gaagttttta	gagccatagg	acttggatta	ttgtgaaaga	600
gtgtctctag	ggggccaggt	taaaccattt	caaggactct	ccttctctca	tctcccttgt	660
tccacccagg	gtggcgaccc	ccaaaaagca	caaagcctcc	ctttcttcat	gggaagggtg	720
aggaaacggaa	gggaacc					737

<210> 201

<211> 493

<212> DNA

<213> Homo sapien

<400> 201

tctagaaatg	cagcttttat	ttattacccc	atttctttca	agtccttggg	aaataacata	60
ttaagggtag	aagaaattaa	cacatgatgg	aaaagtcatt	gtgacgcca	tgaatttcat	120
tgagtataaa	ctcatctact	tcaaatttat	tttataacac	aacctaagat	actcaagata	180
attattttaat	ggtttagctct	taagttgaat	tgggtctacat	aatgcgtggg	aagaaaacca	240
gattttttagc	cttcttgcca	aatccagacc	tctgggtgat	ttttctttga	cagaagatgc	300
aagttatttt	ccaatttcac	aattaaatgt	atttaacatg	aacattatct	tgctttaaaa	360
actataaaca	ttgtaggaga	attatagcca	gtcttcagtt	ataaccactc	caccctcctc	420
actttctctc	tctctctctc	tttttttttt	gctatgggat	ttaatgggaa	aaatatgtaa	480
aaactgtcac	ttaa					493

<210> 202

<211> 283

<212> DNA

<213> Homo sapien

<400> 202

cctttttatc	tcagtgcac	cgtccgggga	cgcagggtgg	ggtagctcaa	ggctagcctc	60
aaagggcagc	cccacctcct	catcctggac	cacagagacc	acctgcttgg	cgcgcgcgtc	120
cttttccgag	agggtggctg	actccggggg	gctgggggct	gggctgccc	ccccgccgct	180

gttgctgtac tcctcgcccc agtcgatggg ggctgccctc ggacagcagg tgcaggttgg 240
gggcactggt acgcaagacc atgctgcccc gagaggtaga tct 283

<210> 203

<211> 713

<212> DNA

<213> Homo sapien

<400> 203

ctgcttttgc gcaaggtgcc actggacgag cgcctcgtct tctcggggaa cctcttccag 60
caccaggagg acagcaagaa gtggagaaac cgcttcagcc tcgtgcccc caactacggg 120
ctggtgctct acgaaaacaa agcggcctat gagcggcagg tcccaccacg agccgtcatc 180
aacagtgcag gctacaaaat cctcacgtcc gtggaccaat acctggagct cattggcaac 240
tccttaccag ggaccacggc aaagtcgggc agtccccca tcctcaagtg cccacacacag 300
ttcccgtca tcctctggca tccttatgag cgtcactact acttctgcat gatgacagaa 360
gccgagcagg acaagtggca ggctgtgctg caggactgca tccggcactg caacaatgga 420
atccctgagg actccaaggt agagggccct gcgttcacag atgccatccg catgtaccga 480
cagtccaagg agctgtacgg cacctgggag atgctgtgtg ggaacgaggt gcagatcctg 540
agcaacctgg tgatggagga gctgggccct gagctgaagg cagagctcgg cccgcggtcg 600
aaggggaaac ccgcaggagc ggcaccgcag gtggatccag atcttcggac gccgtgtacc 660
acatgggtga cgagcaggcc aaaggcgcgc cttcgaagga gggggctgtc caa 713

<210> 204

<211> 275

<212> DNA

<213> Homo sapien

<400> 204

gtagacaagt acagcagatc cagacaccag atctagctag gctaaatgta cagtattctaa 60
cttgatctga actgaacctg tattccttga tgatgcctaa aactacatcc atagaattct 120
ggtagaacctg taatacagtt ctgaaagtac agttttatat aataagatgc tgatctcttt 180
attctttcaa gtaagagtgc tagagaacaa attgtgttac ttgccttggg atttattgaa 240
cgtctggaaa atgctgtctt cctagatcca aacag 275

<210> 205

<211> 694

<212> DNA

<213> Homo sapien

<400> 205

ctgttcctgt acatttaact gaaaaaaaaaag taacttaaaa taatataaaa atagcactca 60
tgtatgtcct acagttatag gtgaaatttg atattgtttg tcttacatag catacctata 120
gacagcttaa gtaaagtac tgtaagagg gttatgctta ttgatgaact cttgtagttg 180
cttaccagct ctgtagtat agttaaatg atctcagtag cttcaagtat ttataaaatg 240
gttgaagtcc aaatacatgt gataattaca atacactttg aattaatgga ggggtggagg 300
ctagttgaaa tgcattttat ttacccaagg agtatgttaa aatgatagtt ataaatgttg 360
gaagtttaaa gcaagatact cagttagtt ctttacaat cataagaaga acaaaattag 420
atgttgacat tgctatttta ggctgtgtgt tttccatatg cttcttgett tccctgtcac 480
aggtgggtgc agcaatattg gtgtgattga gggtatgctg gcaccactcg cacacaggcg 540
cacaatggtg ttagctgggc agaaagagtg gcatctctgg ctaccgggct gggggcgacc 600
tttaccatag gatgaagtaa ccttgcattc ggctgcaagg tgtactgtac cgtacacagg 660
tgctgggtcg atggccactt tctgcttttc tttc 694

<210> 206

<211> 704

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(704)

<223> n = A,T,C or G

<400> 206

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ctcaggggat	ttgcccgcct	cacccaattc	aactttcgta	agtcagtatt	taccatctaa	120
ctcagtgccc	caaaatttaa	aatttccttg	cactttacag	caaaaataca	tattggggct	180
ctactgaagc	aatatataca	tgtcaaaact	aaaaatcaga	aaagcaaaag	gggccattca	240
acatatagca	gcttatattt	aaatatgtac	aggtatgtat	gttttcacag	ttagatcttt	300
aaaaaaattt	atatttgata	tgttcaaaaa	tacttctatt	ggctataaat	aatattttaa	360
aagctcaact	gatcaaaatg	cattccaaga	acatatcaaa	ttaaataaat	cttctacgtc	420
tttaaaaaca	gataattgaa	gtcagtaaag	cttgagggtt	gtgttaagt	tattctgtca	480
gtccctacta	ctaggggaag	cagaatcttc	taaatacgat	acgaaagaaa	ctcccaaagc	540
ttggaaggaa	tcggcagctc	ctgaactttt	tggggggggc	atccctcttc	gggattgaca	600
tcgcacataa	atgttgcaag	ctaagggacc	ccccccgggg	gagtggggcc	caaaaaaac	660
cacaccttcc	ccgtcaatgg	tggtccccc	accaacctta	aaaa		704

<210> 207

<211> 225

<212> DNA

<213> Homo sapien

<400> 207

ccattttaac	tgtactgcc	atagaattct	ggaattgtg	aaaattgtat	cattgaagtt	60
cagtaggatg	tgtggcttaa	aaatttatca	ggaccacaaa	aaagaaaaca	aaaatatttg	120
gtactgaggt	tcattgccag	ggcaggaggt	atttccagaa	aatactcatg	cctgtgttct	180
gttccttgct	ttcccaaata	ctgcatgtga	ctttcctaag	cygca		225

<210> 208

<211> 678

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(678)

<223> n = A,T,C or G

<400> 208

cctatatcta	tcaaaaaaaa	tccagttcct	aactaataat	ctcccaaaaa	gaaagcacca	60
ggaccagatg	atataaatgg	caaatttttt	caatcattta	aggacaaaat	aataccaatt	120
ctgtatcatt	tcttccagaa	cacttcctaa	ctcatcgat	gaggccagca	tcactcta	180
agcaaaacca	gataaagcca	ttacaagaga	gagtgcagca	ccaatgtggt	tttattgagg	240
atgcaaacaa	aatttaacat	aataattaat	agtgaataac	tggatgctct	ttccctaagt	300
tagagattaa	ggaaagaatg	tccccttcac	tactcccata	caacacctta	ctgaaaattc	360
tagctagctt	tataaaataa	anaaaaacca	naaaataaaa	taaaagggtg	acagactgga	420
agatacagtg	aaggaggaag	aaataaaatt	ttctttgcgc	ataacatgat	tcttctatgt	480
ggaaatcaca	gagatttgaa	catttttttt	ttttgagaca	gtttttgctc	ttgttgccca	540
ggttggagtg	taatggcgcg	atctcggtc	actgcaacct	tcacctcccg	aattcaaggt	600
gatttctctg	ccctcagcct	tcccggagta	agcttgggga	ttaacagggc	atggcacccc	660

ccatgcccc agctaaat

678

<210> 209

<211> 720

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(720)

<223> n = A,T,C or G

<400> 209

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aaagtatgca	aagagtagga	aattattctg	atgacatatg	gaggggttaca	aaggagaaaa	120
ctttttgcta	cctctgataa	agaatagact	aaattctcca	agaccaatct	gactgggtgct	180
ataataaaag	gaggtacaca	cggaagcaca	agggatgtgt	gcctctggag	gaaaggtcag	240
gtgaggactc	agtgagaaga	caagccaagg	agccagggtct	tggaagaagt	caaccctgtt	300
gacaccttga	tcttggaacta	accctgtgga	caccttgatc	ttggactttt	agcttccaga	360
actgcnagaa	aataaaattt	tcttggttaa	gccaccana	gtgtantgtt	ttggtatggc	420
agccctaaca	aattaaaatt	atattttaac	agagaatata	aaattcta	ataacatttt	480
acagtaaagc	atcatggctc	tttttttct	tattaataaa	tccatcaaaa	cagaaagt	540
tgcaaaattt	taacacattt	ctctaccact	actgtttcta	ctctcttaaa	actactccgc	600
aaatataaaa	atagaaggcc	aaaatgcac	attaaaacga	tgtttgggga	ctaattggcct	660
taaaattcta	ttacacttgg	aaatatacaa	atattcaaa	attatctatt	gatcacctca	720

<210> 210

<211> 277

<212> DNA

<213> Homo sapien

<400> 210

tccatgtatt	tttatacaga	atggaacaat	atgtatgtat	gcaatyktta	cattccacca	60
tgaataaaaa	cagtataatg	aaaataacaa	tagattcaaa	caatgatatg	ctattttttt	120
ttacctatga	cattggcaag	gtcttcttaa	aaaatctgcg	aataaccgat	gttgagagaga	180
tcatggggaa	atagccactc	aaatgttact	catgagagtg	tacatatgtg	taacttcact	240
tgaggggcaa	tttggtgata	catttaaaaa	gttttgg			277

<210> 211

<211> 715

<212> DNA

<213> Homo sapien

<400> 211

gtggtagaaa	tactaatttt	gcaattacag	aaaaaaacaa	atgccattca	catgggttyct	60
aacaaaaagt	gtctgaccac	ccccaccccc	caccctcaa	aaagccctta	aataaagagg	120
aagatcaaaa	gaaaacaaaa	taattcccga	gtttcacctc	atacatacaa	tatagcacag	180
gaagtggcaa	agtttaaaat	aatgccttta	ctgttaggac	tagtatgctg	tcaaaagcca	240
caatcctttt	gttttagtga	gttgattttc	aatagaaaaa	tacaaatgaa	catgtgttta	300
agttccaaca	tggattgagc	acctctgaat	ttagtatcaa	atgatttaatt	ttattttttca	360
gatgtcaaat	cttagtataa	aattttccat	tattttaaac	ttcacttgaa	tctttaaaaa	420
agctgtctaa	attgtactat	atgagttcag	tttaattctc	tgtaaaatgc	taacaaattg	480
aatgtcagc	agtcctttta	aaaaaaatgg	gggctgggtt	atttctagaa	gaactctcat	540
taagctttga	aaatcagaaa	tcagagacaa	ataacttcag	atatagacta	gctccacaag	600
caaatttata	caattatctg	taacagtcta	tacatatatg	tgtatatata	tataccgtaa	660

ccactttcat aggtaaaaaa tattaacttc atgtcacact atgatcagaa gtata 715

<210> 212

<211> 717

<212> DNA

<213> Homo sapien

<400> 212

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gaaactcttc	ccacaaccca	gcagtagata	tattaaaacc	tacaattttc	agggatacaa	120
ccaatattta	attcttttga	gggttttgtg	tttaatacaa	ggacacaaaac	acacgtataa	180
aatgacgatg	tcaatactga	ttaaacagaa	caacaaaata	agaagctcaa	attatcatca	240
gctatttgtg	atatctgaaa	taacaataat	gcacttgatt	ctgaaagaat	gattagagtt	300
cctactctga	aaatctaatt	gtcttgatgt	ggcgaagtga	gaagaaagga	tgatttttct	360
aatgaaaagc	atgtatacgg	gtagcccttt	gcgagattct	gtcaaaaacc	tgaattttgc	420
attagctgtt	ttaccaccca	aacgttttta	cccagggatg	tgcagcaatg	ggaactctca	480
tacactgctt	gtgggaatat	aaatcagtat	aaccactttg	gaaaaccatt	taacattgtc	540
aactacagct	ctacacacaa	gtgctataac	caccatttcc	actccagggt	atacaccccta	600
aaaatatgaa	gtgcccattg	ctacccaaaa	ggccgcctaa	aaggaatgct	tttgagaagg	660
gttaaccttg	ttaattagtg	gcaaaacttg	gaaaacaacc	cccaaatggt	cccatcc	717

<210> 213

<211> 599

<212> DNA

<213> Homo sapien

<400> 213

cctgttttgg	cgaggcagga	gggaagcggg	atgggagtgg	tggttaggcc	aagggtagtt	60
caaagcgatt	cagcaggatg	atgaccacag	gagtgctgga	gccgggcctt	tcagcccccg	120
tgtggatgat	gaccggccat	ccaggacatg	cgagggcttg	ggacagtgga	cagccagtgc	180
cacacaagga	aggaccgatt	aaatgacaca	gttaaaggaa	tttggcctag	ggagtgcagg	240
ccagaaaggt	ttggtctttt	tatatatgta	acattggaaa	aaaggaacat	ctcctgttcc	300
ctgtattaag	ttttgacttt	agctcagcaa	atgcagtgtt	tgtggcagta	aatatactct	360
gataacaatg	ttctttccca	ggaatttaga	gttttatgat	ggttattgaa	aatgtttaca	420
tgacaggctg	tcaataatat	tttttgcttc	taaaaataaa	acatacataa	agtgtacgga	480
ttttaagtat	gcaactcact	gaacttttca	taccgtaata	caccacccta	gtaaccttcc	540
cccagttcaa	gatgtagact	gtttccaata	accctcatc	ctgttcctta	atagcccc	599

<210> 214

<211> 789

<212> DNA

<213> Homo sapien

<400> 214

ccttatgaca	aaccttgcta	tgccaaggat	atgcttcact	atcttcatct	atcaaaacac	60
tatgcatcat	agatatctaa	ttttttcatc	tcttgcatga	agtctttcct	gatttccctc	120
tgctgaaatt	tcctctttca	aatgatgtgt	ttccatagta	ctttgtccct	tttcaaagat	180
atatctcaca	tcgcatattt	taccacagtt	agtttcatct	cttaactctc	acactagatt	240
acaaagtcaa	tatagacaaa	gaaatgttca	accttatata	acctcctctg	cctatgctgg	300
taaattgcac	ctactatgtg	ttcaataaga	gcttgctctt	ttcaatatat	aaaactttgt	360
aaagattaaa	gaccttgtag	aaagtcaaga	ggaagatagc	aatttctact	ctaagaactt	420
accctaagga	aacattcatg	aagagatata	aggggttatg	tgcatggatg	ttcattatca	480
tattattctt	cattatgaag	attatgatgg	taataatgaa	aatgattatc	ttgtattggg	540
ccttatttga	agtcaagcat	tgagaatgta	ctttatctgc	attatctcac	tgagtctctg	600
tagcagccct	ataaggtaca	gactgttatc	taagcttaaa	aaaataaagt	taatgtccaa	660

ggtcaaacaa	ctagtaaaag	aaggggggcta	ggaaatttgg	aacccccaaa	ggggcaacct	720
ctcaagggct	atgaatcctt	accattatta	taagggaagct	tggcccatgg	tggcccaaaa	780
aaaaccggg						789

<210> 215
 <211> 765
 <212> DNA
 <213> Homo sapien

<400> 215						
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gagtcctgagt	atcaaagact	tgtattagag	agggttgttg	tagtaatcta	gtcagggtat	120
gagaaatgg	ttgtattaga	gtgtcaggag	tagtcgtggc	aaaaatatat	agatcaggat	180
gagggatggg	cctcatctca	cacctgact	ccagtcaatg	gcagtggctc	cctggagtac	240
actactatag	gaaggatttt	gtaaagtttt	gtctggcctc	agtggagggt	gaggtagggg	300
aggagtctta	tgaacagtta	gtgggtgtctg	ccatggttga	aacaatggag	aagggggaca	360
ccttttctgt	gcagatgttg	cttctggtag	atataatcca	caatgtaatg	ggagaagtac	420
taagaatcag	taaattatgg	aggggtgtaaa	agactactga	tatttaagcc	tgcggaccgg	480
acttagagaa	atgatagtta	aaggagaaat	atccagcaaa	caaagatatg	acattgaagt	540
ttgggactgc	gatttagtacc	agagatttgg	attggagggtg	atttgtatag	aatggatagg	600
tgattttact	cttgcaattt	ggattgaggg	gtggggaaaa	ccagaaaggg	gctggggggg	660
aaattagtag	aagggtcacct	tgaattcatt	gtggtccata	tcaatgctga	aactgattgg	720
ggaacttttt	actcttgagt	ccctttgtaa	gggaacccca	gaaag		765

<210> 216
 <211> 780
 <212> DNA
 <213> Homo sapien

<400> 216						
cctttttctg	tggcaaatgg	aggcttttca	ctgcctgtag	agacaataca	gtaagcatag	60
tttaaggggtg	ggtcagaaca	tgttaagata	acttactgta	tatgtattcc	cttgtatttt	120
gttaaagctg	gaacatttga	tatttttcca	tttatttatg	aaaaaatatg	aacctatttt	180
catttgtaca	aggtaattgt	tttttaaaagc	aagtcacctt	aggggtggctt	taattgtata	240
agtcaagcac	atgtaataaa	ttcaaaacct	gcagttaaca	ggatattaga	catcaatcct	300
ggtaacccaaa	tattaaagat	tctctttaaa	aaagactgaa	catgtttaca	ggtttgaatt	360
aggctaaaag	gtcttgcagt	ggcttttcat	ggcccttcaa	attggaatgg	aactactgta	420
ctttgccatt	tttctataaa	tcagtacttt	ttttttaatt	ttgatataca	ttgtgtgaaa	480
aaagaaaatg	gctaataaac	tgtattaaat	cttaaacaaat	gtataaagat	tgcacttagc	540
cagttcaaag	tgtatactta	ttcataatga	attataacag	ttatatttct	gtgttttctt	600
gtaaatgttt	cttttccctt	aaatacagat	aattcatttg	tattgcttat	tttattatga	660
gctacaacaa	aaggacttca	ggaacaagta	atgtattagt	atgggttcaag	attgttgata	720
ggaactgtct	caaaaggatg	gtggttattt	taaatataaa	tagctaattg	gggtggtaaa	780

<210> 217
 <211> 810
 <212> DNA
 <213> Homo sapien

<400> 217						
cttttaggca	gcccggcacc	ttcatccata	ggcagagaga	gaactgggtg	ttggagacct	60
attcgagggt	ataggaaggg	ccctgtgaag	ttgatttaac	ttttggatgt	cagactgtga	120
aagctcctga	gaaacttggg	gtaataggat	cttcttttgg	ggatgaaaat	ggggaaggcg	180
tgaggaccta	gactacttct	ccctaggcca	gaaaaagaga	attaccctt	gacaaatatg	240
atacctgcta	ggtatttccc	agggaaattt	agggattggc	gtctttccct	agcatgtgga	300

ggaattggca	gacagcttcc	taagggcggg	gagcgggggc	ccaaggctga	caactgcttgc	360
atccacgtga	ccttaagtta	tggcagatga	ctctgaaacg	gactgaggcc	aatgagaaca	420
gatggatgga	gcactcaggt	tagacttgtt	ccttctccta	tgctggagga	gagggatggt	480
tctctagaat	gttggagggtg	agttgagagc	tcgcctcttg	aatgttgaac	agtgtactct	540
tctgaaaact	gcatattcac	tttatgtggt	ttcagaatac	tgggctcaat	actaacataa	600
gaaagacact	tcattgagaa	attcttaagc	ttacagaaaa	cctatctctt	tgacatttcc	660
acataacccc	tagcaaaatg	caggttcttc	atacttctgt	cctttttcca	ttggaagaat	720
tgcttaagga	aaaattaatt	cctattttatt	cccacaaaag	gttgggcatt	gctttgattt	780
taccccatgg	gggaatgtgc	ctttgaattt				810

<210> 218

<211> 817

<212> DNA

<213> Homo sapien

<400> 218

ctgctccctt	atggagggtct	cttcattaat	aattattgga	tagatagaga	aggtgagcct	60
gtggcttcca	agtaccggct	tttgctgaag	gtctacatgg	gaagaagagc	atcattttgat	120
attcagtaga	tctgccacac	ccaactggct	ccatctcctg	gaaaacagca	ctcactacaa	180
gcaactgtaa	tagcaccag	caatgaccac	gctgctcctg	ctggctcttc	cgtacaccag	240
taaaatgaact	caccaatgta	ttgcacacat	acatttcaca	gtagtacaat	aaagccctgt	300
atcaggagtg	gtaattcaat	gacttgactc	tatagtgcac	tcagcttcta	tgcatacca	360
acattcaaat	attcaaatat	ccttccaatc	catttggaac	aaaatacacc	atggctgcca	420
agacacatgt	atttttcttt	cttccatgga	ctcctaaact	gctcccacaa	tcagcagtggt	480
tcttctctca	gaaattatct	taagcttctc	tactcaatgg	gaggtacaca	cagagacctg	540
agaatatgca	gaggccagaa	tctctgtctg	tgctagagat	caactgtact	ctgcccacct	600
ggggaacaca	tcctctgggt	aaagtactcg	gaagtaaatt	acattccctg	gagacagata	660
cgggctttca	ctgcagcctg	ttagaaaaca	caatgtctgt	aagttacctc	ataggtcaaa	720
gagtttttga	ttatatattt	cataatgggg	ctatggcctt	tttaccctgg	ttttaatata	780
gaaccacctg	cagaaaggac	attgaaatta	aaagcca			817

<210> 219

<211> 661

<212> DNA

<213> Homo sapien

<400> 219

ggatgctgag	gcaggaggat	tgagtcctgg	agtttcagga	tacagtgagc	tatgatcatg	60
ccattgcact	ccagcctggg	caacagagca	agattctgtc	tctaagaaaa	ggaaaaagaa	120
aatgaataga	tagtggatatt	agatgttaat	gacatcagtt	gtttttattc	tttattcttt	180
cttagaaaca	gatttagttt	ctcgaattaa	agaactacca	tttttctttt	ttctacaact	240
ttcaagagct	ggtgaagaaa	tgatgttttag	atttaataga	tatagtagca	gtcatatatt	300
aatagaatag	aaactgagac	tctaggaaaa	agatagacat	gagataagga	gtaggcatgg	360
tagacatttc	tagattattt	atgaaaatgt	tgtagaattc	attttttttt	ttggtctgac	420
ctttggcaat	ggtgctgagg	aagggaagc	cagcccatca	ggcaaggctc	tgttttctgc	480
attttatccc	gtttgattct	tctcgttagg	attggagcaa	ataatttcaa	tatgttcttc	540
gctgggttta	tcatagtgac	ccttcattta	aagggaactt	taacaattga	cttaaaagaa	600
actgagatgt	gatattttat	tgggatttga	aagttgccat	tgggttttac	cttccctaat	660
t						661

<210> 220

<211> 792

<212> DNA

<213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (792)
 <223> n = A,T,C or G

<400> 220
 cctctttttaa ttcctacaaa taatttttcaa gtacacacaaa ttgggtaaac aaagaaacaa 60
 agccaccaag aatgaaaatc agtaggaata acgaacaaga ctcacagatg tcaaacagat 120
 ctgtgggtct tgcagacttc agatgttgga attattagtc gtggcaagng nncaaacat 180
 tagctattac cattatgttt accaactagt gaagtgaact atgagaggat atattaacca 240
 cagaagttaa tagaagaata gactcctgaa aatatctgga tgctacaaac taaaatatag 300
 tatataatcc ttcataagagt gtcagtgact tcatatttat aattacattt ttgtatatta 360
 gcagtgttct agttcttact gccttatctt taagctgann nnaaataaaa ttatattttg 420
 ggattcaaaa acacatagct aatgattact atgtggcagt gttacattac tttatcacat 480
 atcattaaca taatctgcat gtgttcaaag agatcttcat acttctttgt agctccact 540
 tctttgtcgt cttttagctt cccacaacat ctagaacagc acaaccgtat atggagaaaa 600
 ctgagtctag tattcgttga atgactaatg gaaaatttag ttnataaaca gaactttctt 660
 cattgnacaa attatcttgc agaagaataa tggccttagt ttaaaattat catattttacc 720
 catntcncca ngttatttta tctcttttgg ctaanaattt tgaaaacggt accttttacc 780
 ctttggcatt tt 792

<210> 221
 <211> 759
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (759)
 <223> n = A,T,C or G

<400> 221
 cttttctgct gctccgggag gtggagtggc ctggcagagg gcacatggct gccacctgct 60
 gcaaggaaaa ttctcagtga agactcctca gtatgaagga gataagcctg cacaatcagt 120
 cactgataga tgcttagtgg aaaaacttcc aattcccatc tacagctctc agagctagga 180
 ttaaaaaactc ctggtcataa actcatgtga tgagaagtta tagcacgccc tcattttcta 240
 catanccact tgcatttatg gttggctttt gaacttgcta gaagggaaag aagtgcacaa 300
 gtgtcctcct tagagctact ctctccctt tgggtgggtt ccagtttggt cattgtccag 360
 atggcccagg agctgacgat caaagggaag aagtcattgt tgcattgaga atgctttgct 420
 gcatcaggat tcagtgaagc tgttcaccgc ctggagccca tgcagcctca agaggcagga 480
 tggagctcag aaaccatcac tgagggttaga aagtgagcac caaagttgag ggaagcccac 540
 aggagtgagc cgaagtgtc cctttggatt tccaaagtgg gtgctgctgc ttcttccatc 600
 agccttgctt ctgaccccaa tgcgttcctg gtgccttctt cttggcattt tgctgtcggg 660
 ggcccaagga aaaaaattcc tgcattggcag tggtgaaaaa agatggctgc ctgctgaaac 720
 ctgatttggc ctgggtaagc cttttggagc cccggttaa 759

<210> 222
 <211> 699
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (699)
 <223> n = A,T,C or G

<400> 222
 ccttntnaag agttggcatt aattcttcac taaatgtagg agtagaattt atcaggtaag 60
 ccacactgac ctctggncct nttnncgccc gatgattttt aattagttga atccctttac 120
 ttgttatata tgtattcata tattctgttc cttcttggat ttacttttat gattggtgcc 180
 tattgaggta tttatttcta gtttgtggta cttcatgtgt ttaggttttc tagacagtgg 240
 acatagaaga ttcaagaagc taaatgtagg agaagtnta atgtaggana ntgaggcnac 300
 natatcatca atgaatgact tgaagtttcc tctgttgtaa agaatgatat taccataact 360
 gccatagnta atattgatgg tgtaagtcaa ataanaaggc aggaggaaag ggacatccat 420
 cactgaacca canatcagag nctcattgaa gcctttgaga agaatccaca aaattttaca 480
 ggataattca tttcctgcga tcaccacnag aagagaaact ggtaaacag acaggtattc 540
 cagagtccaa aaatttacat ttggtttcng aaccaaagac ctcagctccc aggccacagc 600
 aaaagggggc ttatgaattc cctggcacc agncccaaga cccaanaacc tcactttgat 660
 tggtttnggg cttgggaaac caaaaaacca atgggtggc 699

<210> 223

<211> 598

<212> DNA

<213> Homo sapien

<400> 223
 aaaaagagaa agtttcagat ttgccattca aggcttattt atatatatgt gtgtgtatat 60
 aaatacatgc acacacttgc atacatatat atttttggct gggggagtgt gagttttgcc 120
 tttctaaggg agggaccgag caggctcctt tgttctgtat tctggcggag atgggtcctg 180
 gccctgtgtc actggcctat ccttaaagat catctcccat cctccccagc gccatctgtg 240
 tgcagcaacc agaaagggat gaacttggcc ctcttgccgg cctggacaag gtctcttcc 300
 taccctttct gttgccagtc agcaacctgt aactcacatt ctcttcccag tgaatccctg 360
 ggagcgcctg accctgggtg gctgttcagc ttctgtctgc tggggccagc aatttttgag 420
 gatttatctt taggccaggc ttgcctccgt acttatccct gctctcccat ttctctcttg 480
 tttgagagag aatgaggaag caaagagtga gaaagaatag gggctgaaga cgccactccc 540
 agatggctct ttctatcctg ctcttctgtt gaaacacacg tgctgtgggc ctcaggcg 598

<210> 224

<211> 501

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(501)

<223> n = A,T,C or G

<400> 224
 aaacctttat gatgacttcc ttatgaatta ctgaacgaac actggaatgg gactcaggta 60
 tcctgaggac atctctcaac tctggcctta gttccccctc tgtaaaatta gggtgccaac 120
 taaatgatct acaagggtccc ttccagcgcc gccattctgt aattacatca tgtgtaactg 180
 tattaaacat acacaagtga ctgccaggca tgggaatgta acttccgagt aaatgctttg 240
 gtttgttcag aatacactat gaacttcttt ccaaagacgg gttgtggtaa atagtggata 300
 ttttgattat aagaaataga gtttccttga agctttagct ggagatacag caatagtgtg 360
 gtgttcctac aaatatcaca gtgtattcaa acatatcttt ctatcaaaaa tcatttttgc 420
 aaaagctgtg tgtttttatc caacttgtga taataaatgt tctttatttt agaacaaana 480
 aaaaaaaaaa aaaaaaaaaa a 501

<210> 225

<211> 295

<212> DNA

<213> Homo sapien

<400> 225

cctgtatagg gctcgtttcc ccacacatgc ctatttctga agaggcttct gtcttatttg	60
aaggccagcc cacacccagc tactttaaca ccaggtttat ggaaaatgtc aggaaaaaaa	120
aaaaaaaaa cacatgcact cacacaatac ccaaacaatca raattagaag ggcataaaac	180
aggggggcttt ataggctgaa aaatatctta ratttcaraa cagaatacca atcaaatatt	240
gaaaattcct ttgttcaaaa cacaagatg ttttgttttt aatgggagtt ttttt	295

<210> 226

<211> 372

<212> DNA

<213> Homo sapien

<400> 226

agattcctgg cttagagcat gcgagcattg aaggaccaat agcaaactta tcagtacttg	60
gaacagaaga acttcggcaa cgagaacact atctcaagca gaagagagat aagttgatgt	120
ccatgagaaa ggatatgagg actaaacaga taaaaaatat ggagcagaaa ggaaaaccca	180
ctggggagggt agaggaaatg acagagaaac cagaaatgac agcagaggag aagcaaacat	240
tactaaagag gagattgctt gcagagaaac tcaaagaaga agttattaat aagtaataat	300
taagaacaat ttaacaaaat ggaagttaa attgtcttaa aaataaatta tttagtccgt	360
atgaaatgaa at	372

<210> 227

<211> 599

<212> DNA

<213> Homo sapien

<400> 227

ggcccccgct gcgggagccg cttcgggcct tctgggcatg tctgccatat ggctccagggt	60
ttgtttttct ccccggcact ctgacgggga gggctcccgg catctcctgg catccgggta	120
gaggacgcgg aggatgctga gctgctggcg cactgcagca caactagaga tgtacggatg	180
cccccatctt gatcttacag aatcagagggt acagccgcga gaaagagtca agaacagaca	240
gagtcgcttg aggactcagg aggggtgttg ctgcgttgac aacagactac accctcacag	300
tttgctctgc tctccaaca ccagtgaag atgatcacat cccagggatc agtgtcgttt	360
agggatgtga ctgtgggctt cactcaagag gagtggcagc atctggaccc tgctcagagg	420
accctgtaca gggatgtgat gctggagaac tacagccacc ttgtctcagt aggggtattgc	480
attcctaaac cagaagtgat tctcaagttg gagaaaggcg aggagccatg gatattagag	540
gaaaaatttc caagccagag tcatctggaa ttaattaata ccagtagaaa ctattcaat	599

<210> 228

<211> 343

<212> DNA

<213> Homo sapien

<400> 228

aaagtaaatt gtatgaaaaa ttcatttctt caattgcatt agccacattt tgagtattca	60
tgtggctggg agattctgta ttagcacaaa gatatggaac atttccatca ccacagaaag	120
ttctgttggg cagcactgca ttagaatatt ttcatactgc tcttcctcaa ttaatttttg	180
ttgttaatgt tgatgtcttc attggatggg tcataatgtt ccatgaaacc gctcaagtac	240
acaattgtat gttctttgta tcccttacca caaatatctc gctctgctca tttcttttgc	300
agcttcctat aaagtttgc ttcctcaaaa aaaaaaaaaa aaa	343

<210> 229

<211> 417
 <212> DNA
 <213> Homo sapien

<400> 229
 ctcaagctgc agtccaccgg gtatggttct ggatggttcc cccaagggag caggatgta 60
 ggagggtgaag aaaactgaga tttcaagtat gggagagttt ttactatctc cattcctgga 120
 ttaaaagtgc tgaaaaagtc cacagttaaa cattccttta ttcacctat ggctcccaag 180
 aaaagcattc ttcctctgga gtactgggtg actaagggga caatacacca aatttggtga 240
 gtttacaatc aagtctacta aggttggact tccttatcag tttggcagag tcccagggca 300
 gaataatcat ccatctacag gtctctgttt cctctccctc cgcagcagtg gagagcatcc 360
 cagtgtttgg ggcactgtgt tcctcttcgt ccctgcacca gaccctggaa gccttgg 417

<210> 230
 <211> 462
 <212> DNA
 <213> Homo sapien

<400> 230
 gaaataccag aagagaaagt ttcattgtgc aaatctaact tcatggcctc gctggctgta 60
 ttccttatat gatgctgaga ccttaatgga cagaatcaag aaacagctac gtgaatggga 120
 cgaaaatcta aaagatgatt ctcttccttc aaatccaata gatttttctt acagagtagc 180
 tgcttgctct cctattgatg atgtattgag aattcagctc cttaaaattg gcagtgtat 240
 ccagcgactt cgctgtgaat tagacattat gaataaatgt acttcccttt gctgtaaaca 300
 atgtcaagaa acagaaataa caaccaaaaa tgaaatattc agtttatcct tatgtgggcc 360
 gatggcagct tatgtgaatc ctcatggata tgtgcatgag acacttactg tgtataagggc 420
 ttgcaacttg aatctgatag gccggccttc tacagaacac ag 462

<210> 231
 <211> 328
 <212> DNA
 <213> Homo sapien

<400> 231
 ctgtgggttt tcctaaacgc cctcatctg gttgaagccc tagtgtttct ttctcacatc 60
 agaggcfaat gcattgggtt gggctctggtt tggacaataa atttcctctg gtttggacca 120
 agaaaaacag agttctttga cgcctaacat atatgtaaaa agaaagtgtt taaaaacaag 180
 agttaaaatg cttctaacag tgtggtcatc actgcacagg acactggaat tggcattcgg 240
 ggttggtgtc gtccatgtgg tttcgttgta tgtcatgtgc tctcagctca gacagagaca 300
 tccaattgac ttctgacttg gggcattt 328

<210> 232
 <211> 595
 <212> DNA
 <213> Homo sapien

<400> 232
 cgccaatttt agcaataaag agattgtaaa agaagcagat tgaatgaaga attttttagct 60
 gtgcagatag gtgatgttgg gatggaaaat gctaataaac taccctttct tttatcaagt 120
 aattaaaata aatctacata aagaacaaa aaggctgttt tataaaagtg aaatatccag 180
 tatttcagag gccagggcaa gagcacttca gatgaggcag tcaaaatcat tttttccag 240
 tgaggataga ccacaagtgg gtggtgagac cattgaaagc ctttatcaac tgaagagtcc 300
 atttaacagc ataatttgtg ggaagactgg aatagggctg aataaatgtg tttgaatctc 360
 taattttata ctttcttttc ctgaggaact tgatttttct gtccctggat cgccttgta 420
 taattgggtc tgttcctttt actaccactc ttgagtccat atatgaaatc attaaagttg 480

gatgatcagt tttttataaa aatatatatt tttgtccaag aaaaaaaaaa gcatacatat 540
gtgattatgg ctaaatacaaa ggtaactgga atgtatatac ttttgctaatt gttcc 595

<210> 233

<211> 600

<212> DNA

<213> Homo sapien

<400> 233

atgaaggtaa actctaaaat cttcataggt caacaaagaa aattttatcct tcacacttat 60
ttctagaaag cagcaggggt tattttcctag attgcttaca atgaagctag aatatctgcg 120
ataactgtag agtttcaaaa aggatcccta gggctacttc tacgttctcc ttaccagttg 180
agcactctcc ataatttcca gacgggtcat cacaatggtg tagaatgcta agagcaggga 240
gaaagacaat gaaattagaa atgggtgaga cacaatggtg tagaatgcta agagcaggga 300
tcaggacaat caaccaggtg tctaggaagg gtcaagtcac cagtgtcatc tgctgaccaa 360
tgtaggaag aaataaactc aaaggaaaca ccacattttt ccaattaaac tcaaactctat 420
tgacttgtgg tggttctttg atgttgtggg gactgctata acagaaacca attggatttt 480
caagggcaag aaactttgcc actgaataag atgatgtcat ccttcctgat aacaaatagg 540
aatgggtggt cagctctaaa cagcgtggac tgaggaggtt gcttttctac aatattactt 600

<210> 234

<211> 500

<212> DNA

<213> Homo sapien

<400> 234

aaattcctaa ttcttttact atctttctcaa cttttcccaa agataaaata aatttcacat 60
aatttcagtg aggggaaatg gtagttgtaa aaaactacct caagtagcaa tcaccgctgg 120
cagtgttttc tcactttctg ttctgcaatt gcaatcacac ttccaaaaag aaaagcaaat 180
gtttgctaaa ccatagacag acaacctctt tgtgactggt attataagggt ttataatgaa 240
aacttatcaa atataaaaagg tgctccctct tgaaaatgtg tattttattt gaagttttga 300
gtaagagggt agtgtttggc aattttcaac actccctca aaaatctccc aaagttgcaa 360
aaaagtcagt ttagtaaaat tccaagcact taaatgcttc attgagggcc agttgatata 420
cgcaatgcac taatgtgtaa aaattaaccg aatgcaacta ttttataatg gagagctctt 480
accttttctt tccagttttt 500

<210> 235

<211> 159

<212> DNA

<213> Homo sapien

<400> 235

aaaatttaca gataaaggca gttcaatact gccactgaga agtacatctc ttaacatata 60
caactttcag gccacagttt tgaaggctct aagtattaag ttggtttgat gaattagtcg 120
gttggcactt acgaacacat ttattgcctt gccatcttt 159

<210> 236

<211> 254

<212> DNA

<213> Homo sapien

<400> 236

aaataagtga ataaagcgata tttattatct gcaagggttt tttgtgtgtg tttttgtttt 60
tattttcaat atgcaagtta ggcttaattt ttttatctaa tgatcatcat gaaatgaata 120
agagggctta agaatttgkc catttgcatt cggaaaagaa tgaccagcaa aaggtttact 180

aatacctctc cctttgggga tttaatgtct ggtgctgccg cctgagtytc aagaattaaa 240
gctgcaagag gact 254

<210> 237
<211> 591
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(591)
<223> n = A,T,C or G

<400> 237
tttttttttt tttttttttt tttttttcta atttttactt tttctcaagt ttaatgtara 60
catacaaraa aacatcaagc aatggtttatt gkgcaattcc aatcattatt tgcaraatct 120
tgggtttaaag tcagtyttta tagccatttc aactgcttg tttaaacaaa aagcaacaat 180
ctggttatyt acctataaat ttcattggtat ttttttaaac actgaagtac taaaagcact 240
gatgatttgt attataattt ttaaaatatt taaaacctac acagatttca taratcattc 300
cttttataaa ataatacaaaa taatttgatt atytggaaaa aaaaattctt gaaacaragc 360
cctttccagg tatyttcaat ctctgtaaaa ccccaaacc caaacagagt aratgatgaa 420
ataaggattt ctcagttgcc caagactgtc tgaaatttaa ggttgaaaaa tggactggcg 480
tttttcatgt ttctgngaa ttcanagctt acaggtggca tcaaaactca aatctctggg 540
atggctttac atggctttca ctttgatttg tttcattttc atttgcttct t 591

<210> 238
<211> 252
<212> DNA
<213> Homo sapien

<400> 238
aaatggcttt tgccacatac atagatcttc atgatgtgtg agtgtaattc catgtggata 60
tcagttacca aacattacaa aaaattttat ggcccaaat gaccaacgaa attgttacia 120
tagaatttat ccaattttga tctttttata ttcttctacc acacctggaa acagaccaat 180
agacattttg gggttttata ataggaattt gtataaagca ttactctttt tcaataaatt 240
gttttttaatt tt 252

<210> 239
<211> 153
<212> DNA
<213> Homo sapien

<400> 239
ccacaataaa gtttacttgt aaaatttttag aggccattac tccaattatg ttgcacgtac 60
actcattgta caggcgtgga gactcattgt atgtataaga atattctgac agtgagtgac 120
ccggagtctc tgggtgtacc tcttaccagt cag 153

<210> 240
<211> 382
<212> DNA
<213> Homo sapien

<400> 240
aaaaaaacca tctaaaagt gttttttaat atatatattt tttccaaagg aagaaatttc 60
ctgcttttac tcagggaata aaaaaaatta aggtacattt gagtagaatg atttcatcta 120

aaagagttct	ttcaggagac	atctgtgatt	cactgcattg	tttttatttt	cttctttttc	180
ctcttctttt	ccaacatttc	taccattttc	ctcttcttgg	ttgatatcag	gccactttct	240
tttggtgctt	tcttactgtc	acctgttaaa	ccgcgtttct	ttgtgttagg	ttttgaccgc	300
ttttcttctt	tgtgcactgt	gtcaccaggc	tcctttttgc	caattttgga	ctgttcttta	360
cttacaggag	aaggctctgc	ag				382

<210> 241

<211> 400

<212> DNA

<213> Homo sapien

<400> 241

ggcatgagcc	accgcgccc	gccctatctt	ttactttttat	aaatagagat	gaagtttcac	60
catgttgccc	aggttggtat	cgagctcctg	ggetcaagcg	atcccccaac	cttggccttc	120
caaagtgtctg	ggattacaag	cgcgagccac	cgaaattatt	cttaactagc	aagactaggc	180
tctgacatca	catccttata	gttacatccc	tttaagcagg	gttcagccac	tcactctgca	240
cctggagaac	ttgatggtta	tccctcgaag	tgacagtcct	gcaaatagaca	aaaacactcc	300
aaatctatta	ggttgggtgca	aaagtaatta	cgctttttgc	cactgaaagt	aagtcccaca	360
ggaccctgag	ggaaatggga	gggtggggta	tacatagcag			400

<210> 242

<211> 75

<212> DNA

<213> Homo sapien

<400> 242

actcacatat	gcagacctga	cactcaagag	tggttagcta	cacagagtcc	atctaatttt	60
tgcaacttcc	tgtgg					75

<210> 243

<211> 192

<212> DNA

<213> Homo sapien

<400> 243

gctccacatt	tgtagcgaac	actttgactc	caaagagaag	gaggaagaca	aagacaagaa	60
ggaaaagaaa	gacaaggaca	agaagggaagc	ccctgctgac	atgggagcac	atcagggagt	120
ggctgttctg	gggattgccc	ttattgctat	gggggaggag	attggtgcag	agatggcatt	180
acgaaccttt	gg					192

<210> 244

<211> 616

<212> DNA

<213> Homo sapien

<400> 244

aatttttatag	caatatactg	accatttctaa	aaataacaaa	atacatgttg	ctctcaacta	60
catagttaaa	aaaggttagta	aattctctta	cccaaaatag	aggaggggtg	ggctagttag	120
ctgctcaaac	atttgaaca	aataaaaatg	tatctatata	catataatga	tcattgtttc	180
atagcctaaa	atcaccatac	aaaatctaata	aataaaattg	tgtcgtgttc	aggagtgtgg	240
aagccaacac	attaaattaa	caaagtattt	ttggtatatg	taaataatgg	gatagaatct	300
ctcgaatcag	gattgtccca	gaagttctaa	ggcagatgtc	aatgacatgc	acattgtcca	360
tgttcagtaa	ttttcaaaga	ctagaataaa	ctatgtaaac	tattcaatac	aattcaatat	420
tacttaactg	ctaaaaagta	cttcaagatc	ttgcactgcc	ttgagttagt	ataatcaaat	480
tagtaattgg	aaaatagctg	taatagcagg	cactgaagaa	ttctgacaaa	taccaataa	540

ctgtttgttt ttaccaaaata aactggtaag atgatatcac aaagggtttt aagttatttt 600
gctatacaag gttttt 616

<210> 245

<211> 165

<212> DNA

<213> Homo sapien

<400> 245

ttggaacagt ggattaaaat ccagaagggg aggggtcatg aagaagaaac caggggagta 60
atttcttacc aaacattacc aagaaatatg ccaagtcaca gagcccagat tatggcccgc 120
taccctgaag gttatagaac actcccaaga aacagcaaga caagg 165

<210> 246

<211> 229

<212> DNA

<213> Homo sapien

<400> 246

tgtactggat ccctccaggt gggggcgact ctcacctgac tattacaata gcctcctaag 60
tggtttccct acttgcaacc ttgcccgat aatatctatc ctccacacag caggcagggc 120
gatcctttaa gaatagaagt tagatcatga aaatgctctg ctctgatccc tgcaaaagct 180
cgccacctcc ttacagtcac cgctgaactc gtagcagagg ttcaggagg 229

<210> 247

<211> 338

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(338)

<223> n = A,T,C or G

<400> 247

ggaaaccgtg tgtacttata ctggatgatg ccaccagtgc cctggatgca aacagccagt 60
tacaggngga gcagctcctg tacgaaagcc ctgagcggta ctcccgtca gtgcttctca 120
tcaccagca cctcagcctg gtggagcagg ctgaccacat cctctttctg gaaggaggcg 180
ctatccggga ggggggaacc caccancagc tcatggagaa aaagggtgct tactgggcca 240
tggngcaggc tcctgcagat gctccagaat gaaagccttc tcagacctgc gcactccatc 300
tccctccctt ttcttctctc tgtggtggag aaccacag 338

<210> 248

<211> 177

<212> DNA

<213> Homo sapien

<400> 248

tgaaaacaaa tgatttctca actcctacgg ttcattgtaga gtttagagaa aatttccatc 60
attgtcatca ttgaactgtg aacctgggaa gccagatcat gattaacact gacatcaagt 120
ttcaagttgc agatcaatgc acccagtgtt cagatgaggg aaacttctcc gtgacaa 177

<210> 249

<211> 263

<212> DNA

<213> Homo sapien

<400> 249

aaagtaatga ctttattaat aaatatacat ccatatgatg atgtagatac aaatcatgaa	60
cactactcca ttcccataca cataattgca cacgagtagc tcaagttcat ggacataaaa	120
acatacacag tatctattca gactttttac agcagaggac agcgtgctta ttatcagtta	180
attggttaatt attttctcca aaattacctg tggaaaaaag aaattctgaa aacttaaaag	240
aatcaaaagt atctgattac ttt	263

<210> 250

<211> 333

<212> DNA

<213> Homo sapien

<400> 250

aaaaaaaaa acagcgtaaa tattagccca caagagcagt cctaaacaat cacaattaca	60
ctgtactacc caagaagact gtttattgtg aagcattttac ctttcaaaaa atcattacat	120
ttctatttct tgggtggagca gcacattgtg gagtgtgatt cttaattctt cattgagttt	180
gtcaatagga cattgatgct ggataggttg tcttttgttt ttatgcctca gaccatcttg	240
tgagattggt tgcctatctc ataatacagt tttatgcaga aagggtgaaa ctatgtaaat	300
ggtttttatg gaaattatca gttacaatat ttt	333

<210> 251

<211> 384

<212> DNA

<213> Homo sapien

<400> 251

aaaccatttg tacaaaaactt ctataaattt ttctctctct ttctctctta tgtacaaaaa	60
tatcttaata tatccccgaa ctggttagga tagatacaaa tagatttttt ataataaaaa	120
attcacaaaa gattggaagc attctataat gaaaatggta gaaaagacag tgtgagggaa	180
gccatggggt ttgggaatcg ggcctggag gagaagcaga gtttcaaagg gctgagaata	240
gcatagtttc actgtaaacc aatgtctaca gcttattggg gtgggggcta ctgagacgaa	300
agacaccaac tcgtttctag agggctaaga actgcacttt aagaaagggc ggggaggtga	360
agggaccoga gcaagaactt tcag	384

<210> 252

<211> 211

<212> DNA

<213> Homo sapien

<400> 252

aaagcagtct gaaaatggga catctgtaga gaaattcatt tccttcttct cctccggatg	60
tggaaatggaa gctttgaggg aaggaaaagt aggaaaagag cgggatggga tgggatggga	120
tgggatggga tgggatagga agagaggctg gggaatgggc agagaagggg gtgctgagtg	180
tgctgtgaga tagagcaaga tcacaagaag g	211

<210> 253

<211> 135

<212> DNA

<213> Homo sapien

<400> 253

aaaaattggt tcttgacaag ctgacttggc acttaagtgc acttttttat gaagaaaaag	60
tacaatgaac tgcttttctt caagcaataa ttgtttccaa cttgtctggg aattgtgtgt	120

ctggtaactg gaagg

135

<210> 254

<211> 361

<212> DNA

<213> Homo sapien

<400> 254

cctgtagccc	ctgctacacg	ggaggctgaa	gtgggaggat	cacttgaacc	aatgaggggtg	60
aggttacagt	gagcccagat	catgccacta	ctctacaggc	tgggtgataa	gagtgaagacc	120
ctgtatcaaa	aaaaagacaa	ggaaaaaaaa	aactgggccg	tttgtttttg	cagaatgtct	180
ctcaatttgg	acttttttggg	caggaatata	atacaagtga	tacaaatgct	tctttaacat	240
tagaacctgt	ataaaattac	cattacagac	cttgctattt	tacttatagg	taaatacactg	300
tttaccaagg	taagtctttt	gggaatttcc	aaaaatgaag	tccatggaca	gttaaaaact	360
g						361

<210> 255

<211> 331

<212> DNA

<213> Homo sapien

<400> 255

aaaaaaataa	ataatccacc	aacgtgattg	accttggcga	gatcatgttt	ctagtctata	60
cctcagtttc	cccacatgta	aagtgaggat	aatgtccac	cccatgtaac	tgtgggtgagg	120
accaactgca	acactgtgcc	tgcgagtctc	cttggaaaag	tgtaagggtc	tacacaaatg	180
gaaagtgatc	tgatcacact	cagtgtcccc	agcccagcct	ttcagtgtcc	tggccctggg	240
gtgggggaca	atactctcct	caccccttcc	actagtcttc	atgaatagca	aggaggccat	300
aacataatth	ggtctaaacc	ccttcctttt	t			331

<210> 256

<211> 186

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(186)

<223> n = A,T,C or G

<400> 256

cctttggggc	cttgcacttt	gacctgcaat	ggggccacac	cagccttgct	tgtgtccacc	60
tgggaaggact	gagggaggtt	ggcacgaacc	atgcctgggc	tcaggccggg	cccanagcac	120
ttgaccttgg	acgcatctgt	cacatcatgc	acagggacct	tgaaaggact	gcctggcact	180
tgatgg						186

<210> 257

<211> 255

<212> DNA

<213> Homo sapien

<400> 257

ctgggggtccg	tcaccgacct	ttgggggaact	gggctacggg	gaccacaagc	ccaagtcttc	60
cactgcagcc	caggaggtta	agactctgga	tggcattttc	tcagagcagg	tcgccatggg	120
ctactcacac	tccttgggtga	tagcaagaga	tgaaagttag	actgagaaag	agaagatcaa	180
gaaactgccca	gaatacaacc	cccgaaccct	ctgatgtctcc	cagagactcc	tccgactcca	240

cacctctcgc ggcag

255

<210> 258

<211> 604

<212> DNA

<213> Homo sapien

<400> 258

ctgaatttgc aatggagttt ggtggtgcaa tcggtattga ttagtttggc atagacagat	60
gcagcagttt agagcaaaat cgagaaaatg attttttttt tcctccttga tttcctggca	120
gaagatatct tactttttca gcaaaactttt cttttaacac taaagcagcc tagggcaatg	180
ccagatactt agagcttttc tcttgattat aagtagaaat gggggtgtct gggctagagg	240
tggagggttg atgtgctgtc gtcacagtct agctggcagc aagcaaggca aaagcagaga	300
ctgctctaga agcggttcca agcagcagag acgtcaggaa aggcacttct tagtaccaac	360
ctctatgctt taatagtgtc ttgttaagct gcttcattggg ttgagacaaa ctaccagcac	420
ttcaaagagc tcagttctct gctcaactct cttctctagt tacattatct tttttccttc	480
aggagactga ggcaggaaaa tcgcttgaac tcaggagggtc gaggccgcag tgagccaaga	540
tcacaccacc gcactccagc ctgggccttg caaagtgcta ggattacagg aatgagccac	600
cagg	604

<210> 259

<211> 429

<212> DNA

<213> Homo sapien

<400> 259

aaaaatgtct gtatcgagat cttccagttt gaagtcttcc tcctctgtgt cttcccaagg	60
ctctgtggca agctccactg gttctcccgc ttccatcaga accactgact tccacaatcc	120
tggctatccc aagtacctgg gcacccccca cctggaactg tacttgagtg actcacttag	180
aaacttgaac aaagagcggc aattccactt cgctgggtatc aggtcccggc tcaaccacat	240
gctggctatg ctgtcaagga gaacactctt tactgaaaac caccttggcc ttcattctgg	300
caatttcage agagttaatt tgcttgctgt tagagatgta gcactttatc cttectatca	360
gtaactgtct cgtgttcaga ctctcggttt cttccaggct tacagtggac atcatcagct	420
tcctgcttt	429

<210> 260

<211> 385

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(385)

<223> n = A,T,C or G

<400> 260

ctgcaacaca tgcagcacca gtctcagcct tctcctcggc agcactcccc tgtcgcctct	60
cagataacat ccccatccc tgccatcggg agccccagc cagcctctca gcagcaccag	120
tcgcaaatac agtctcagac acagactcaa gtattatcgc aggtcagtat tttctgaana	180
cgcatatggc agacggattt gcgtatacca aggagagtgg cataggaggg aaaagcatat	240
gtggctgaaa cctgtaagtt ggtgttggtt atgcagaaat gtgtaacaga tcaaacggtc	300
ctctcaagtg tctattanat aggcaataag aactgcagtg tagctgagta acatctttta	360
gctgactata aatcactttg ttttt	385

<210> 261

<211> 230
 <212> DNA
 <213> Homo sapien

<400> 261
 ctgtactgga tccctccagg tgggggagac tctcacctga ctattacaat agcctcctaa 60
 gtggtttccc tacttgcaac cttgcccga taatatctat cctccacaca gcaggcaggg 120
 cgatccttta agaatagaag ttagatcatg aaaatgctct gctctgatcc ctgcaaaagc 180
 tcgccacctc cttacagtca ccgctgaact cgtagcagag gttcaggagg 230

<210> 262
 <211> 198
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(198)
 <223> n = A,T,C or G

<400> 262
 atgttaagta aacatgaaat ctatataaca gaacaaaaat tcactcttat gtcaatgtca 60
 gcgtgttaat gtagatctat ttactganac agactctgta gtggcagaga gtggccttgt 120
 taagccagga ccctgttctg caggctgtgg gtagaagcta ggaagtcctt ggagtttcac 180
 ccagcttttc catgaatg 198

<210> 263
 <211> 157
 <212> DNA
 <213> Homo sapien

<400> 263
 aaaatatatt tctaaacaga atgggcccag tcagtcacag taactgttga tctccatagt 60
 agagcaaccc acaagacag aactgatttt ttcccataa tcagggtgta aaaatataca 120
 acttgtttct gaaccaaacc cacaatttct gcagttt 157

<210> 264
 <211> 290
 <212> DNA
 <213> Homo sapien

<400> 264
 ctggctactc caagaccctg gcatgaggct gaggacaact tacaagggct tcaccgaagc 60
 agtggacctt tattttgacc acctgatgtc cagggtgggtg ccactccagt acaagcgtgg 120
 gggacctatc attgccgtgc aggtggagaa tgaatatggg tcctataata aagaccccg 180
 atacatgccc tacgtcaaga aggcactgga ggaccgtggc attgtggaac tgctcctgac 240
 ttcagacaac aaggatgggc tgagcaaggg gattgtccag ggagtccttg 290

<210> 265
 <211> 234
 <212> DNA
 <213> Homo sapien

<400> 265
 aaaaaaagga aaggaaagag aggaaaagaa aataaaataa gacgatttat tgcttctcct 60

cagcatcctc cttggtctcc tccttcaccc agagagcttc tagcttttcc gccacttttt	120
cggcatgatc atttttgccc gatcccttct tttctctctc ttcgatctct ttcttgcat	180
cttcaaacctt tgttttgaat ttctgtgcat tctcagcatt caggaagcgg atgg	234

<210> 266

<211> 335

<212> DNA

<213> Homo sapien

<400> 266

gtcctcatca tcccagtttg aggcagtgcg ggagtgggga aggccgtctt agaccataga	60
ggttggaaga cgctgagaga tcatccagcc cagccccttg atgttacaga gcagaagaca	120
gatgccccaa caggagaagg cacttgccca cggtcatacg gcaggttgcc acaaaaccaa	180
gatggcagcc ctctctcagc gtgcctcact gccactccca gagccaggga gccccataaa	240
accacatca tgtcttaaga gtatatctgg ctcttgacc agcaatcggc cctgggagcc	300
accaggtggg aaaagcgcct ctgccagagt ccagg	335

<210> 267

<211> 619

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (619)

<223> n = A,T,C or G

<400> 267

tggagctctg acgaagggat cggggagggtg ctggagaagg aagactgcat gcaggccctg	60
agcggccana tcttcatggg catggngtcc tcccagtacc aggcccggtt ggacatcgng	120
cgcctcattg atgggcttgt caacgcctgc atccgctttg tctacttctc tttggaggat	180
gagctcaaaa gcaagggtgt tgcanaaaa atgggcctgg agacaggctg gaactgccac	240
atctccctca cacccaatgg tgacatgcct ggctccgaga tccccccctc cagccccagc	300
cacgcaggct ccctgcatga tgacctgaat cagggtgtcc gagatgatgc anaagggtc	360
ctcctcatgg aggaggaggg ccactcggac ctcatcagct tccagcctac ggacagcgac	420
atccccagct tccggagga ctccaaccgg gccaaagtgc cccgggggat ccaccaagtg	480
cggccccacc tgcagaacat tgacaacgtg cccctgctag tgcccctttt caccgactgc	540
accccanaga ccatgtgtga gatgataaag atcatgcaan agtacgggga ggtgacctgc	600
tgcttgggca nctctgcca	619

<210> 268

<211> 147

<212> DNA

<213> Homo sapien

<400> 268

cctataaccc agacaccagc atggacaaaa ctcaattata ctgaattcag agacaaaatt	60
cagtgcact cttctaccac ttatttaggg ttctacagca tttcactgag cagacttagt	120
ttttgtttt tgttttacaa acctttt	147

<210> 269

<211> 325

<212> DNA

<213> Homo sapien

<400> 269

ctgagctgta ggaatgggtt cttggtacac aagatagtat tgttgagcta gttttcgagc	60
tctgtgcaca agcactctgt aatcggggcc catgccactg tacaccaaac ctatatgctt	120
ggtaattggt tctactttgt gtacacttcg ctcatcatac agaatggatt tctgtttttt	180
ctcagttgct aataccacac catttgcagc ttttaattccc acggacgggg ctcctccagc	240
tacagcagcc aaagcatatt caatctggac aagtttacca gacgggctga atgtagtcag	300
cgaaaagctg taccgcgct ccgcc	325

<210> 270

<211> 428

<212> DNA

<213> Homo sapien

<400> 270

aaacatatgg taaattaccg agtgacacct ctgggctaga gacctctttt gaggggagtt	60
tgcaactac ggattcaatt tctttaacag ttatgaagtt ctttaaagaa cctgtttggt	120
attggggggt tgtggtcacc tgtgcttttc tgagatttgg cccctacatc taagtgttg	180
aatgcatgtg tgtagagttg tttatggtgc ttccctttct tcttagaagg gtctatagta	240
atatcccctg ccttatccct agtagtacta atttgtgttt tcttacttct tgacaggcaa	300
acacatcaga gcataagtgg ttccctaatgc caagctgacc tcccttgatc tctgtcttct	360
acaggatatt gacatgggac ttctttatta ccttttcagt tccctgatac cttcaaatag	420
ctttattt	428

<210> 271

<211> 206

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(206)

<223> n = A,T,C or G

<400> 271

cgtcccggag cccacgngg ncatggctgg canagcgctc tgcattgctg ggctggctct	60
ggccttgctg tcctccagct ctgctgagga gtacgtgggc ctgtctgcaa accagtngc	120
cgtgccagcc aaggacaggg tggactgcgg ctaccccat gtcaccccca aggagtgc	180
caaccggggc tgctgctttg actcca	206

<210> 272

<211> 83

<212> DNA

<213> Homo sapien

<400> 272

ctggcttccc tgagaactca acaatgcctt ttccctgaggg ccttcctcga tcatccaaa	60
tgactacagc cctctctacc tgg	83

<210> 273

<211> 472

<212> DNA

<213> Homo sapien

<400> 273

ctggagaagg tgtgcagggg aaaccctgct gatgtcaccg aggccagggt gtctttctac	60
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tcgggacact cttccttttg gatgtactgc atgggtgttct tggcgctgta tgtgcaggca      120
cgactctgtt ggaagtgggc acggctgctg cgacccacag tccagtctct cctggtggcc      180
tttgccctct acgtgggcta caccgcgtg tctgattaca aacaccactg gagcgatgtc      240
cttgttggcc tcctgcaggg ggcaactggtg gctgccctca ctgtctgcta catctcagac      300
ttcttcaaag cccgaccccc acagcactgt ctgaaggagg aggagctgga acggaagccc      360
agcctgtcac tgacgttgac cctgggcgag gctgaccaca accactatgg ataccgcac      420
tcctcctcct gaggccggac cccgcccgag cagggagctg ctgtgagtcc ag              472

```

<210> 274

<211> 205

<212> DNA

<213> Homo sapien

<400> 274

```

ccaggcggcc cgaggactta cggtcggcac ttctctgttc tcccgtgtca gcgtgtggtg      60
tcgcctgcat gggctcgtacc tggatgggtg gtccaccatc gacacggagg ggctggattt      120
gtttctcagg caatcctgta ttttaatttt agatgtattt cctgaagcat atttttcata      180
gaatgtagcg tgtaaatagc tttttt                                205

```

<210> 275

<211> 308

<212> DNA

<213> Homo sapien

<400> 275

```

ctcctcgccc tccccaccga catcatgctc cagttccagc ttggatttac actgggcaac      60
gtggttgga tgtatctggc tcagaactat gatataccaa acctggctaa aaaacttgaa      120
gaaattaaaa aggacttgga tgccaagaag aaacccccta gtgcatgaga ctgcctccag      180
cactgccttc aggatatact gattctactg ctcttgaggg cctcgtttac tatctgaacc      240
aaaagctttt gttttcgtct ccagcctcag cacttctctt ctttgctaga cctgtgttt      300
tttgctttt                                308

```

<210> 276

<211> 201

<212> DNA

<213> Homo sapien

<400> 276

```

aaattaactt tttcttgcaa aatattcatt tcattttttc caagaaaatc ttataaaggc      60
aaaaataaaa ttttattttg gcaaatgtca tgaagtcgat actggcagca tatggagtta      120
gttaaaaaata gacaacaact gctagatata ttcaaaattc tatttttttt tctgagcata      180
gtcaaagaga aattttcatt t                                201

```

<210> 277

<211> 520

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (520)

<223> n = A,T,C or G

<400> 277

```

aaaaaaaaag tattcagcac catttgctca tnggtctttc agagtttggt cttaaagttt      60

```

ctggaacttt cctgtctgta aagtaacagg aattactgag ctacattgga aagcctctct	120
gggacaggca gtggggagtt aagcagtcac cataaaggaa tcagtgtaca ttcagcatgg	180
tgacttgact acacaacaat cccttccccct ctactgtagc tcaagagaga catgcttcta	240
accactgagg tatgaggagt ctccagactgt tatttgctgt tagaattggc ctccccagct	300
aataacagta catctctggc acagatgcta ttggctccta atgtcctgtg attttaggaa	360
atagtttggg ttttagttcaa tttattcaga aaccaaactg gtttaattag cttcactact	420
ctggcagagt aagggtatgc tggtttagta tctttataaa atatatataa tgtataggta	480
aatcatagtc ttaaatacata cctaaaatac tgtatcattt	520

<210> 278

<211> 264

<212> DNA

<213> Homo sapien

<400> 278

cgcgccgggc ggaactttcc agaacgctcg gtgagaggcg gaggagcggc aactaccccg	60
gctgcgcaca gctcggcgct ccttcccgcct ccctcacaca ccggcctcag cccgcaccgg	120
cagtagaaga tgggtgaaaga aacaacttac tacgatgttt tgggggtcaa acccaatgct	180
actcaggaag aattgaaaaa ggcttatagg aaactggcct tgaagtacca tcctgataag	240
aacccaaatg aaggagagaa gttt	264

<210> 279

<211> 414

<212> DNA

<213> Homo sapien

<400> 279

aaacatacaa taatttttat tatggaaatt aatctttaca tacaaaatca gctacgtaat	60
tttacttaca aaacaataaa aactgttctt tactgtggca acaaaaagaag cattttgaca	120
aatgaaaaaa attaatgcaa acaaatataa acaatgcttt tctttttact tgcttcaactg	180
tctcttctat ttattttcta tgatcatctg acacaaacat ggattacttt gatattctact	240
gaaacataaa tgataagggt cttaaagggt gaattaaaag tctgggtggt caatatttta	300
gaagctgaat aaacaaaacg aaattggggg ttgtgattac agaggattta tcattttttc	360
cctttgtcca tatgaaaata tataatagaa aattaccac gggaaaacat tttt	414

<210> 280

<211> 262

<212> DNA

<213> Homo sapien

<400> 280

ccaccatgcc tggcctgctt caattttttg atgccacttt gtaaacggca cttaattatg	60
gaaaatagga aaaagcaaaa ctaaaataag gaagaggata tatatataac ttttcacaat	120
ctcttttctg atccccttta gatgccagc caaccaggac cacacacaga tttcatttta	180
ttttagaggt atatgaaaag atttaatagt ctcatgcatt ttattttacg tatactgatt	240
tctacgtttt gactgactat tt	262

<210> 281

<211> 349

<212> DNA

<213> Homo sapien

<400> 281

ctgtgacccg ggtgcatcag tggatatagt tgtgtctccc catgggggtt taacagtctc	60
tgcccaagac cgttttctga taatggtgac agaaatggaa cagtcactctg gcacaggccc	120


```

agcagaatta actcagtttt ggaaagaagt tcccagaaac aaagtgatgg aacataggtt      180
aagatgccat actgttgaaa gcagtaaacc aaacactctt acgttaaaag acaatgcttt      240
caatatgtca gataaaacca gtgaagatat atgtctacaa cttagtcgtt tactagaaag      300
caataggaag cttgaagacc aagttcagcg ttgtatctgg ttccagcag      349

```

<210> 282

<211> 381

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(381)

<223> n = A,T,C or G

<400> 282

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aaacactaaa tgaagcttct cacaatttct aattataaac aaaaggctga aaacagtatg      60
ggaaacaaaag tttcaaaaaca agaaaaagtt gagtaaaagg tgccccctct atggctcatc      120
tgaaagaaac attttactca gagaggcaaa catttctgat ctaggagtaa gtttccact      180
cactttgcaa ggaccactc attctgcana aagacctaca agtctttctg gtctcaattg      240
caaagtacgt gaaaatgtgt atgaaagatc taaaagctaa atattagaat aaggctaatt      300
gaaatcaaaa ttgtgtgctg gtctaaatat acatcttcgg cttcttcctt tttagtaagt      360
atttttatct cagatgtatt t

```

381

<210> 283

<211> 543

<212> DNA

<213> Homo sapien

<400> 283

```

aatatagctc ctccctaccc ccaacaatgg accctgccc a ttgcctccca gttccttgat      60
cttcctaggt tccacaactc tctttttcct tttagtttta ttccctccag ccaaacctct      120
cttattcaat attttgagcc aatgggggag ttatgtagat ttttttccct acacattagc      180
tgcccccttt tatgaccaat gactcataag gcaagatgtg tgggtggcatc ttcggacagg      240
cagcaggctt taatagggca gcctgggttg gtggaggcaa gcaaagctaa ttggcatgcg      300
tggaatcaa accccaggcc ctgggctcat tagcccatgg tcaaaacaac tgagccagag      360
gaggaataaa tttgcccagg aatatcagta gttcctttat tagaagaaaa tggctgatat      420
ggaagtggg gaatctgaat tgccagagaa tcttgggaag agtaataagc tcttagtctc      480
aacaataaagt gttttttcat ctgagcgcgt aaagggtgct atatgggaac aaagaagtat      540
ttt

```

543

<210> 284

<211> 147

<212> DNA

<213> Homo sapien

<400> 284

```

aaactggtat tttatctttg attctccttc agccctcacc cctgggtctc atctttcttg      60
atcaacatct tttcttgctt ctgtcccttc ctctcatctc ttagctcccc tccaacctgg      120
ggggcagtgg tgtggagaag ccacagg

```

147

<210> 285

<211> 316

<212> DNA

<213> Homo sapien

<400> 285

cggccgaggt ctggcttcac tcctactccc tctctgctcg cagcacgctg gccgccagct	60
ctttgatgtg ttcccaggcc cgctgcacat gggcagattc caccgtgcga gaacagatgg	120
caaagcgtag gacaaacttg tccctgaggt gacatggaac caagtggatt tttttggcac	180
tgtttattct ttgcagaaga gcttcattca ctttgttggg acccttttagc cgaaagcaga	240
caagccccag aatgacttcc acacagattt caaagcgggg atcctggcgc accagtgact	300
caaaactcatg ggacag	316

<210> 286

<211> 322

<212> DNA

<213> Homo sapien

<400> 286

cctggggagc cttttagtgg ggtgggacct caggcagacc cccaaaccaa agggagccag	60
atgcccaggt tcaagtcatt agtgatatgt ggcagggctg acagagaaat aatcctggag	120
gtctccaaag ctgctgggaa tgggaatggcg atgaaaagcg caggagtggg cagggtgtgg	180
tgggtgatgg tggcctcact cagagtggac caaggcccca gctccttgcc caaaaccaa	240
gcccttgggc ccgaagtttt tagcataaca tcctttgcag taaatctcgc catccttgtc	300
tgccagggtg gttgactcaa gg	322

<210> 287

<211> 364

<212> DNA

<213> Homo sapien

<400> 287

ctgcccagcg tcaaaccaat tctggctgat atcgagtacc tgcaggacca gcacctctcg	60
ctcacagtca agtccatgga tggctatgaa tcctatggg agtggtgtgtg tgcactcaaa	120
tccatgatcg gcagcacggc ccaacagttc ctgaccttcc tatcccaccg tggcgaggag	180
acaggcaata tcagaggctc catgaagggtg cgggtgcccc cggagcgcct gggcacccgt	240
gagcggctct acgagtggat cagcattgat aaggatgagg caggagcaaa gagcaaagcc	300
ccctctgtgt cccgagggag ccaggagccc aggtcaggga gccgcaagcc agccttcaca	360
gagg	364

<210> 288

<211> 261

<212> DNA

<213> Homo sapien

<400> 288

aaaattataa ctactcattc tttcttttagc cttagttaat ttgagcagaa gccacaacaa	60
gcaaaccaca ataaatttag aattggcaga aatccacatt aactcctctt cccaagtttc	120
cacactacta ccatttacag ttgtaggttt gtaatgtata attatgtaat gcagaaacta	180
gctttgactt gtgtaacgat gcactgtcaa agtaagcaaa gtaagaattg aaattccaca	240
ttcccagaat ttaacactca g	261

<210> 289

<211> 261

<212> DNA

<213> Homo sapien

<400> 289

ctgagtgtta aattctggga atgtggaatt tcaattctta ctttgcttac tttgacagtg	60
---	----

catcggttaca caagtcaaag ctagtttctg cattacataa ttatacatta caaacctaca	120
actgtaaatg gtagtagtgt ggaaacttgg gaagaggagt taatgtggat ttctgccaat	180
tctaaattta ttgtggtttg cttgttggg cttctgctca aattaactaa ggctaaagaa	240
agaatgagta gttataattt t	261

<210> 290

<211> 92

<212> DNA

<213> Homo sapien

<400> 290

ccactacccg aacttacagg tgccaaaaga agaaagggtg taaacggaga ccacctatca	60
ctcatcagaa cctaggatca tcacattcct tt	92

<210> 291

<211> 287

<212> DNA

<213> Homo sapien

<400> 291

ccatggctcc gctcagggcc ccgggtcacct ccgagtcact ctgttccttg actgtctttg	60
tgtttctgta cctcaaggca ctgaagctgg aggactctgt ccatgcctgt gtcaccctcg	120
tgtgggagcc tctgggctcg gcagggtccac atttcatgag ctgaggcgtg ggccagggcc	180
atctggaaag ggaactcggc ttttcagaa cgtggtggat catctgtcgg gtgtgtggtg	240
aacacgttca gttcatcagg gcctacgctc cgggaagggg cccccag	287

<210> 292

<211> 270

<212> DNA

<213> Homo sapien

<400> 292

ccattgtttc ctgctggcg aagggtcctt gaacatccct caccttcctc tcccgcctct	60
gccttctgct ggggtcaaagg tggccttttc tctccagcct tgaattgttc cctgttggct	120
tccaaggcc ccatctgctg gtacagtcca cacttcaca gccaagacc gagagggtt	180
tcactgcccc aagcctctct cctgtgacct tgggattctg tcttggcaga atcctttgtc	240
agcggctctt actctgtcct tctgttttg	270

<210> 293

<211> 333

<212> DNA

<213> Homo sapien

<400> 293

ccatgctcgt caacctgggtg tccactgctt gctacgtctc ctctctcttc ctgggctgcg	60
acactggccc tgtggctggg gttactgttc cctatggaaa cagcacagca cctggctcag	120
ccctggaccc ctactcgccc tgcaataata actgtgaatg ccaaaccgat tccttcactc	180
cagtgtgtgg ggcagatggc atcacctacc tgtctgctg ctttctgtgg tgcaacagca	240
cgaatctcac gggctgtgcg tgcctacca ccgtccctgc tgagaacgca accgtggttc	300
ctggaaaatg cccagtcctt gggcgccaag agg	333

<210> 294

<211> 123

<212> DNA

<213> Homo sapien

<400> 294
 ctgatacaaa tacagaaaac tctgcccatt atccaagaaa caaataatta agactaaaat 60
 gcaagctgat gtgttcgagc attgtagggc cactaaatag ccatctgtga ttcgtggcaa 120
 ttt 123

<210> 295
 <211> 311
 <212> DNA
 <213> Homo sapien

<400> 295
 ctgcatacag acatttggtt aggtcatctg gattatcttg attgtcacca tggcaactat 60
 ccacaaccag tgcctaggtg tgtgagaaga gtgatacaat aatactgtgg catgggtcatt 120
 tagctaattcc agtctaagcc taacagaaaac cttttccatc aaagtttttc agagaataac 180
 aacatctcat aagaggccag aggatggctt gtgcttaata tcacacctgt acagtagggc 240
 agtgcttccc aggtgtctg cttacatttt agcttgtctt acggttacat atggtttttag 300
 tattttcatt t 311

<210> 296
 <211> 241
 <212> DNA
 <213> Homo sapien

<400> 296
 ctgcggaaga tctgcaacca cccctacatg ttccagcaca tcgaggagtc cttttccgag 60
 cacttggggt tcaactggcg cattgtccaa gggctggacc tgtaccgagc ctcgggtaaa 120
 tttgagcttc ttgatagaat ttttcccaa ctccgagcaa ccaaccacaa agtgctgctg 180
 ttctgcaaaa tgacctccct catgaccatc atggaagatt actttgcgta tcgcggcttc 240
 a 241

<210> 297
 <211> 295
 <212> DNA
 <213> Homo sapien

<400> 297
 aaacacaaga tgaaaatact ctgttctgtc caaagcatca cctaattggtg tgaggcatct 60
 cacttagctg tggagaagtc cttggaatta gatctcagaa agacagcttt aagacagttaa 120
 aaccttttgg caatgggcta attgccttaa aagaagagtt ctacctgaaa gaccttgcag 180
 gtggagaaat tgtcctacaa agattcttgg atatgttagt ggagataact gacatgggta 240
 gctgtgggtc aaccaggaac tgtcaacaac ctgatctctg caaaaccagg atgga 295

<210> 298
 <211> 347
 <212> DNA
 <213> Homo sapien

<400> 298
 ccaaaataaa gcttcaggca agaggcaaag atccagtgga atatgggaga atgggtggagg 60
 accaacacct gctaccccag agagcttttc taaaaaaagc aagaaagcag tcatgagtgg 120
 tattcacct gcagaagaca cgaaggttac tgagtttgag ccagagggac ttccagaagt 180
 tgtaaagaaa gggtttgctg acatcccagc aggaagact agcccatata tcctgcgaag 240
 aacaacctg gcaactcgga ccagccccg cctggctgca cagaagttag cgctatcccc 300
 actgagtctc ggcaaagaaa atcttgcaga gtcctccaaa ccaacag 347

<210> 299
<211> 268
<212> DNA
<213> Homo sapien

<400> 299
aaaaagtaaa catgaaaaca tcacgaattg taccatgatt caagaataac ttttgtaata 60
gaaaacacat gaccttttgc agtatagtgt gataccgaag taaaagtga agaaataaat 120
gcaggaaagt ttaagtggat gtaagttttt ataaggaaag taataagagg aggctgcttt 180
tgaaggctct ttgatcttcc atgatgataa tatcggtgca aagttcttta acttgtattc 240
aagtaattag cagttgacca cttggttt 268

<210> 300
<211> 185
<212> DNA
<213> Homo sapien

<400> 300
aaattggaga aggaagtttt cctgaagagc cagaatcctt gctaagtcatt ttagatccaa 60
ctgaccatct ttatttctgt caaaaatctt catcatgggtg ccggtgtatt cttccagttt 120
agcctcagaa atggcctttc tgtggtgaag aaagagggtct cggaggaagt tgcggagctc 180
agcag 185

<210> 301
<211> 75
<212> DNA
<213> Homo sapien

<400> 301
aaaattggaa agtgggataa gaaatctaaa gtaaccagct tatctttgaa acaatattat 60
tttgaaattg gcttt 75

<210> 302
<211> 247
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(247)
<223> n = A,T,C or G

<400> 302
ccatgttctc tgaattgggt gcagaagaca agggcagagt ggctgcggcc cctattacct 60
ttgtagcagc cacatcagaa agcagaagaa aacagtattt ctgaaggcat tgtttgaggt 120
tgatctcagc actgaacgat ttcaagccct acgcaccana acagaaggag ggtggaggaa 180
gtgatcanag ggaacgagct gtaggtttgc anaaatgtgt gaaaccaaaa tgatcactgc 240
ctacttg 247

<210> 303
<211> 535
<212> DNA
<213> Homo sapien

<400> 303

ctgcttcaga	ggaaatcact	gaaaaataaa	gaaaaaccat	ccatgcatgg	ctgcatccag	60
tgtacctgta	atcctgaaga	aaaggctcta	attccttcca	tgtgaaatg	ctagctttgg	120
tttcagagag	agactttatt	gcaactgtga	ccaccgtcac	tggtagagcac	tgtgtttcgg	180
ccccagcgg	acttaaaaga	ctggaatgtg	gtagtggcgg	tcgttctcgg	tcagcagggg	240
gatctccggc	cagtcacctga	gaggctcctc	tgggtagcag	acttcaaagt	ctctggagtt	300
aaacttgaac	agtctgaaca	cttttatctt	tacttcaagg	gagtatccaa	gtataaacat	360
atcaatctgc	tctagtccac	atgtgtcgcc	tacagaattc	aggtgattca	tcataaagct	420
caaaggatca	gaggatgtct	ccctggaaaa	caggagtcta	aaaagactgg	gaatgacctt	480
tttagtcttc	atttgttcat	aaacttcagt	gacttgatac	agcatgatga	actttt	535

<210> 304

<211> 522

<212> DNA

<213> Homo sapien

<400> 304

ccgcgctcgg	tctacaatca	cgttttatta	ttggctcgtc	tagtcatggg	atagagaagg	60
taaaatagcaa	aatagaaga	aaagggggaa	aaggtagaag	gcaaggggaa	aactattggt	120
tttagatctt	tatcctgggc	ctgtcaatga	tcaggtaat	ggaaggatca	aaattaggcc	180
aaacttggtg	attgggcca	aattgaacca	aagtttgtgt	caagaagacc	tggggcagag	240
atatgtgact	aatcatcttg	gaatatgccc	agacccaag	aatatttatg	cccaacttga	300
atgctaacca	gaagtccctt	actgtagaag	attgtaagg	tgtattttt	ttgccccgac	360
accaaaatat	tgatgtattt	tccaacacca	attctccaat	tctctgacac	caactcgatg	420
ttcaacaatt	cagttatatt	ctgtcactaa	ttcctgcagc	tatcagcagg	ccccacaggt	480
aaaggattca	gtctcacaag	attgcccccc	caccacttc	ag		522

<210> 305

<211> 165

<212> DNA

<213> Homo sapien

<400> 305

cctaaagcgc	tcctcgctga	agctcaagg	gtccacaatg	atttgtttgt	caaagttatt	60
gagtgcata	gccagttctc	ctcctcctcc	accctgggtc	tgtgaggcat	cgtctgaggc	120
agtggcctgg	gctgcattgg	aaatgcctgt	gaccgcctgc	tgcag		165

<210> 306

<211> 294

<212> DNA

<213> Homo sapien

<400> 306

ctgcacctaa	gacatggccc	tggctaggcg	ggaacagctc	acagtagcga	tacattcaca	60
ggacacagtt	ggtgtccaga	aaagggggct	cagaacacag	tttctacaca	agcacttggc	120
acccacacga	cagagacgtc	actcaagcag	cacagccaca	aatagtttac	agcagctcat	180
gcccggcatc	cgcccatgct	gggagactcc	ctgaaagggtg	ggcacctgcc	gtctatgagg	240
aggtgtctcc	ctccatcatt	aacccccaa	cacacaatgt	gtgaggagag	cagg	294

<210> 307

<211> 181

<212> DNA

<213> Homo sapien

<400> 307

```

aaaaatccat gacaccttga tagaaattag agtttacaca aacaaaaaag gaaccttcga      60
tattgccagc agctataaag tgaacgtact gagaccgaca ggacagcaag aaggcatttg      120
cacatttata tctgacaccc gaccatactt tcagtcacca gaatatcttc tctccagatt      180
t                                                                    181

```

```

<210> 308
<211> 179
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(179)
<223> n = A,T,C or G

```

```

<400> 308
aaggctgagg actgctggga gctcagatca gcccggagct actggctcat gggcagccaa      60
aaaaactagg atctgctgaa cgaaggctca gcccgagatc tccgcagtct tcagcgcatc      120
ggcccgaaga aggcccanct aatcgtgggc tggcgggagc tccacggccc cttcagcca      179

```

```

<210> 309
<211> 129
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(129)
<223> n = A,T,C or G

```

```

<400> 309
ctgcccgcctt gcccgtagct gactcagntt cctcatcttc atctccatcc tcttcctcac      60
catcaccttc ttcttctctc tctcttctct cccacacctc ttctctctct tcgtctacct      120
cattgtcag                                                                    129

```

```

<210> 310
<211> 390
<212> DNA
<213> Homo sapien

```

```

<400> 310
tgaggctggg ggagagccgt ggtccctgag gatgggtcag agctaaactc ctctcctggcc      60
tgagagtcag ctctctgccc tgtgtacttc ccgggccagg gctgccccta atctctgtag      120
gaaccgtggt atgtctgcat gttgcccctt tctcttttcc cctttcctgt cccaccatac      180
gagcacctcc agcctgaaca gaagctctta ctctttccta ttccagtgtt acctgtgtgc      240
ttggtctggt tgactttacg cccatctcag gacacttccg tagactgttt aggttcccct      300
gtcaaatatc agttaccacac tcggtcccag ttttgttgcc ccagaaaggg atgttattat      360
ccttggggggc tcccagggca agggttaagg                                                                    390

```

```

<210> 311
<211> 355
<212> DNA
<213> Homo sapien

```

```

<220>

```

<221> misc_feature
 <222> (1)...(355)
 <223> n = A,T,C or G

<400> 311

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<210> 312

<211> 498

<212> DNA

<213> Homo sapien

<400> 312

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<211> 653

<212> DNA

<213> Homo sapien

<400> 313

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<211> 513

<212> DNA

<213> Homo sapien

<400> 314

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<210> 315
<211> 222
<212> DNA
<213> Homo sapien

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<210> 316
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<212> DNA
<213> Homo sapiens

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<210> 317

<211> 4235

<212> DNA

<213> Homo sapiens

<400> 317

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<210> 318

<211> 3347

<212> DNA

<213> Homo sapiens

<400> 318

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<210> 319

<211> 1814

<212> DNA

<213> Homo sapiens

<400> 319

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1814

<210> 320

<211> 3132

<212> DNA

<213> Homo sapiens

<400> 320

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3132

<210> 321

<211> 2280

<212> DNA

<213> Homo sapiens

<400> 321

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tcgtttctca tctccttgat gttcctgttg tcttacttgt ttggatttta caaaagattt 240
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<210> 322

<211> 1398

<212> DNA

<213> Homo sapiens

<400> 322

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ctaaccctaaa ggaattgaaa ggaaccactc attcacttct agacgacaaa atgcaaaaaa 180
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1398

<210> 323

<211> 1316

<212> DNA

<213> Homo sapiens

<400> 323

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<210> 324

<211> 200

<212> PRT

<213> Homo sapiens

<400> 324

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Ala Phe Phe Val Gln Thr Cys Arg Glu Glu His Lys Lys Lys Asn Pro
      20              25              30

Glu Val Pro Val Asn Phe Ala Glu Phe Ser Lys Lys Cys Ser Glu Arg
      35              40              45

Trp Lys Thr Val Ser Gly Lys Glu Lys Ser Lys Phe Asp Glu Met Ala
      50              55              60

Lys Ala Asp Lys Val Arg Tyr Asp Arg Glu Met Lys Asp Tyr Gly Pro
      65              70              75              80

Ala Lys Gly Gly Lys Lys Lys Lys Asp Pro Asn Ala Pro Lys Arg Pro
      85              90              95

Pro Ser Gly Phe Phe Leu Phe Cys Ser Glu Phe Arg Pro Lys Ile Lys
      100             105             110

Ser Thr Asn Pro Gly Ile Ser Ile Gly Asp Val Ala Lys Lys Leu Gly
      115             120             125

Glu Met Trp Asn Asn Leu Asn Asp Ser Glu Lys Gln Pro Tyr Ile Thr
      130             135             140

Lys Ala Ala Lys Leu Lys Glu Lys Tyr Glu Lys Asp Val Ala Asp Tyr
      145             150             155             160

Lys Ser Lys Gly Lys Phe Asp Gly Ala Lys Gly Pro Ala Lys Val Ala

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165 170 175
 Arg Lys Lys Val Glu Glu Glu Asp Glu Glu Gln Glu Glu Glu Glu
 180 185 190
 Glu Glu Glu Glu Glu Glu Asp Glu
 195 200

 <210> 325
 <211> 263
 <212> PRT
 <213> Homo sapiens

 <400> 325
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 Gly Arg Ile His Gln Ile Glu Tyr Ala Met Glu Ala Val Lys Gln Gly
 20 25 30
 Ser Ala Thr Val Gly Leu Lys Ser Lys Thr His Ala Val Leu Val Ala
 35 40 45
 Leu Lys Arg Ala Gln Ser Glu Leu Ala Ala His Gln Lys Lys Ile Leu
 50 55 60
 His Val Asp Asn His Ile Gly Ile Ser Ile Ala Gly Leu Thr Ala Asp
 65 70 75 80
 Ala Arg Leu Leu Cys Asn Phe Met Arg Gln Glu Cys Leu Asp Ser Arg
 85 90 95
 Phe Val Phe Asp Arg Pro Leu Pro Val Ser Arg Leu Val Ser Leu Ile
 100 105 110
 Gly Ser Lys Thr Gln Ile Pro Thr Gln Arg Tyr Gly Arg Arg Pro Tyr
 115 120 125
 Gly Val Gly Leu Leu Ile Ala Gly Tyr Asp Asp Met Gly Pro His Ile
 130 135 140
 Phe Gln Thr Cys Pro Ser Ala Asn Tyr Phe Asp Cys Arg Ala Met Ser
 145 150 155 160
 Ile Gly Ala Arg Ser Gln Ser Ala Arg Thr Tyr Leu Glu Arg His Met
 165 170 175
 Ser Glu Phe Met Glu Cys Asn Leu Asn Glu Leu Val Lys His Gly Leu
 180 185 190
 Arg Ala Leu Arg Glu Thr Leu Pro Ala Glu Gln Asp Leu Thr Thr Lys
 195 200 205
 Asn Val Ser Ile Gly Ile Val Gly Lys Asp Leu Glu Phe Thr Ile Tyr

Gln Arg Lys Ala Gln Pro Ala Gln Pro Ala Asp Glu Pro Ala Glu Lys
245 250 255

Ala Asp Glu Pro Met Glu His
260

<211> 539

<212> PRT

<213> Homo sapiens

Met Pro Glu Asn Val Ala Pro Arg Ser Gly Ala Thr Ala Gly Ala Ala
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Gly Gly Arg Gly Lys Gly Ala Tyr Gln Asp Arg Asp Lys Pro Ala Gln
20 25 30

Ile Arg Phe Ser Asn Ile Ser Ala Ala Lys Ala Val Ala Asp Ala Ile
35 40 45

Arg Thr Ser Leu Gly Pro Lys Gly Met Asp Lys Met Ile Gln Asp Gly
50 55 60

Lys Gly Asp Val Thr Ile Thr Asn Asp Gly Ala Thr Ile Leu Lys Gln
65 70 75 80

Met Gln Val Leu His Pro Ala Ala Arg Met Leu Val Glu Leu Ser Lys
85 90 95

Ala Gln Asp Ile Glu Ala Gly Asp Gly Thr Thr Ser Val Val Ile Ile
100 105 110

Ala Gly Ser Leu Leu Asp Ser Cys Thr Lys Leu Leu Gln Lys Gly Ile
115 120 125

His Pro Thr Ile Ile Ser Glu Ser Phe Gln Lys Ala Leu Glu Lys Gly
130 135 140

Ile Glu Ile Leu Thr Asp Met Ser Arg Pro Val Glu Leu Ser Asp Arg
145 150 155 160

Glu Thr Leu Leu Asn Ser Ala Thr Thr Ser Leu Asn Ser Lys Val Val
165 170 175

Ser Gln Tyr Ser Ser Leu Leu Ser Pro Met Ser Val Asn Ala Val Met
180 185 190

Lys Val Ile Asp Pro Ala Thr Ala Thr Ser Val Asp Leu Arg Asp Ile

195	200	205
Lys Ile Val Lys Lys Leu Gly Gly Thr Ile Asp Asp Cys Glu Leu Val		
210	215	220
Glu Gly Leu Val Leu Thr Gln Lys Val Ser Asn Ser Gly Ile Thr Arg		
225	230	235 240
Val Glu Lys Ala Lys Ile Gly Leu Ile Gln Phe Cys Leu Ser Ala Pro		
	245	250 255
Lys Thr Asp Met Asp Asn Gln Ile Val Val Ser Asp Tyr Ala Gln Met		
	260	265 270
Asp Arg Val Leu Arg Glu Glu Arg Ala Tyr Ile Leu Asn Leu Val Lys		
	275	280 285
Gln Ile Lys Lys Thr Gly Cys Asn Val Leu Leu Ile Gln Lys Ser Ile		
	290	295 300
Leu Arg Asp Ala Leu Ser Asp Leu Ala Leu His Phe Leu Asn Lys Met		
305	310	315 320
Lys Ile Met Val Ile Lys Asp Ile Glu Arg Glu Asp Ile Glu Phe Ile		
	325	330 335
Cys Lys Thr Ile Gly Thr Lys Pro Val Ala His Ile Asp Gln Phe Thr		
	340	345 350
Ala Asp Met Leu Gly Ser Ala Glu Leu Ala Glu Glu Val Asn Leu Asn		
	355	360 365
Gly Ser Gly Lys Leu Leu Lys Ile Thr Gly Cys Ala Ser Pro Gly Lys		
	370	375 380
Thr Val Thr Ile Val Val Arg Gly Ser Asn Lys Leu Val Ile Glu Glu		
385	390	395 400
Ala Glu Arg Ser Ile His Asp Ala Leu Cys Val Ile Arg Cys Leu Val		
	405	410 415
Lys Lys Arg Ala Leu Ile Ala Gly Gly Gly Ala Pro Glu Ile Glu Leu		
	420	425 430
Ala Leu Arg Leu Thr Glu Tyr Ser Arg Thr Leu Ser Gly Met Glu Ser		
	435	440 445
Tyr Cys Val Arg Ala Phe Ala Asp Ala Met Glu Val Ile Pro Ser Thr		
	450	455 460
Leu Ala Glu Asn Ala Gly Leu Asn Pro Ile Ser Thr Val Thr Glu Leu		
465	470	475 480
Arg Asn Arg His Ala Gln Gly Glu Lys Thr Ala Gly Ile Asn Val Arg		
	485	490 495

100

Lys Gly Gly Ile Ser Asn Ile Leu Glu Glu Leu Val Val Gln Pro Leu
 500 505 510

Leu Val Ser Val Ser Ala Leu Thr Leu Ala Thr Glu Thr Val Arg Ser
 515 520 525

Ile Leu Lys Ile Asp Asp Val Val Asn Thr Arg
 530 535

<210> 327

<211> 144

<212> PRT

<213> Homo sapiens

<400> 327

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Thr Ala Ala Leu Ile Phe Phe Ala Ile Trp His Ile Ile Ala Phe Asp
 20 25 30

Glu Leu Lys Thr Asp Tyr Lys Asn Pro Ile Asp Gln Cys Asn Thr Leu
 35 40 45

Asn Pro Leu Val Leu Pro Glu Tyr Leu Ile His Ala Phe Phe Cys Val
 50 55 60

Met Phe Leu Cys Ala Ala Glu Trp Leu Thr Leu Gly Leu Asn Met Pro
 65 70 75 80

Leu Leu Ala Tyr His Ile Trp Arg Tyr Met Ser Arg Pro Val Met Ser
 85 90 95

Gly Pro Gly Leu Tyr Asp Pro Thr Thr Ile Met Asn Ala Asp Ile Leu
 100 105 110

Ala Tyr Cys Gln Lys Glu Gly Trp Cys Lys Leu Ala Phe Tyr Leu Leu
 115 120 125

Ala Phe Phe Tyr Tyr Leu Tyr Gly Met Ile Tyr Val Leu Val Ser Ser
 130 135 140

<210> 328

<211> 138

<212> PRT

<213> Homo sapiens

<400> 328

Met Pro Asn Phe Ser Gly Asn Trp Lys Ile Ile Arg Ser Glu Asn Phe
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Glu Glu Leu Leu Lys Val Leu Gly Val Asn Val Met Leu Arg Lys Ile

20 25 30
 Ala Val Ala Ala Ala Ser Lys Pro Ala Val Glu Ile Lys Gln Glu Gly
 35 40 45
 Asp Thr Phe Tyr Ile Lys Thr Ser Thr Thr Val Arg Thr Thr Glu Ile
 50 55 60
 Asn Phe Lys Val Gly Glu Glu Phe Glu Glu Gln Thr Val Asp Gly Arg
 65 70 75 80
 Pro Cys Lys Ser Leu Val Lys Trp Glu Ser Glu Asn Lys Met Val Cys
 85 90 95
 Glu Gln Lys Leu Leu Lys Gly Glu Gly Pro Lys Thr Ser Trp Thr Arg
 100 105 110
 Glu Leu Thr Asn Asp Gly Glu Leu Ile Leu Thr Met Thr Ala Asp Asp
 115 120 125
 Val Val Cys Thr Arg Val Tyr Val Arg Glu
 130 135

 <210> 329
 <211> 346
 <212> PRT
 <213> Homo sapiens

 <400> 329
 Met Phe Leu Ser Ile Leu Val Ala Leu Cys Leu Trp Leu His Leu Ala
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 Leu Gly Val Arg Gly Ala Pro Cys Glu Ala Val Arg Ile Pro Met Cys
 20 25 30
 Arg His Met Pro Trp Asn Ile Thr Arg Met Pro Asn His Leu His His
 35 40 45
 Ser Thr Gln Glu Asn Ala Ile Leu Ala Ile Glu Gln Tyr Glu Glu Leu
 50 55 60
 Val Asp Val Asn Cys Ser Ala Val Leu Arg Phe Phe Phe Cys Ala Met
 65 70 75 80
 Tyr Ala Pro Ile Cys Thr Leu Glu Phe Leu His Asp Pro Ile Lys Pro
 85 90 95
 Cys Lys Ser Val Cys Gln Arg Ala Arg Asp Asp Cys Glu Pro Leu Met
 100 105 110
 Lys Met Tyr Asn His Ser Trp Pro Glu Ser Leu Ala Cys Asp Glu Leu
 115 120 125
 Pro Val Tyr Asp Arg Gly Val Cys Ile Ser Pro Glu Ala Ile Val Thr

130 135 140
 Asp Leu Pro Glu Asp Val Lys Trp Ile Asp Ile Thr Pro Asp Met Met
 145 150 155 160
 Val Gln Glu Arg Pro Leu Asp Val Asp Cys Lys Arg Leu Ser Pro Asp
 165 170 175
 Arg Cys Lys Cys Lys Lys Val Lys Pro Thr Leu Ala Thr Tyr Leu Ser
 180 185 190
 Lys Asn Tyr Ser Tyr Val Ile His Ala Lys Ile Lys Ala Val Gln Arg
 195 200 205
 Ser Gly Cys Asn Glu Val Thr Thr Val Val Asp Val Lys Glu Ile Phe
 210 215 220
 Lys Ser Ser Ser Pro Ile Pro Arg Thr Gln Val Pro Leu Ile Thr Asn
 225 230 235 240
 Ser Ser Cys Gln Cys Pro His Ile Leu Pro His Gln Asp Val Leu Ile
 245 250 255
 Met Cys Tyr Glu Trp Arg Ser Arg Met Met Leu Leu Glu Asn Cys Leu
 260 265 270
 Val Glu Lys Trp Arg Asp Gln Leu Ser Lys Arg Ser Ile Gln Trp Glu
 275 280 285
 Glu Arg Leu Gln Glu Gln Arg Arg Thr Val Gln Asp Lys Lys Lys Thr
 290 295 300
 Ala Gly Arg Thr Ser Arg Ser Asn Pro Pro Lys Pro Lys Gly Lys Pro
 305 310 315 320
 Pro Ala Pro Lys Pro Ala Ser Pro Lys Lys Asn Ile Lys Thr Arg Ser
 325 330 335
 Ala Gln Lys Arg Thr Asn Pro Lys Arg Val
 340 345

 <210> 330
 <211> 826
 <212> PRT
 <213> Homo sapiens

 <400> 330
 Met Glu Gly Ala Gly Gly Ala Asn Asp Lys Lys Lys Ile Ser Ser Glu
 5 10 15
 Arg Arg Lys Glu Lys Ser Arg Asp Ala Ala Arg Ser Arg Arg Ser Lys
 20 25 30
 Glu Ser Glu Val Phe Tyr Glu Leu Ala His Gln Leu Pro Leu Pro His

35 40 45
 Asn Val Ser Ser His Leu Asp Lys Ala Ser Val Met Arg Leu Thr Ile
 50 55 60
 Ser Tyr Leu Arg Val Arg Lys Leu Leu Asp Ala Gly Asp Leu Asp Ile
 65 70 75 80
 Glu Asp Asp Met Lys Ala Gln Met Asn Cys Phe Tyr Leu Lys Ala Leu
 85 90 95
 Asp Gly Phe Val Met Val Leu Thr Asp Asp Gly Asp Met Ile Tyr Ile
 100 105 110
 Ser Asp Asn Val Asn Lys Tyr Met Gly Leu Thr Gln Phe Glu Leu Thr
 115 120 125
 Gly His Ser Val Phe Asp Phe Thr His Pro Cys Asp His Glu Glu Met
 130 135 140
 Arg Glu Met Leu Thr His Arg Asn Gly Leu Val Lys Lys Gly Lys Glu
 145 150 155 160
 Gln Asn Thr Gln Arg Ser Phe Phe Leu Arg Met Lys Cys Thr Leu Thr
 165 170 175
 Ser Arg Gly Arg Thr Met Asn Ile Lys Ser Ala Thr Trp Lys Val Leu
 180 185 190
 His Cys Thr Gly His Ile His Val Tyr Asp Thr Asn Ser Asn Gln Pro
 195 200 205
 Gln Cys Gly Tyr Lys Lys Pro Pro Met Thr Cys Leu Val Leu Ile Cys
 210 215 220
 Glu Pro Ile Pro His Pro Ser Asn Ile Glu Ile Pro Leu Asp Ser Lys
 225 230 235 240
 Thr Phe Leu Ser Arg His Ser Leu Asp Met Lys Phe Ser Tyr Cys Asp
 245 250 255
 Glu Arg Ile Thr Glu Leu Met Gly Tyr Glu Pro Glu Glu Leu Leu Gly
 260 265 270
 Arg Ser Ile Tyr Glu Tyr Tyr His Ala Leu Asp Ser Asp His Leu Thr
 275 280 285
 Lys Thr His His Asp Met Phe Thr Lys Gly Gln Val Thr Thr Gly Gln
 290 295 300
 Tyr Arg Met Leu Ala Lys Arg Gly Gly Tyr Val Trp Val Glu Thr Gln
 305 310 315 320
 Ala Thr Val Ile Tyr Asn Thr Lys Asn Ser Gln Pro Gln Cys Ile Val
 325 330 335

Cys Val Asn Tyr Val Val Ser Gly Ile Ile Gln His Asp Leu Ile Phe
 340 345 350
 Ser Leu Gln Gln Thr Glu Cys Val Leu Lys Pro Val Glu Ser Ser Asp
 355 360 365
 Met Lys Met Thr Gln Leu Phe Thr Lys Val Glu Ser Glu Asp Thr Ser
 370 375 380
 Ser Leu Phe Asp Lys Leu Lys Lys Glu Pro Asp Ala Leu Thr Leu Leu
 385 390 395 400
 Ala Pro Ala Ala Gly Asp Thr Ile Ile Ser Leu Asp Phe Gly Ser Asn
 405 410 415
 Asp Thr Glu Thr Asp Asp Gln Gln Leu Glu Glu Val Pro Leu Tyr Asn
 420 425 430
 Asp Val Met Leu Pro Ser Pro Asn Glu Lys Leu Gln Asn Ile Asn Leu
 435 440 445
 Ala Met Ser Pro Leu Pro Thr Ala Glu Thr Pro Lys Pro Leu Arg Ser
 450 455 460
 Ser Ala Asp Pro Ala Leu Asn Gln Glu Val Ala Leu Lys Leu Glu Pro
 465 470 475 480
 Asn Pro Glu Ser Leu Glu Leu Ser Phe Thr Met Pro Gln Ile Gln Asp
 485 490 495
 Gln Thr Pro Ser Pro Ser Asp Gly Ser Thr Arg Gln Ser Ser Pro Glu
 500 505 510
 Pro Asn Ser Pro Ser Glu Tyr Cys Phe Tyr Val Asp Ser Asp Met Val
 515 520 525
 Asn Glu Phe Lys Leu Glu Leu Val Glu Lys Leu Phe Ala Glu Asp Thr
 530 535 540
 Glu Ala Lys Asn Pro Phe Ser Thr Gln Asp Thr Asp Leu Asp Leu Glu
 545 550 555 560
 Met Leu Ala Pro Tyr Ile Pro Met Asp Asp Asp Phe Gln Leu Arg Ser
 565 570 575
 Phe Asp Gln Leu Ser Pro Leu Glu Ser Ser Ser Ala Ser Pro Glu Ser
 580 585 590
 Ala Ser Pro Gln Ser Thr Val Thr Val Phe Gln Gln Thr Gln Ile Gln
 595 600 605
 Glu Pro Thr Ala Asn Ala Thr Thr Thr Thr Ala Thr Thr Asp Glu Leu
 610 615 620

Lys Thr Val Thr Lys Asp Arg Met Glu Asp Ile Lys Ile Leu Ile Ala
 625 630 635 640
 Ser Pro Ser Pro Thr His Ile His Lys Glu Thr Thr Ser Ala Thr Ser
 645 650 655
 Ser Pro Tyr Arg Asp Thr Gln Ser Arg Thr Ala Ser Pro Asn Arg Ala
 660 665 670
 Gly Lys Gly Val Ile Glu Gln Thr Glu Lys Ser His Pro Arg Ser Pro
 675 680 685
 Asn Val Leu Ser Val Ala Leu Ser Gln Arg Thr Thr Val Pro Glu Glu
 690 695 700
 Glu Leu Asn Pro Lys Ile Leu Ala Leu Gln Asn Ala Gln Arg Lys Arg
 705 710 715 720
 Lys Met Glu His Asp Gly Ser Leu Phe Gln Ala Val Gly Ile Gly Thr
 725 730 735
 Leu Leu Gln Gln Pro Asp Asp His Ala Ala Thr Thr Ser Leu Ser Trp
 740 745 750
 Lys Arg Val Lys Gly Cys Lys Ser Ser Glu Gln Asn Gly Met Glu Gln
 755 760 765
 Lys Thr Ile Ile Leu Ile Pro Ser Asp Leu Ala Cys Arg Leu Leu Gly
 770 775 780
 Gln Ser Met Asp Glu Ser Gly Leu Pro Gln Leu Thr Ser Tyr Asp Cys
 785 790 795 800
 Glu Val Asn Ala Pro Ile Gln Gly Ser Arg Asn Leu Leu Gln Gly Glu
 805 810 815
 Glu Leu Leu Arg Ala Leu Asp Gln Val Asn
 820 825

 <210> 331
 <211> 92
 <212> PRT
 <213> Homo sapiens

 <400> 331
 Met Ala Tyr Arg Gly Gln Gly Gln Lys Val Gln Lys Val Met Val Gln
 5 10 15
 Pro Ile Asn Leu Ile Phe Arg Tyr Leu Gln Asn Arg Ser Arg Ile Gln
 20 25 30
 Val Trp Leu Tyr Glu Gln Val Asn Met Arg Ile Glu Gly Cys Ile Ile
 35 40 45

Gly Phe Asp Glu Tyr Met Asn Leu Val Leu Asp Asp Ala Glu Glu Ile
 50 55 60

His Ser Lys Thr Lys Ser Arg Lys Gln Leu Gly Arg Ile Met Leu Lys
 65 70 75 80

Gly Asp Asn Ile Thr Leu Leu Gln Ser Val Ser Asn
 85 90

<210> 332

<211> 235

<212> PRT

<213> Homo sapiens

<400> 332

Met Asp Pro Ala Arg Pro Leu Gly Leu Ser Ile Leu Leu Leu Phe Leu
 5 10 15

Thr Glu Ala Ala Leu Gly Asp Ala Ala Gln Glu Pro Thr Gly Asn Asn
 20 25 30

Ala Glu Ile Cys Leu Leu Pro Leu Asp Tyr Gly Pro Cys Arg Ala Leu
 35 40 45

Leu Leu Arg Tyr Tyr Tyr Asp Arg Tyr Thr Gln Ser Cys Arg Gln Phe
 50 55 60

Leu Tyr Gly Gly Cys Glu Gly Asn Ala Asn Asn Phe Tyr Thr Trp Glu
 65 70 75 80

Ala Cys Asp Asp Ala Cys Trp Arg Ile Glu Lys Val Pro Lys Val Cys
 85 90 95

Arg Leu Gln Val Ser Val Asp Asp Gln Cys Glu Gly Ser Thr Glu Lys
 100 105 110

Tyr Phe Phe Asn Leu Ser Ser Met Thr Cys Glu Lys Phe Phe Ser Gly
 115 120 125

Gly Cys His Arg Asn Arg Ile Glu Asn Arg Phe Pro Asp Glu Ala Thr
 130 135 140

Cys Met Gly Phe Cys Ala Pro Lys Lys Ile Pro Ser Phe Cys Tyr Ser
 145 150 155 160

Pro Lys Asp Glu Gly Leu Cys Ser Ala Asn Val Thr Arg Tyr Tyr Phe
 165 170 175

Asn Pro Arg Tyr Arg Thr Cys Asp Ala Phe Thr Tyr Thr Gly Cys Gly
 180 185 190

Gly Asn Asp Asn Asn Phe Val Ser Arg Glu Asp Cys Lys Arg Ala Cys
 195 200 205

Ala Lys Ala Leu Lys Lys Lys Lys Lys Met Pro Lys Leu Arg Phe Ala

210
225
230
235

215
220

Ser Arg Ile Arg Lys Ile Arg Lys Lys Gln Phe
225 230 235

<210> 333
<211> 291
<212> PRT
<213> Homo sapiens
<400> 333

Met Gln Arg Ala Arg Pro Thr Leu Trp Ala Ala Ala Leu Thr Leu Leu
5 10 15

Val Leu Leu Arg Gly Pro Pro Val Ala Arg Ala Gly Ala Ser Ser Gly
20 25 30

Gly Leu Gly Pro Val Val Arg Cys Glu Pro Cys Asp Ala Arg Ala Leu
35 40 45

Ala Gln Cys Ala Pro Pro Pro Ala Val Cys Ala Glu Leu Val Arg Glu
50 55 60

Pro Gly Cys Gly Cys Cys Leu Thr Cys Ala Leu Ser Glu Gly Gln Pro
65 70 75 80

Cys Gly Ile Tyr Thr Glu Arg Cys Gly Ser Gly Leu Arg Cys Gln Pro
85 90 95

Ser Pro Asp Glu Ala Arg Pro Leu Gln Ala Leu Leu Asp Gly Arg Gly
100 105 110

Leu Cys Val Asn Ala Ser Ala Val Ser Arg Leu Arg Ala Tyr Leu Leu
115 120 125

Pro Ala Pro Pro Ala Pro Gly Asn Ala Ser Glu Ser Glu Glu Asp Arg
130 135 140

Ser Ala Gly Ser Val Glu Ser Pro Ser Val Ser Ser Thr His Arg Val
145 150 155 160

Ser Asp Pro Lys Phe His Pro Leu His Ser Lys Ile Ile Ile Ile Lys
165 170 175

Lys Gly His Ala Lys Asp Ser Gln Arg Tyr Lys Val Asp Tyr Glu Ser
180 185 190

Gln Ser Thr Asp Thr Gln Asn Phe Ser Ser Glu Ser Lys Arg Glu Thr
195 200 205

Glu Tyr Gly Pro Cys Arg Arg Glu Met Glu Asp Thr Leu Asn His Leu
210 215 220

Lys Phe Leu Asn Val Leu Ser Pro Arg Gly Val His Ile Pro Asn Cys

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<210> 334
<211> 582
<212> PRT
<213> Homo sapiens
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<400> 334

Glu Ser Lys Gly Ala Ser Ser Cys Arg Leu Leu Phe Cys Leu Leu Ile
5 10 15

Ser Ala Thr Val Phe Arg Pro Gly Leu Gly Trp Tyr Thr Val Asn Ser
20 25 30

Ala Tyr Gly Asp Thr Ile Ile Ile Pro Cys Arg Leu Asp Val Pro Gln
35 40 45

Asn Leu Met Phe Gly Lys Trp Lys Tyr Glu Lys Pro Asp Gly Ser Pro
50 55 60

Val Phe Ile Ala Phe Arg Ser Ser Thr Lys Lys Ser Val Gln Tyr Asp
65 70 75 80

Asp Val Pro Glu Tyr Lys Asp Arg Leu Asn Leu Ser Glu Asn Tyr Thr
85 90 95

Leu Ser Ile Ser Asn Ala Arg Ile Ser Asp Glu Lys Arg Phe Val Cys
100 105 110

Met Leu Val Thr Glu Asp Asn Val Phe Glu Ala Pro Thr Ile Val Lys
115 120 125

Val Phe Lys Gln Pro Ser Lys Pro Glu Ile Val Ser Lys Ala Leu Phe
130 135 140

Leu Glu Thr Glu Gln Leu Lys Lys Leu Gly Asp Cys Ile Ser Glu Asp
145 150 155 160

Ser Tyr Pro Asp Gly Asn Ile Thr Trp Tyr Arg Asn Gly Lys Val Leu
165 170 175

His Pro Leu Glu Gly Ala Val Val Ile Ile Phe Lys Lys Glu Met Asp

180	185	190
Pro Val Thr Gln Leu Tyr Thr Met Thr Ser Thr Leu Glu Tyr Lys Thr		
195	200	205
Thr Lys Ala Asp Ile Gln Met Pro Phe Thr Cys Ser Val Thr Tyr Tyr		
210	215	220
Gly Pro Ser Gly Gln Lys Thr Ile His Ser Glu Gln Ala Val Phe Asp		
225	230	235
Ile Tyr Tyr Pro Thr Glu Gln Val Thr Ile Gln Val Leu Pro Pro Lys		
245	250	255
Asn Ala Ile Lys Glu Gly Asp Asn Ile Thr Leu Lys Cys Leu Gly Asn		
260	265	270
Gly Asn Pro Pro Pro Glu Glu Phe Leu Phe Tyr Leu Pro Gly Gln Pro		
275	280	285
Glu Gly Ile Arg Ser Ser Asn Thr Tyr Thr Leu Thr Asp Val Arg Arg		
290	295	300
Asn Ala Thr Gly Asp Tyr Lys Cys Ser Leu Ile Asp Lys Lys Ser Met		
305	310	315
Ile Ala Ser Thr Ala Ile Thr Val His Tyr Leu Asp Leu Ser Leu Asn		
325	330	335
Pro Ser Gly Glu Val Thr Arg Gln Ile Gly Asp Ala Leu Pro Val Ser		
340	345	350
Cys Thr Ile Ser Ala Ser Arg Asn Ala Thr Val Val Trp Met Lys Asp		
355	360	365
Asn Ile Arg Leu Arg Ser Ser Pro Ser Phe Ser Ser Leu His Tyr Gln		
370	375	380
Asp Ala Gly Asn Tyr Val Cys Glu Thr Ala Leu Gln Glu Val Glu Gly		
385	390	395
Leu Lys Lys Arg Glu Ser Leu Thr Leu Ile Val Glu Gly Lys Pro Gln		
405	410	415
Ile Lys Met Thr Lys Lys Thr Asp Pro Ser Gly Leu Ser Lys Thr Ile		
420	425	430
Ile Cys His Val Glu Gly Phe Pro Lys Pro Ala Ile Gln Trp Thr Ile		
435	440	445
Thr Gly Ser Gly Ser Val Ile Asn Gln Thr Glu Glu Ser Pro Tyr Ile		
450	455	460
Asn Gly Arg Tyr Tyr Ser Lys Ile Ile Ile Ser Pro Glu Glu Asn Val		
465	470	475
		480

Thr Leu Thr Cys Thr Ala Glu Asn Gln Leu Glu Arg Thr Val Asn Ser
 485 490 495
 Leu Asn Val Ser Ala Ile Ser Ile Pro Glu His Asp Glu Ala Asp Glu
 500 505 510
 Ile Ser Asp Glu Asn Arg Glu Lys Val Asn Asp Gln Ala Lys Leu Ile
 515 520 525
 Val Gly Ile Val Val Gly Leu Leu Ala Ala Leu Val Ala Gly Val
 530 535 540
 Val Tyr Trp Leu Tyr Met Lys Lys Ser Lys Thr Ala Ser Lys His Val
 545 550 555 560
 Asn Lys Asp Leu Gly Asn Met Glu Glu Asn Lys Lys Leu Glu Glu Asn
 565 570 575
 Asn His Lys Thr Glu Ala
 580

 <210> 335
 <211> 709
 <212> PRT
 <213> Homo sapiens

 <400> 335
 Met Ala Glu Val Glu Asp Gln Ala Ala Arg Asp Met Lys Arg Leu Glu
 5 10 15
 Glu Lys Asp Lys Glu Arg Lys Asn Val Lys Gly Ile Arg Asp Asp Ile
 20 25 30
 Glu Glu Glu Asp Asp Gln Glu Ala Tyr Phe Arg Tyr Met Ala Glu Asn
 35 40 45
 Pro Thr Ala Gly Val Val Gln Glu Glu Glu Asp Asn Leu Glu Tyr
 50 55 60
 Asp Ser Asp Gly Asn Pro Ile Ala Pro Thr Lys Lys Ile Ile Asp Pro
 65 70 75 80
 Leu Pro Pro Ile Asp His Ser Glu Ile Asp Tyr Pro Pro Phe Glu Lys
 85 90 95
 Asn Phe Tyr Asn Glu His Glu Glu Ile Thr Asn Leu Thr Pro Gln Gln
 100 105 110
 Leu Ile Asp Leu Arg His Lys Leu Asn Leu Arg Val Ser Gly Ala Ala
 115 120 125
 Pro Pro Arg Pro Gly Ser Ser Phe Ala His Phe Gly Phe Asp Glu Gln
 130 135 140

Leu Met His Gln Ile Arg Lys Ser Glu Tyr Thr Gln Pro Thr Pro Ile
 145 150 155 160
 Gln Cys Gln Gly Val Pro Val Ala Leu Ser Gly Arg Asp Met Ile Gly
 165 170 175
 Ile Ala Lys Thr Gly Ser Gly Lys Thr Ala Ala Phe Ile Trp Pro Met
 180 185 190
 Leu Ile His Ile Met Asp Gln Lys Glu Leu Glu Pro Gly Asp Gly Pro
 195 200 205
 Ile Ala Val Ile Val Cys Pro Thr Arg Glu Leu Cys Gln Gln Ile His
 210 215 220
 Ala Glu Cys Lys Arg Phe Gly Lys Ala Tyr Asn Leu Arg Ser Val Ala
 225 230 235 240
 Val Tyr Gly Gly Gly Ser Met Trp Glu Gln Ala Lys Ala Leu Gln Glu
 245 250 255
 Gly Ala Glu Ile Val Val Cys Thr Pro Gly Arg Leu Ile Asp His Val
 260 265 270
 Lys Lys Lys Ala Thr Asn Leu Gln Arg Val Ser Tyr Leu Val Phe Asp
 275 280 285
 Glu Ala Asp Arg Met Phe Asp Met Gly Phe Glu Tyr Gln Val Arg Ser
 290 295 300
 Ile Ala Ser His Val Arg Pro Asp Arg Gln Thr Leu Leu Phe Ser Ala
 305 310 315 320
 Thr Phe Arg Lys Lys Ile Glu Lys Leu Ala Arg Asp Ile Leu Ile Asp
 325 330 335
 Pro Ile Arg Val Val Gln Gly Asp Ile Gly Glu Ala Asn Glu Asp Val
 340 345 350
 Thr Gln Ile Val Glu Ile Leu His Ser Gly Pro Ser Lys Trp Asn Trp
 355 360 365
 Leu Thr Arg Arg Leu Val Glu Phe Thr Ser Ser Gly Ser Val Leu Leu
 370 375 380
 Phe Val Thr Lys Lys Ala Asn Ala Glu Glu Leu Ala Asn Asn Leu Lys
 385 390 395 400
 Gln Glu Gly His Asn Leu Gly Leu Leu His Gly Asp Met Asp Gln Ser
 405 410 415
 Glu Arg Asn Lys Val Ile Ser Asp Phe Lys Lys Lys Asp Ile Pro Val
 420 425 430

Leu Val Ala Thr Asp Val Ala Ala Arg Gly Leu Asp Ile Pro Ser Ile
 435 440 445
 Lys Thr Val Ile Asn Tyr Asp Val Ala Arg Asp Ile Asp Thr His Thr
 450 455 460
 His Arg Ile Gly Arg Thr Gly Arg Ala Gly Glu Lys Gly Val Ala Tyr
 465 470 475 480
 Thr Leu Leu Thr Pro Lys Asp Ser Asn Phe Ala Gly Asp Leu Val Arg
 485 490 495
 Asn Leu Glu Gly Ala Asn Gln His Val Ser Lys Glu Leu Leu Asp Leu
 500 505 510
 Ala Met Gln Asn Ala Trp Phe Arg Lys Ser Arg Phe Lys Gly Gly Lys
 515 520 525
 Gly Lys Lys Leu Asn Ile Gly Gly Gly Gly Leu Gly Tyr Arg Glu Arg
 530 535 540
 Pro Gly Leu Gly Ser Glu Asn Met Asp Arg Gly Asn Asn Asn Val Met
 545 550 555 560
 Ser Asn Tyr Glu Ala Tyr Lys Pro Ser Thr Gly Ala Met Gly Asp Arg
 565 570 575
 Leu Thr Ala Met Lys Ala Ala Phe Gln Ser Gln Tyr Lys Ser His Phe
 580 585 590
 Val Ala Ala Ser Leu Ser Asn Gln Lys Ala Gly Ser Ser Ala Ala Gly
 595 600 605
 Ala Ser Gly Trp Thr Ser Ala Gly Ser Leu Asn Ser Val Pro Thr Asn
 610 615 620
 Ser Ala Gln Gln Gly His Asn Ser Pro Asp Ser Pro Val Thr Ser Ala
 625 630 635 640
 Ala Lys Gly Ile Pro Gly Phe Gly Asn Thr Gly Asn Ile Ser Gly Ala
 645 650 655
 Pro Val Thr Tyr Pro Ser Ala Gly Ala Gln Gly Val Asn Asn Thr Ala
 660 665 670
 Ser Gly Asn Asn Ser Arg Glu Gly Thr Gly Gly Ser Asn Gly Lys Arg
 675 680 685
 Glu Arg Tyr Thr Glu Asn Arg Gly Ser Ser Pro Ser Gln Ser Arg Arg
 690 695 700
 Asp Trp Gln Ser Ala
 705

<400> 336

Met Ile Arg Ala Ala Pro Pro Leu Phe Leu Leu Leu Leu Leu Leu
5 10 15

Leu Leu Leu Val Ser Trp Ala Ser Arg Gly Glu Ala Ala Pro Asp Gln
20 25 30

Asp Glu Ile Gln Arg Leu Pro Gly Leu Ala Lys Gln Pro Ser Phe Arg
35 40 45

Gln Tyr Ser Gly Tyr Leu Lys Ser Ser Gly Ser Lys His Leu His Tyr
50 55 60

Trp Phe Val Glu Ser Gln Lys Asp Pro Glu Asn Ser Pro Val Val Leu
65 70 75 80

Trp Leu Asn Gly Gly Pro Gly Cys Ser Ser Leu Asp Gly Leu Leu Thr
85 90 95

Glu His Gly Pro Phe Leu Val Gln Pro Asp Gly Val Thr Leu Glu Tyr
100 105 110

Asn Pro Tyr Ser Trp Asn Leu Ile Ala Asn Val Leu Tyr Leu Glu Ser
115 120 125

Pro Ala Gly Val Gly Phe Ser Tyr Ser Asp Asp Lys Phe Tyr Ala Thr
130 135 140

Asn Asp Thr Glu Val Ala Gln Ser Asn Phe Glu Ala Leu Gln Asp Phe
145 150 155 160

Phe Arg Leu Phe Pro Glu Tyr Lys Asn Asn Lys Leu Phe Leu Thr Gly
165 170 175

Glu Ser Tyr Ala Gly Ile Tyr Ile Pro Thr Leu Ala Val Leu Val Met
180 185 190

Gln Asp Pro Ser Met Asn Leu Gln Gly Leu Ala Val Gly Asn Gly Leu
195 200 205

Ser Ser Tyr Glu Gln Asn Asp Asn Ser Leu Val Tyr Phe Ala Tyr Tyr
210 215 220

His Gly Leu Leu Gly Asn Arg Leu Trp Ser Ser Leu Gln Thr His Cys
225 230 235 240

Cys Ser Gln Asn Lys Cys Asn Phe Tyr Asp Asn Lys Asp Leu Glu Cys
245 250 255

Val Thr Asn Leu Gln Glu Val Ala Arg Ile Val Gly Asn Ser Gly Leu

260 265 270
 Asn Ile Tyr Asn Leu Tyr Ala Pro Cys Ala Gly Gly Val Pro Ser His
 275 280 285
 Phe Arg Tyr Glu Lys Asp Thr Val Val Val Gln Asp Leu Gly Asn Ile
 290 295 300
 Phe Thr Arg Leu Pro Leu Lys Arg Met Trp His Gln Ala Leu Leu Arg
 305 310 315 320
 Ser Gly Asp Lys Val Arg Met Asp Pro Pro Cys Thr Asn Thr Thr Ala
 325 330 335
 Ala Ser Thr Tyr Leu Asn Asn Pro Tyr Val Arg Lys Ala Leu Asn Ile
 340 345 350
 Pro Glu Gln Leu Pro Gln Trp Asp Met Cys Asn Phe Leu Val Asn Leu
 355 360 365
 Gln Tyr Arg Arg Leu Tyr Arg Ser Met Asn Ser Gln Tyr Leu Lys Leu
 370 375 380
 Leu Ser Ser Gln Lys Tyr Gln Ile Leu Leu Tyr Asn Gly Asp Val Asp
 385 390 395 400
 Met Ala Cys Asn Phe Met Gly Asp Glu Trp Phe Val Asp Ser Leu Asn
 405 410 415
 Gln Lys Met Glu Val Gln Arg Arg Pro Trp Leu Val Lys Tyr Gly Asp
 420 425 430
 Ser Gly Glu Gln Ile Ala Gly Phe Val Lys Glu Phe Ser His Ile Ala
 435 440 445
 Phe Leu Thr Ile Lys Gly Ala Gly His Met Val Pro Thr Asp Lys Pro
 450 455 460
 Leu Ala Ala Phe Thr Met Phe Ser Arg Phe Leu Asn Lys Gln Pro Tyr
 465 470 475 480

 <210> 337
 <211> 543
 <212> PRT
 <213> Homo sapiens

 <400> 337
 Met Ala Ala Ala Lys Ala Glu Met Gln Leu Met Ser Pro Leu Gln Ile
 5 10 15
 Ser Asp Pro Phe Gly Ser Phe Pro His Ser Pro Thr Met Asp Asn Tyr
 20 25 30
 Pro Lys Leu Glu Glu Met Met Leu Leu Ser Asn Gly Ala Pro Gln Phe

35	40	45
Leu Gly Ala Ala Gly Ala	Pro Glu Gly Ser Gly Ser Asn Ser Ser Ser	
50	55	60
Ser Ser Ser Gly Gly Gly Gly Gly Gly Gly Gly Ser Asn Ser Ser		
65	70	75 80
Ser Ser Ser Ser Thr Phe Asn Pro Gln Ala Asp Thr Gly Glu Gln Pro		
85	90	95
Tyr Glu His Leu Thr Ala Glu Ser Phe Pro Asp Ile Ser Leu Asn Asn		
100	105	110
Glu Lys Val Leu Val Glu Thr Ser Tyr Pro Ser Gln Thr Thr Arg Leu		
115	120	125
Pro Pro Ile Thr Tyr Thr Gly Arg Phe Ser Leu Glu Pro Ala Pro Asn		
130	135	140
Ser Gly Asn Thr Leu Trp Pro Glu Pro Leu Phe Ser Leu Val Ser Gly		
145	150	155 160
Leu Val Ser Met Thr Asn Pro Pro Ala Ser Ser Ser Ser Ala Pro Ser		
165	170	175
Pro Ala Ala Ser Ser Ala Ser Ala Ser Gln Ser Pro Pro Leu Ser Cys		
180	185	190
Ala Val Pro Ser Asn Asp Ser Ser Pro Ile Tyr Ser Ala Ala Pro Thr		
195	200	205
Phe Pro Thr Pro Asn Thr Asp Ile Phe Pro Glu Pro Gln Ser Gln Ala		
210	215	220
Phe Pro Gly Ser Ala Gly Thr Ala Leu Gln Tyr Pro Pro Pro Ala Tyr		
225	230	235 240
Pro Ala Ala Lys Gly Gly Phe Gln Val Pro Met Ile Pro Asp Tyr Leu		
245	250	255
Phe Pro Gln Gln Gln Gly Asp Leu Gly Leu Gly Thr Pro Asp Gln Lys		
260	265	270
Pro Phe Gln Gly Leu Glu Ser Arg Thr Gln Gln Pro Ser Leu Thr Pro		
275	280	285
Leu Ser Thr Ile Lys Ala Phe Ala Thr Gln Ser Gly Ser Gln Asp Leu		
290	295	300
Lys Ala Leu Asn Thr Ser Tyr Gln Ser Gln Leu Ile Lys Pro Ser Arg		
305	310	315 320
Met Arg Lys Tyr Pro Asn Arg Pro Ser Lys Thr Pro Pro His Glu Arg		
325	330	335

Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Arg Ser
 340 345 350
 Asp Glu Leu Thr Arg His Ile Arg Ile His Thr Gly Gln Lys Pro Phe
 355 360 365
 Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp His Leu Thr
 370 375 380
 Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile
 385 390 395 400
 Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg Lys Arg His Thr Lys
 405 410 415
 Ile His Leu Arg Gln Lys Asp Lys Lys Ala Asp Lys Ser Val Val Ala
 420 425 430
 Ser Ser Ala Thr Ser Ser Leu Ser Ser Tyr Pro Ser Pro Val Ala Thr
 435 440 445
 Ser Tyr Pro Ser Pro Val Thr Thr Ser Tyr Pro Ser Pro Ala Thr Thr
 450 455 460
 Ser Tyr Pro Ser Pro Val Pro Thr Ser Phe Ser Ser Pro Gly Ser Ser
 465 470 475 480
 Thr Tyr Pro Ser Pro Val His Ser Gly Phe Pro Ser Pro Ser Val Ala
 485 490 495
 Thr Thr Tyr Ser Ser Val Pro Pro Ala Phe Pro Ala Gln Val Ser Ser
 500 505 510
 Phe Pro Ser Ser Ala Val Thr Asn Ser Phe Ser Ala Ser Thr Gly Leu
 515 520 525
 Ser Asp Met Thr Ala Thr Phe Ser Pro Arg Thr Ile Glu Ile Cys
 530 535 540

<210> 338
 <211> 148
 <212> PRT
 <213> Homo sapiens

<400> 338
 Pro Pro Ala Thr Ser Tyr Ala Pro Ser Asp Val Pro Ser Gly Val Ala
 5 10 15
 Leu Phe Leu Thr Ile Pro Phe Ala Phe Phe Leu Pro Glu Leu Ile Phe
 20 25 30
 Gly Phe Leu Val Trp Thr Met Val Ala Ala Thr His Ile Val Tyr Pro
 35 40 45

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<210> 339
<211> 196
<212> PRT
<213> Homo sapiens
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<400> 339
Met Pro Gly Met Phe Phe Ser Ala Asn Pro Lys Glu Leu Lys Gly Thr
          5                      10                      15
Thr His Ser Leu Leu Asp Asp Lys Met Gln Lys Arg Arg Pro Lys Thr
          20                      25                      30
Phe Gly Met Asp Met Lys Ala Tyr Leu Arg Ser Met Ile Pro His Leu
          35                      40                      45
Glu Ser Gly Met Lys Ser Ser Lys Ser Lys Asp Val Leu Ser Ala Ala
          50                      55                      60
Glu Val Met Gln Trp Ser Gln Ser Leu Glu Lys Leu Leu Ala Asn Gln
          65                      70                      75                      80
Thr Gly Gln Asn Val Phe Gly Ser Phe Leu Lys Ser Glu Phe Ser Glu
          85                      90                      95
Glu Asn Ile Glu Phe Trp Leu Ala Cys Glu Asp Tyr Lys Lys Thr Glu
          100                     105                     110
Ser Asp Leu Leu Pro Cys Lys Ala Glu Glu Ile Tyr Lys Ala Phe Val
          115                     120                     125
His Ser Asp Ala Ala Lys Gln Ile Asn Ile Asp Phe Arg Thr Arg Glu
          130                     135                     140

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Ser Thr Ala Lys Lys Ile Lys Ala Pro Thr Pro Thr Cys Phe Asp Glu
 145 150 155 160

Ala Gln Lys Val Ile Tyr Thr Leu Met Glu Lys Asp Ser Tyr Pro Arg
 165 170 175

Phe Leu Lys Ser Asp Ile Tyr Leu Asn Leu Leu Asn Asp Leu Gln Ala
 180 185 190

Asn Ser Leu Lys
 195

<210> 340

<211> 316

<212> PRT

<213> Homo sapiens

<400> 340

Met Ala Thr Phe Val Glu Leu Ser Thr Lys Ala Lys Met Pro Ile Val
 5 10 15

Gly Leu Gly Thr Trp Lys Ser Pro Leu Gly Lys Val Lys Glu Ala Val
 20 25 30

Lys Val Ala Ile Asp Ala Gly Tyr Arg His Ile Asp Cys Ala Tyr Val
 35 40 45

Tyr Gln Asn Glu His Glu Val Gly Glu Ala Ile Gln Glu Lys Ile Gln
 50 55 60

Glu Lys Ala Val Lys Arg Glu Asp Leu Phe Ile Val Ser Lys Leu Trp
 65 70 75 80

Pro Thr Phe Phe Glu Arg Pro Leu Val Arg Lys Ala Phe Glu Lys Thr
 85 90 95

Leu Lys Asp Leu Lys Leu Ser Tyr Leu Asp Val Tyr Leu Ile His Trp
 100 105 110

Pro Gln Gly Phe Lys Ser Gly Asp Asp Leu Phe Pro Lys Asp Asp Lys
 115 120 125

Gly Asn Ala Ile Gly Gly Lys Ala Thr Phe Leu Asp Ala Trp Glu Ala
 130 135 140

Met Glu Glu Leu Val Asp Glu Gly Leu Val Lys Ala Leu Gly Val Ser
 145 150 155 160

Asn Phe Ser His Phe Gln Ile Glu Lys Leu Leu Asn Lys Pro Gly Leu
 165 170 175

Lys Tyr Lys Pro Val Thr Asn Gln Val Glu Cys His Pro Tyr Leu Thr
 180 185 190

Gln Glu Lys Leu Ile Gln Tyr Cys His Ser Lys Gly Ile Thr Val Thr
 195 200 205
 Ala Tyr Ser Pro Leu Gly Ser Pro Asp Arg Pro Trp Ala Lys Pro Glu
 210 215 220
 Asp Pro Ser Leu Leu Glu Asp Pro Lys Ile Lys Glu Ile Ala Ala Lys
 225 230 235 240
 His Lys Lys Thr Ala Ala Gln Val Leu Ile Arg Phe His Ile Gln Arg
 245 250 255
 Asn Val Ile Val Ile Pro Lys Ser Val Thr Pro Ala Arg Ile Val Glu
 260 265 270
 Asn Ile Gln Val Phe Asp Phe Lys Leu Ser Asp Glu Glu Met Ala Thr
 275 280 285
 Ile Leu Ser Phe Asn Arg Asn Trp Arg Ala Cys Asn Val Leu Gln Ser
 290 295 300
 Ser His Leu Glu Asp Tyr Pro Phe Asn Ala Glu Tyr
 305 310 315

<210> 341

<211> 422

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(422)

<223> n = A,T,C or G

<400> 341

gatganattt	ttncnagaga	gaggaagang	ctattcagtt	ggatgggatt	aaatgcatca	60
caaataagag	aacttagaga	gaagtcggaa	aagtttgcct	tccaagcccg	aagttaacag	120
aatgatgaaa	cttatcatca	attcattgta	taaaaataaa	gagattttcc	tgagagaact	180
gatttcaa	gcttctgatg	cttagataa	gataaggcta	atatcactga	ctgatgaaaa	240
tgctctttct	ggaaatgagg	aactaacagt	caaaattaag	tgtgataagg	agaagacctg	300
ctgcatgtca	cagacaccgg	tgttaggaatg	accagagaag	agttgggttaa	aaaccttggt	360
accatagcca	aatctgggac	aagcgagttt	ttaaacaaaa	tgactgaagc	acaggaagat	420
gg						422

<210> 342

<211> 472

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(472)

<223> n = A,T,C or G

<400> 342

ctggagaagg tgtgcagggg aaaccctgct gatgtcaccg aggccagggtt gtctttctac	60
tcgggacact cttccttttg gatgtactgc atggtgttct tggcgctgna tgtgcaggca	120
cgactctgtt ggaagtgggc acggctgctg cgaccacag tccagttctt cctggtggcc	180
tttgccctct acgtgggcta caccgcgtg tctgattaca aacaccactg gagcgatgtc	240
cttggtggcc tctgcaggg ggcactggtg gctgccctca ctgtctgcta catctcagac	300
ttcctcaaag cccgaccccc acagcactgt ctgaaggagg aggagctgga acggaagccc	360
agcctgtcac tgacgttgac cctgggagag gctgaccaca accactatgg ataccgcac	420
tctcctcctt gaggccggac cccgcccagg caggagagcta ctgtgagtcc ag	472

<210> 343

<211> 139

<212> DNA

<213> Homo sapien

<400> 343

gtcctggggc tccccctcc ctcaagccag ggctcctcct cctgtcgtgg gctcattgtg	60
accactggcc tctctacagc acggcctgtg gcctgtcaa ggcagaacca cgacccttga	120
ctcccgggtg gggaggtgg	139

<210> 344

<211> 235

<212> DNA

<213> Homo sapien

<400> 344

ctgcgggctc agcacagtag acatgactgg gatccccacc ttggacaacc tccagaagg	60
agtccaattt gctctcaagt accagtcgct gggccagtgt gtttacgtgc attgtaaggc	120
tgggcgctcc aggagtgcc ctatggtggc agcatacctg attcaggtgc acaaattggag	180
tccagaggag gctgtaagag ccatacgcaa gatccgggtca tacatccaca tcagg	235

<210> 345

<211> 458

<212> DNA

<213> Homo sapien

<400> 345

ctgtaagggtg ctattcagtc ctgtgaccct ttttttgaa tgctcttcat tactgttgct	60
ctgttttgtg acttctctgg aaaccgccta ctttgggtgtg gtgtcacctt gagctgtgca	120
cataggacac cagttttgac ttaacctaac aggcagtttt tatctctagc tttttcaagc	180
cagggtattga gcagtttctt ggccaatggc ctgagaaaacc acctgtccct gtcaaggggt	240
gattttattg gttttaagtg gggaagtaat cccatgtact tatttcttaa atacctagga	300
agttcttctt ggtggctcct cttggccctc cctctttct cccccaaccc accatcctgc	360
aaggcaagga atggcctctc cctccacaga ggcaacggct gcagagggag cactgtggct	420
gccatcccag ttcctcttca aagccaaaca gacacgcg	458

<210> 346

<211> 525

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(525)

<223> n = A,T,C or G

<400> 346

ccagagcaca	acgcctcacc	atggactgga	cctggaggat	ntctctnnng	gtggcagcag	60
ccacaggtgt	ccactcccaa	gccccacttg	tgcagtctgg	ggctgaggag	aagaagcctg	120
gggcctcagt	gactatttct	tgtaaggctt	ctggatatat	ncttactaaa	tatactttac	180
attgggtgcg	ccaggccccc	cccggacaaa	gacctgaatg	ggtgggatgg	atcaacactg	240
gcattgatac	cgttaaatat	tcacagaagt	ttcaggacag	agtctccatt	acctgggact	300
catccgcgac	cacagnctac	ctgnanntga	gtagcctgga	atccgaagac	acggctgtgt	360
attactgtgc	gagacttang	gcccgttcgc	tgtgggtggga	cttaatgacg	cttttgacat	420
ctggggccaa	gggacagtgg	tcaccgtctc	ttcanggagt	gcattcgccc	caaccctttt	480
ccccctctct	cctgtgaaga	attccccgnc	ggatacgagc	agcgt		525

<210> 347

<211> 423

<212> DNA

<213> Homo sapien

<400> 347

ccagacgctg	acttgtttct	gagtccttaa	gcaggaagga	tttgaaatcc	tggagcttgg	60
cagtcttget	cttcacctct	aagccaatgt	tgacccttcc	atctataaag	tccacaactc	120
tccggaagtc	atcctcacgg	aactgtcag	aagttaaggc	tggggcccca	agccgcagggc	180
cgcccggtgt	gatggcactt	cggtctccag	gacaggtgtt	cttgttggca	gtgatggata	240
caagctctag	cacccgctca	gcccagagtc	catccaggcc	cttgggccgc	aggtccacca	300
gcaccaggtg	gttgtcagta	ccacctgata	ccagttagta	gcctcgctct	agcagggcat	360
ctgccatggc	ccgagcattc	ttcagaacct	gcagggagta	ctcccgaac	atgggggtgc	420
agg						423

<210> 348

<211> 513

<212> DNA

<213> Homo sapien

<400> 348

cctctaggcc	tgatgctctc	agaggcaata	gaagaaaagt	aaaaggaagg	tctcacttca	60
cagacaatga	aacctccta	accctcttcc	ccactaccca	caactcccta	cactgccaat	120
ctaaataaaa	agaggacaat	gcatgagtgt	gagatacaca	tacacacaca	cacatacaca	180
cacacacacg	cacagcttcc	tttcagccaa	agaactgcaa	aatccttccc	cggaaggagg	240
acaactggca	acaccaatca	aggcttggtg	gtctaagggtg	atggctggaa	tcatgtgaga	300
ctggtaaaaa	tccagggaga	aaatgtttca	ccttcagctc	attcccaagt	ctctatgaag	360
cccggcccac	ttccacatag	gggaactgtg	gctctggggg	cagcctctgc	agctactcag	420
aataggtggg	aggaggggct	ggctttgagg	ctgccttagc	catgaggctc	tttgccctagg	480
aatagctgga	gatgggagct	gcagggggct	cag			513

<210> 349

<211> 231

<212> DNA

<213> Homo sapien

<400> 349

ccttatttct	cttgtccttt	cgtacagggg	ggaatttgaa	gtagatagaa	accgacctgg	60
attactccgg	tctgaactca	gatacagtag	gactttaatc	gttgaacaaa	cgaaccttta	120
atagcggctg	caccatcggg	atgtcctgat	ccaacatcga	ggtcgtaaac	cctattgttg	180
atatggactc	tagagtagga	ttgcgctggt	atccctaggg	taacttggtc	c	231

<210> 350

<211> 341
 <212> DNA
 <213> Homo sapien

<400> 350
 ctgcccagg gcgttcgtaa cgggaatgcc gaagcgtggg aaaaaggagg cggtggcgga 60
 agacggggat gagctcagga cagagccaga ggccaagaag agtaagacgg ccgcaaagaa 120
 aaatgacaaa gaggcagcag gagaggggccc agccctgtat gaggaccccc cagatcagaa 180
 aacctcacc agtggcaaac ctgccacacc caagatctgc tcttggaatg tggatgggct 240
 tcgagcctgg attaagaaga aaggattaga ttgggtaaag gaagaagccc cagatatact 300
 gtgccttcaa gagaccaaat gttcagagaa caaactacca g 341

<210> 351
 <211> 256
 <212> DNA
 <213> Homo sapien

<400> 351
 ggcgttgggg acggttgtag gacgtggctc tttattcgtg agttttccat ttacctccgc 60
 tgaacctaga gcttcagacg ccctatggcg tccgcctcga cccaaccggc ggccttgagc 120
 gctgagcaag caaagggtgg cctcgcggag gtgatccagg cgttctccgc cccggagaat 180
 gcagtgcgca tggacgaggc tcgggataac gcctgcaacg acatgggtaa gatgctgcaa 240
 ttcgtgctgc ccgtgg 256

<210> 352
 <211> 368
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)... (368)
 <223> n = A,T,C or G

<400> 352
 cctttcttgt aagtgaagaa naaggaatgc agcaaagaag agttcgacat tggagtcctt 60
 agttccatca ggatccatt cgcagccttt agcatcatgt agaagcaaac tgcacctatg 120
 gctgagatag gtgcaatgac ctacaagatt ttgtgttttc tagctgtcca ggaaaagcca 180
 tcttcagtct tgctgacagt caaagagcaa gtgaaacat ttccagccta aactacataa 240
 aagcagccga accaatgatt aaagacctct aaggctccat aatcatcatt aaatatgccc 300
 aaactcattg tgacttttta ttttatatac aggattaaaa tcaacattaa atcatcttat 360
 ttacatgg 368

<210> 353
 <211> 368
 <212> DNA
 <213> Homo sapien

<400> 353
 ctgaggggtg gcagtaagca atgaggatgg gctataaagc tgtaactgg ctaagggccca 60
 tccttgggca ggcatttcag acacatctgt agagagggca gtagcatctc cgataggcca 120
 gctctgaagg aagcttaatg cttaatacag tcacactgca taaattagct tagaatgctc 180
 tcttgggtaa aaaatattaa tagtgatat gcaactgaag agcaaaaattc ctcaagaaaa 240
 aaagttaat agcaaggagt ttccatcagt cccggtcttt gtgaggatta ccacaaçaaa 300
 cacttaaaag gatacaacag gtacttatta aatgctgcct tgcctttttac ctcttccctt 360

tttttttt

368

<210> 354
<211> 380
<212> DNA
<213> Homo sapien

<400> 354

ccatggcttc	tcacccagac	agtctttctg	ggcaacttgg	ggaagccctt	gttctgctca	60
agtctcacc	catggaagag	gtgggggaag	ggggccttgg	tttttcagga	agacagggtg	120
gagagcacga	gtcactacaa	agcagtaaaa	gtgaatgggt	tctccagggg	ctgggtccag	180
aacaccacgg	agagccccag	ccataaagg	gtgttccgcc	tctggcctgc	aggaatctct	240
ttgaatctct	ttgattgggt	gctccaagag	caatgggaag	tcaacagcca	ggaggctgga	300
ctgggttccc	tgggaccccg	aggtcccaga	gctgctgggc	agtggttgtc	ggcaaagaag	360
aaaggtccaa	gagggtcagg					380

<210> 355
<211> 347
<212> DNA
<213> Homo sapien

<400> 355

ccagtggagg	ggtgggggta	tcgatcccg	cgggggctgg	cttgggtgct	ggtgccctga	60
gcccttctct	gcpcgcctgg	gtgttgccct	cactgatgga	ggtaggcgtc	cagccagatg	120
tcaccagact	tcttcgggga	cctgacgatg	tccaccagcg	cggtgaggaa	gggcttcact	180
tcgtagctga	ggccgtgctt	ggcacacagc	gacttgacca	gcggggccac	ccggctgtag	240
ttgtgtctcg	gcacccctgg	gaagaggtgg	tgctcgatct	ggaagttgag	gtgcccgtg	300
aaccagttgg	tgaaaagtga	gggctccacg	ttgcagggtg	ctgccag		347

<210> 356
<211> 157
<212> DNA
<213> Homo sapien

<400> 356

cctggagctg	ctgaagactg	ctattgggaa	agctggctac	actgataagg	tggtcategg	60
catggacgta	gcggcctccg	agttcttcag	gtctgggaag	tatgacctgg	acttcaagtc	120
tcccgatgac	cccagcaggt	acatctcgcc	tgaccag			157

<210> 357
<211> 323
<212> DNA
<213> Homo sapien

<400> 357

ccatacaggg	ctggtgccc	ggccctagag	gtcactcttc	gtaccctgat	ccagaactgt	60
ggggccagca	ccatccgtct	acttacctcc	cttcggggcca	agcacaccca	ggagaactgt	120
gagacctggg	gtgtaaatgg	tgagacgggt	actttgggtg	acatgaagga	actgggcata	180
tgggagccat	tggctgtgaa	gctgcagact	tataagacag	cagtggagac	ggcagttctg	240
ctactgcgaa	ttgatgacat	cgtttcaggc	cacaaaaaga	aaggcgatga	ccagagccgg	300
caaggcgggg	ctcctgatgc	tgg				323

<210> 358
<211> 555
<212> DNA

<213> Homo sapien

<400> 358

aaaagggttc taaaacatga cggagggttg gatgaagctt ctccatggag taaaaaatgt	60
atttaaaaga aaattgagag aaaggactac agagccccga gttaatacca atagaagggc	120
aatgctttta gattaaaatg aagggtgactt aaacagctta agttagtt taagaattgt	180
agggtgattaa aataatttga aggcgatctt ttaaaaagag attaaaccga aggtgattaa	240
aagaccttga aatccatgac gcaggagaaa ttgcgtcatt taaagcctag ttaacgcatt	300
tactaaacgc agacgaaaat ggaaagatta attgggagtg gtaggatgaa acaatttggg	360
gaagatagaa gtttgaagt gaaaactgga agacagaagt acgggaaggc gaagaaaaga	420
atagagaaga tagggaaatt agaagataaa aacatacttt tagaagaaaa aagataaatt	480
taaacctgaa aagtaggaag cagaagaaaa aagacaagct aggaacaaaa aagctaaggg	540
caaatgtac accac	555

<210> 359

<211> 549

<212> DNA

<213> Homo sapien

<400> 359

ctgccaggct gaaaagaagc ctcagctccc acaccgccct cctcaccgcc ctctctcggc	60
agtcacttcc actggtggac cacgggcccc cagccctgtg tcggccttgt ctgtctcagc	120
tcaaccacag tctgacacca gagccactt ccctctctc tgggtgtgagg cacagcgagg	180
gcagcatctg gaggagctct gcagctcca cactaccac gacctccag ggctgggctc	240
aggaaaaacc agccactgct ttacaggaca gggggttgaa gctgagcccc gcctcacacc	300
cacccccatg cactcaaaga ttggatttta cagctacttg caattcaaaa ttcagaagaa	360
taaaaaatgg gaacatacag aactctaaaa gatagacatc agaaattgtt aagttaagct	420
ttttcaaaaa atcagcaatt cccagcgta gtcaagggtg gacactgcac gctctggcat	480
gatgggatgg cgaccgggca agctttcttc ctcgagatgc tcttgctgct tgagagctat	540
tgctttggt	549

<210> 360

<211> 289

<212> DNA

<213> Homo sapien

<400> 360

tttaaat ttt actagtgtta cttaatgtat attctaaaaa gagaatgcag taactaatgc	60
cctaaatggt tgatctctgt ttgtcattac tttttcaaaa ttattttttt ctgtaaagta	120
taatataata aacttcttgc ttaaattgaa tttctatatt agtgggttaatt tgcagtttat	180
taaagggatc attatcagta atttcatagc aactgttcta gtgtttttgtg tttttaaaac	240
agaattagga atttgagata tctgattata tttttcatat gaatcacag	289

<210> 361

<211> 311

<212> DNA

<213> Homo sapien

<400> 361

ctgttcagta tggcaaaggg cagacttact ccttcattcca ctctgctgcc ttgatgaggt	60
gaacacactg gaataagatg gagggcagga tacctgccaa agcctgagga atgagatgat	120
ctgaaacaat tgggcaaagg ctggacattt caaaaagctg acttccaact gcagtttatg	180
ggtatagaat ttgatgcttc cctcaagtcc tgactgctct ttctgaggca gccaggctag	240
gccaaagaaat gagctgctcc agcttctcca gagcacagca gcctccagg gcctgtcagc	300
atctgcagca g	311

<210> 362
 <211> 496
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(496)
 <223> n = A,T,C or G

<400> 362
 ccagtttcta aaanaatgca catttaaaga gaagcatcta ccacggcttt aaaacaaaac 60
 aactctgaga tgaacaatat gtgttatact cagagattaa caatctcaat catacatact 120
 gattctttca gacatttaat aaccactaca tttttttgca ttaatgaagt ttgactatat 180
 gtgtaaaggg actaaatatt ttgcaacag cctgttcttt gttcattctt ttctggatag 240
 cgtgtcctct gtattgcggg agatttatac attctgttgc cttaaataatgt gtgtaaaatg 300
 agctgataaa ctggagtact acttaaaaaa aagtctgtga ttataagat gcataatgctt 360
 tctatgtgaa tataagcttg tgcacaatgt ttaaaagaaa aacaatgaat tagaagagat 420
 cccccgtccc ccagctcgac atatttcata cagaatgttt aaaagaaaaa ctctgctagt 480
 cttggcaaac atttgg 496

<210> 363
 <211> 673
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(673)
 <223> n = A,T,C or G

<400> 363
 ccaagagggg gataanacaa acttctcaaa caaaaagaaa agaaaaacga atgattcatc 60
 tgctttaate agtgtgatta atgcagcacc cattgccccg ggaaccgttt ctgctgtact 120
 atctggatac taaaatgtta cggaagtagc tctttgttct ccctcactct gcccttagtt 180
 aatagaaatt cagactcgcc aagtaaggct ttgtgcatag tgtcttcattg tcgcgtatag 240
 ttgagcgcgt tcttagcagt tggcttcatg gacagctcat tagtggtttg acttttctta 300
 cccagcggtta attgaattct tgcttttaga caacttcctt tttgtagtgg tgaaccttgc 360
 ccttttagtac agttcaagtg aatctggata attgttcac tttgcttttag cttagataacc 420
 atgtagtggg ctgtggctac aggaagctgg ttctgtctgc ttccacagtc tgcttaaaaa 480
 actgtctgac ttcgtgaata tagagaccaa gtttaccact tctgatgaag agaccaatta 540
 agattcattc ctcatctgt ttctttccag tgggagaaga gtcccatga aataagatga 600
 aactgattcc atgcactagt acatgtaggc ttctcccttg cgcaaagctt aacaatttgt 660
 aggaaacttt ggg 673

<210> 364
 <211> 495
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(495)
 <223> n = A,T,C or G

<400> 364
 ccaaagtgtt gcncaagact agcagagttt ttcttttaaa cattctgtat gaaatatgtc 60
 agactggggg acggggggtc tcttctaatt cattgttttt cttttaaaca ttgtgcacaa 120
 gcttatattc acatagaaag catatacatc ttataaatca cagacttttt ttaagtagt 180
 actccagttt atcagctcat ttacacaca tatttaggca acagaatgta taaatctacc 240
 gcaatacaga ggacacacta tccagaaaag aatgaacaaa gaacaggctg ttgcaaaaat 300
 atttagtccc ttacacata tagtcaaact tcattaatgc aaaaaatgta gtggttatta 360
 aatgtctgaa agaatacagta tgtatgattg agattgttaa tctctgagta taacacatat 420
 tgttcatctc agagttgttt tgttttaaag ccgtggtaga tgcttctctt taaatgtgca 480
 ttttttagaa actgg 495

<210> 365
 <211> 291
 <212> DNA
 <213> Homo sapien

<400> 365
 aactgacaag cccttgcgcc tgcctctcca ggatgtctac aaaattggtg gtattggtac 60
 tgttcctgtt ggcccagtg gagactggtg ttctcaaac ccggtatggtg gtcacctttg 120
 ctccagtc aa cgttacaacg gaagtaaaat ctgtcgaaat gcaccatgaa gctttgagtg 180
 aagctcttcc tggggacaat gtgggcttca atgtcaagaa tgtgtctgtc aaggatgttc 240
 gtcgtggcaa cggtgctggg gacagcaaaa atgacccacc aatggaagca g 291

<210> 366
 <211> 277
 <212> DNA
 <213> Homo sapien

<400> 366
 ctggatggtg cctcagaagg tgcattctgc ttctgcaggg gcttgaaaca ccaaggcact 60
 ccagggatcc tggagtcaaa gcagcagccc cggttgttgc actccttggg ggtgacatgg 120
 gggtagcccg cagtccaccc tgtccttggc tggcacggca cactggtttg cagacaggcc 180
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 gcgctctggc agccatgacc accgtgggct ccgggac 277

<210> 367
 <211> 311
 <212> DNA
 <213> Homo sapien

<400> 367
 ccagagctgc ggggcctcag tacacggagc tgttccggat gccacagcac agcaccatgc 60
 tcaggatcat ctgaagatc atgatcacag cgaccacgat ggcagcaatg ccgatgaggt 120
 acagcttccc ggagaagagg tcategatct tctggtggca gtctccttg aagaggttgc 180
 tgatgatgtt gctgcccag ggacacaaat tgttcttgag cactgaggtg gtcaaagcag 240
 tcagtgtgct ggagccacag cagtcaagcg tctcgtggaa ggtcttcacc acagccttgg 300
 cgttgttggc g 311

<210> 368
 <211> 384
 <212> DNA
 <213> Homo sapien

<400> 368

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ccaaaggggt ctctagctgc tgctctgctg ctccctgctca tggatgagtt tggcgatggg      60
gccggtgatg ccgcctatca aggtccagta ctcctcgaag ctgatgcgcc catcaggatt      120
ggcatccagg ttctggatga gcttatccgc agccttccgg tccctgtgt ccgacagcat      180
gtgggttcagc tctttctgga gcatctcgcg gaagctgctc ttgctgatct tgttcttgac      240
caggctgtac ctagacacat attttagaa gttttccacc aggacaatga ctgccttctc      300
cagctccgtg tagcaagtct gacatctccc tgcttcgcct gctggcgggg cctaaggcgg      360
gggccaaagcc cagttacagc ccag                                           384

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<210> 369

<211> 216

<212> DNA

<213> Homo sapien

<400> 369

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ccaagtgcc a ggtggcttcc agcagcttcc tacgatcagc cgaagaaagc agaagctctg      60
gaggctgcc a tcgagaacct caatgaagcc aagaactatt ttgcaaagg t gactgcaaa      120
gagcgcatca gggacgtcgt ttacttccag gccagactct accataccct ggggaagacc      180
caggagagga accggtgtgc gatgctcttc cggcag                                           216

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<210> 370

<211> 561

<212> DNA

<213> Homo sapien

<400> 370

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ctggctcctt cttttgtggt cgtttggggg atgggctggt ttgggggttta ggtgcagaga      60
atgggttggg gccactgctt actggaccac tctgagcctt cagggcaggg ttcttgtgag      120
tcttcatgtc atcagataca tgtttcaggg catgtgtaat gctctcccc tgattaatct      180
gcgcgaacag tgctgagcgg gaagcagact catctgagcc tgaactggta gagactgggg      240
gaggaggggg gcctgggtgga gggggaggag gacctgatcc ggcagagggt ccagatggca      300
gtccgctcag ttcttttgc acaggccccg ttttgctcca ggccagtcgg gtggtatgga      360
actccttaat gtaagcctgc agctctgtcc atatacttaa ataagctttg acccagtcta      420
catgcttctt atccacatct ttgtactctt tgaggactcg gtttgataaa aacatggcgg      480
catcattcat ttctttcgca taaggggccag gcttggggagc catagccacc cagcccaggg      540
cctggatact ttcgctgaca g                                           561

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<210> 371

<211> 518

<212> DNA

<213> Homo sapien

<400> 371

```

cccacttcca tcgctctctg gtgtgaggca cagcgagggc agcatctgga ggagctctgc      60
agcctccaca cctaccacga cctcccaggg ctgggctcag gaaaaaccag ccactgcttt      120
acaggacagg gggttgaagc tgagccccgc ctcacaccca ccccatgca ctcaaagatt      180
ggattttaca gctacttgca attcaaaatt cagaagaata aaaaatggga acatacagaa      240
ctctaaaaga tagacatcag aaattgttaa gttaagcttt ttcaaaaaat cagcaattcc      300
ccagcgtagt caagggtgga cactgcacgc tctggcatga tgggatggcg accgggcaag      360
ctttcttctt cgagatgctc tgctgcttga gagctattgc ttgttaaga tataaaaagg      420
ggtttctttt tgtcttcttg taagggtggac ttccagcttt tgattgaaag tcctagggtg      480
attctatttc tgctgtgatt tatctgctga aagctcag                                           518

```

<210> 372

<211> 335

<212> DNA

<213> Homo sapien

<400> 372

ctggaggctg ggtgcaccct gccagatcc acacctgtac cccggcggaa aggctcatgg	60
gcattgaaga cgggtggtgaa aaagccaaag ggaaaagcac caacacccaaa tgagaagtgg	120
aagcccccg taccacccaaa tggctggaat cccctctctgc tctccggagc tggctctctgg	180
ccctggggggc ggggtggagt ttttaattctg ggatcctggg gcttctggct ccctcgccca	240
taaagcggga caaccttctc tctgctgac ccagctttac atactggaca ctcttgccgt	300
tctggccgtg tctccagcca ctgatgaaga catgg	335

<210> 373

<211> 467

<212> DNA

<213> Homo sapien

<400> 373

ccactagctg aatcttgaca tggaagggtt tagctaattgc caagtggaga tgcagaaaat	60
gctaagttga cttaggggct gtgcacagga actaaaaggc aggaagtac taaatattgc	120
tgagagcatc caccacagga aggactttac cttccaggag ctccaaactg gcaccacccc	180
cagtgtcac atggctgact ttatctctcg tgttccattt ggcacagcaa gtggcagtgt	240
ctccaccacc tatgatgggt atgcagccc tagaagtggc tttcaccacc tcatccatga	300
gagctttgggt tccccgggca aaagcttccc attcaaatac cccacagga ccattccaca	360
caatctgctt agcccgagt acagcctcag catacttctt gctgctttca ggaccacagt	420
ccaagcccat ccagccagca ggtacgccag aagccacagt ggcttg	467

<210> 374

<211> 284

<212> DNA

<213> Homo sapien

<400> 374

tttccgtaaa agcgtgtaac aagggtgtaa atatttataa ttttttatac ctggttgtag	60
accgagggg cggcggcggt gttttttatg gtgacacaaa tgtatatatt gctaacagca	120
attccaggct cagtattgtg accgcggagc cacaggggac cccacgcaca ttccgttgcc	180
ttaccgatg gcttgtagc cggagagaac cgattaaaac cgtttgagaa actcctccct	240
tgtctagccc tgtgttcgct gtggacgctg tagaggcagg ttgg	284

<210> 375

<211> 307

<212> DNA

<213> Homo sapien

<400> 375

cctactcttc tccgtccatt gtactatctg cccgtggtgg ggatggcagt aggatcatat	60
ttgatgactt ccgagaagca tattattggc tccgtcataa tactccagag gatgcgaagg	120
tcatgtcctg gtgggattat ggctatcaga ttacagctat ggcaaaccga acaattttag	180
tggacaataa cacatggaat aataccata tttctcgagt agggcaggca atggcgcca	240
cagaggaaaa agcctatgag atcatgaggg agctcgatgt cagctatgtg ctggtcattt	300
ttggagg	307

<210> 376

<211> 650

<212> DNA

<213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(650)
 <223> n = A,T,C or G

<400> 376
 ccattgncn ctnacgtgat gtcacatctt gccagggtcat cttggcaaaa gtcggagcat 60
 ttctcagtc ctgcaaagta gcccttctcg ttggagcacc ggaagagacg tgtgtgtttc 120
 atgtactcgg catcgctc atagggcttc tgtgccccaa tgcccaccca gaagaagttc 180
 tcaggctcct caccctcgtt gataacctgc ttgctgtagg aggtgtcaaa catggtgttc 240
 aggatgtctt ctgccaactt ggcttcgtca ggtctgatg cccggcccac ccaggcatac 300
 acgatgccct ggttgtcttc actctcaaag ggaaccttga ggatgaagca gaactcggag 360
 ttgaggagggc ttgagtcggt gttgatctgg atgcaccggg tgcagagggc gctgccgttg 420
 gtgcggatct ggtagaggct gggctgttgg gcgccctgga ccgcttctc cttgccccgg 480
 tggatgatga acttctctt gaaatgggac aggaacttgg ggttctctg ctgctgcgtc 540
 atgctacca cctccagctt cccagggaag aggtctctga acttctttt caggctgaag 600
 gtgaagggtga cccaccata ttgggaggct ttcacggccc tgccagaagt 650

<210> 377
 <211> 306
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(306)
 <223> n = A,T,C or G

<400> 377
 tctagatgca tgctcgagcg gccgccagtg tgatgganat ctgcagaatt cgcccttcga 60
 gcggccgccc gggcagggtc ggggtgctgcc ttcacctgcc aggccttcc ccgctagctt 120
 ggggcgagca gagctgcgtc cagtggaaact aaagccgttc caggattatc aaaaactgag 180
 cagcaacctt gggggacctg gatcatcacg gactccccca actggaaggt ccttctcttg 240
 cctcaattcc cgtctcaagg ccacgccttc cacctacagt ggagtcttcc gcaccagcg 300
 cgtcga 306

<210> 378
 <211> 199
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(199)
 <223> n = A,T,C or G

<400> 378
 ccacangtgg cacttgggtg tggctcctct gttatttgtc ctcatgtgag aaagcagatc 60
 atctccaaat cttgccattt gtatactttt ggtggagact tggatgcat atcttctttg 120
 ttttgggttt tcttccctag cttattttgt ggcttttaaa gaagtggatt gtattgtgag 180
 atcctgtgat tcctggtgg 199

<210> 379
 <211> 216
 <212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(216)

<223> n = A,T,C or G

<400> 379

ccagggcang tcatcaagag gggcattgtc ttgcatgcgg cctgccgtgt ccaccagcac	60
cacgtcaaag ccttggttac gtgcaaaagc aatggcttcc atggcaatgc cagcagcatc	120
cttgccatag cccttttcaa acaactgcac catgggtgcgg ccaccatgct tctctggagg	180
gtgtagggca ctcaaacgcc ggggtgtgtgt acgcag	216

<210> 380

<211> 555

<212> DNA

<213> Homo sapien

<400> 380

ccatgggcct tcctttccac taaaaggaat tccgaacagc aaaaagaagg tcttgagata	60
gtgaaaatgg tgatgatata tttagaaggc gaagatgggt tggatgaaat ttattcattc	120
agtgagagtc tgagaaaact gtgcgtcttc aagaaaattg agaggcattc cattcactgg	180
ccctgccgac tgaccattgg ctccaatttg tctataagga ttgcagccta taaatcgatt	240
ctacaggaga gayttaaaaa gacttggaca gttgtggatg caaaaaccct aaaaaaagaa	300
gatatacaaa aagaacagc ttattgctta aatgatgatg atgaaactga agttttaaaa	360
gaggatatta ttcaagggtt ccgctatgga agtgatatag ttcctttctc taaagtggat	420
gaggaacaaa tgaaatataa atcggagggg aagtgttctc ctgttttggg attttgtaaa	480
tcttctcagg gtcagagaag attcttcatg ggaaatcaag ttctaaaggc ttgccccaa	540
gagatgatga ggcag	555

<210> 381

<211> 406

<212> DNA

<213> Homo sapien

<400> 381

ctgcaccagg tgggcctcta ggtcccatta agcccattgg tccagggccca agtccaactc	60
cttttccatc atactgagca gcaaagttcc caccgagacc agggggggcca ggaggaccag	120
gtggaccagg agggcctgtg ggaccatctt caccatctct gcctgggggg cctgggtggac	180
ccctttctcc acgtggtcct ctatctccgg ctggggccctt tcttacagtt tcctcttgta	240
aagattggca tgttgctagg cataaggcta ctgcaagcag caacaaagtc cgcgtatcca	300
caaagctgag catgtctagc acttagacat gcagactcct tgtgtcgcag agcccctggg	360
tcaccggcgg aggtatcacc tggcgggccc gggcatgcag tcgtgg	406

<210> 382

<211> 528

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(528)

<223> n = A,T,C or G

<400> 382

```

ctgagcagtt tgtgggtntn tcttcccgca agtttcagga agtattcaca aaagaaaaat      60
acattttttc cccagggggt ggggcaagga cagtggagag agtgctagga aatgagtcct      120
ctgggaaagg ggaccgggcc gtgatgttaa atatctccgg ctccaagtg actggatttg      180
cctaggacct tcagaccaac agacttcaga ccctcagacc tgccccgggg ccagggtggag      240
aaagtggagg ccgtacaagg aagtgaatt ctgagttgtt ggggctaagc ctgacccct      300
ctccatgtct cccgccccaa cccactctgg cctcagtaga ttttttttc agttgtgtgt      360
gttggccagg ctggagtgc gtagcgccat cttggctcac tgcacctcca ccttcggggc      420
tcaagcgatt ctccagctc agcctcctga gtagctagga ctgcaggtgc tccaccacgc      480
ccggctaatt tttgtatttt tagtagagat ggggtttccc catgttgg      528

```

<210> 383

<211> 335

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(335)

<223> n = A,T,C or G

<400> 383

```

ccatnttgag tctactcctg cgtcttgtgc cctagcaccg cgagaaccgt cagtttgagc      60
cagatggaag ctgagctgaa cacattacga tggatgatgg aaacataaga ctatcaagaa      120
atccaagtgg taatgggcga agtttattca gcatccggca atggacttat cgtagttggg      180
gaaacgggtg ttccgaataa tatcctggaa gttatcagga cacctatttt aaatataggc      240
ctgaattttg taaagtaata tttaagggtg tccgtgataa ttaaataaaa tgcttaattc      300
atgtggcgaa aaaaaaaaaa naaaaaaaaa aaaaaa      335

```

<210> 384

<211> 333

<212> DNA

<213> Homo sapien

<400> 384

```

agtccaatac ggctattggg gttgtagcag ctttcagagg aaattagtgg tctgggcttg      60
cctccagctc cccaggggca gcccagtag ctacactgtc cagacagcac aagaccaggc      120
tgggtgtcac tccatccgag cgctgcctca gggatcgata aagtttact gcagaaagtc      180
tccactgcgg tatgtgaca tctgccctga accttcaccc tacagcatta caggctttaa      240
tcagattctg ctggaaagac acaggctgat ccacgtgacc tcttctgcct tctctgggct      300
ggggtgatcc ttggtgcctt tgtttccaca agg      333

```

<210> 385

<211> 343

<212> DNA

<213> Homo sapien

<400> 385

```

ctgtgacacc tcagggtgaa agggctcttc tccttgaaca cccaccgagg ggcctggagc      60
aacagccagc cgatatggac ttctagctgc accgggtcac tgaggggtgga gaggtttgtc      120
tggcacctgt acttccact gtcgtcgact gtggcagcgt caatgaagta gctcgaggcc      180
tggcttgaga tgaggctctc attgtgaaac cactgtgtgg aattgtctc aggggagtag      240
gtcccttggc acttcagagt cacactgtcc ttctcgagca ccctgtacca ttgaggctcc      300
aggaacacca cagcctttgg gagatcttca gtccgcatgc caa      343

```

<210> 386

<211> 244
 <212> DNA
 <213> Homo sapien

<400> 386
 tattctttga ttcttgga ataggtgaga gaactaatag caaccaggca actgaggacg 60
 aagtcaaaaa gtcggttaaca gaagaatgga atcagccaac ccacttgata agaaattgct 120
 ccataaacca gcattgaact gattataaac ataagaacag agacggcaaa aagaacacag 180
 gcattatcag ccattctctc agacgaatag taattaccga tgacttcata ctgaatggtg 240
 acag 244

<210> 387
 <211> 504
 <212> DNA
 <213> Homo sapien

<400> 387
 atctggagtc cagcctcagg gatgcgctac ttccattct ctgcattgaa cattcgttct 60
 gtcagcatcc gctccagctt cactgcatca gcggcaaaact tgcggatccc gtcagagagc 120
 ttctccacag ccattctggtc ctggttggtc aaccaacgga aagacttctc atccagggtg 180
 attttttcca ggtcactggc ttgggcccgc ttggctgaga gcacaggcac cagcttggcg 240
 ttgtcctgca gcagctctcc caggagcttg ggtgggatgg tgaggaagtc acagccggcc 300
 agtgctttga tctcgcccggt gttgcggaag gagcgccca tgacaatggt tttgtagcta 360
 aacttcttgt agtagttgta gatttttagtg acactcttta ccccagggtc ttccaggggc 420
 tcataggatt tcttgctgggt gtttgccaca tgccaatcaa ggatgcgccc aacaaatggg 480
 gagatgaggg tcacacccgc ctgc 504

<210> 388
 <211> 450
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(450)
 <223> n = A,T,C or G

<400> 388
 gccaaagtgc tgcntgaatt ccactccctt ggttttcgcc tgcccagcgt tgctgtttgc 60
 gtggaggggtg gggggagctc agtggcaggg aatcagcggc ccgtggggtc gtggggacgg 120
 gaacatgtgc ccgaccgctc catccctcc tcctccttag gatgcataac ctacctgtc 180
 tttttttttt taaattttnt ttccagggtan agtagctntt tgtacataaa naatacttga 240
 aaaattaatt gtatgatgta tgaaaanaca nagtctccta gttttgtatn ttgttgatg 300
 actgccatga gttccaccaa aaagccactn tattttgggc tntgtgacat tttaaatgcg 360
 tgacaaaagt gagcaaataa agngaggaan aaatntatnt atganataat atanattgta 420
 ttgaaatcta aaaaaaaaaa aaaaaaaaaa 450

<210> 389
 <211> 297
 <212> DNA
 <213> Homo sapien

<400> 389
 cctgcacttg aacatggctt tggttttaag caacttctct accctgaccc tctcctggg 60
 acagcgtttc gggaggttct ttggcctcac tgagagggat gtggagctgc tgtaccccg 120

```

caaggagaag gtattctaca gcctgatgag ggagagcggc tacatgcaca tccagtgcac      180
caagcctgac accgtaggct ctgctctgaa tgactctcct gtgggtctgg ctgcctatat      240
tctagagaag ttttccacct ggaccaatac ggaattccga tacctggagg atggagg          297

```

```

<210> 390
<211> 223
<212> DNA
<213> Homo sapien

```

```

<400> 390
ctgggctgga gagggtggtgc tggcaaaaaca gtccttcccc tggggccggg tcttaccag      60
gtccagagaa accaacgcgg gatgtcagac ttcacaaaaa ggactttctg gttgcccttg      120
gctggcctcc tggaggcggt cgcctctagt ttctcaggga tggagcgaga gcccagccag      180
agaacagtaa gaggagctgc tctcctatct gcactcacc agg                      223

```

```

<210> 391
<211> 365
<212> DNA
<213> Homo sapien

```

```

<400> 391
ctgaggaaga aatgaaaaaa gaccctgtcc ctcatggccc gccactggc ctctgtgaa      60
ctctgtcctg ttgccaaccc cagatgaagt cagccaaaaa gtgctttcca catcctctct      120
ctggggctgc ccagcctgac cgtaggggat ccactggcag agccaagggt gatgctggtg      180
cctgaagctg gaagccagca ggacatgaga cccctcctgt agcaggaagt ggttctagaa      240
ctcccagcag aacagaacgg aaaaggagct gattggggat agaatgagtt ctgctaaaca      300
gccagatgct ctgagagagg tgacactgga ctgtctcgga ggtgtgtgca gatggctaca      360
ggtgg                                              365

```

```

<210> 392
<211> 302
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(302)
<223> n = A,T,C or G

```

```

<400> 392
ccaagagcta caatgagcag cgcatacanga cagaacgtgc aggtttttga gttccagttg      60
actgcagagg acatgaaagc catagatggc ctagacagaa atctccacta ttttaacagt      120
gatagttttg ctagccaccc taattatcca tattcagatg aatattaaca tggagagctt      180
tgctgatgt ctaccagaag ccctgtgtgt ggatggtgac gcagaggacg tctctatgcc      240
ggtgactgga catatcacct ctacttaaat ccgtcctggt tagcgacttc agtcaactac      300
ag                                              302

```

```

<210> 393
<211> 213
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(213)

```

<223> n = A,T,C or G

<400> 393

ccaataatca agnacaaana ctggatttga ggatggatca gttctgaaac agtttctttc	60
tgaacacagag aaaatgtccc ctgaagacag agcaaaatgc tttggaaaga atgaggccat	120
acaggcagcc catgatgccg tggcacagga aggccaatgt cgggtagatg acaagggtgaa	180
tttccatttt attctgttta acaacgtgga tgg	213

<210> 394

<211> 334

<212> DNA

<213> Homo sapien

<400> 394

cctacccata atccagagag gcttgcccag aggaggacta cgtgggggac gtgccaccag	60
aacctacttt gggggcgagg tgtcactccg aggtcaaaac ctgctccgag gtggacgagc	120
cgtagctccc cgaatgggct taagaagagg tgggtgttcga ggtcgtggag gtcctgggag	180
agggggccta gggcgtggag ctatgggtcg tggcggaatc ggtggttagag gtcgggggtat	240
gataggtcgg ggaagagggg gctttggagg ccgaggccga ggccgtggac gagggagagg	300
tgcccttgct cgccctgtat tgaccaagga gcag	334

<210> 395

<211> 174

<212> DNA

<213> Homo sapien

<400> 395

ccagatgagg aaaaaaatta ggaaggagat gaagttttcc aaatttcatg gtatatgctg.	60
cacttcccca accttcactc tccatgtagc ctactgggtc tactattcca caaagtgggt	120
caacctccaa atgacctctg gtttaccctt attaaaatcc caaaggactt tcag	174

<210> 396

<211> 140

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(140)

<223> n = A,T,C or G

<400> 396

ctgcaaagcc ttgtgtaacn ttctccagca tttggaccca gtacgtgaaa gccacaaca	60
cgttcattgt ctttagtatt acagattatt tttgcataac atttgttgtt atctcttgac	120
ggaatcgtcc attccaatgg	140

<210> 397

<211> 318

<212> DNA

<213> Homo sapien

<400> 397

cctcgcttgg agggcccccg ggcagcacag ggaggacgag cttgtccagc agagggtctg	60
gcagaggggc ccgcagaggt ttgggcaggg ggtctgacat ccctggctcc tgctctggct	120
ctgggtgccg ggatttgac aggccaggt gcatacagat gccgttttag tcagtctggt	180

tctggaagta gtcgatgacc agggggaagt agtcgtcaag cacttggttg cactggggca 240
 tgagcagctt caaggggagg acgttgact cctgctccag gaacttcctc atcgtgtcct 300
 ggaaaatggc ctccttgg 318

<210> 398
 <211> 517
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (517)
 <223> n = A,T,C or G

<400> 398
 ccttncttcg ccatccattc atcgaccctc tccagcactt gctgcaggct tggctgacca 60
 tccaccatgg cttgaataat cccggtgagc tctgtacaga atggggtaag ctgtggatgg 120
 actacaggct ggacatacat gtgaaaggta gactcaatct ccattgggtccg gccatttagc 180
 tttaggatgg ggaactcgat gatttcctga ggatgaatct gtggcttgtc gcacgtggcc 240
 tcaaagtcca gcactaaaaa gtagtgatac ctctggagag ggaaggacac cattgccgcc 300
 atggatgctc caaagccgtg ggccgccagc tttctggtgg atatggagca gaactccgga 360
 acaccacagg gagaaaataa gtgggagccc agcacttttc ttgctcttga aagtaaatac 420
 gaagaaaatc gagctgtctc agtctgtaaa ggtgctagca ttgaacatcc agaagcatct 480
 aaaactctcc ttacttcgaa gatgccaaga ccggcag 517

<210> 399
 <211> 329
 <212> DNA
 <213> Homo sapien

<400> 399
 ccaacctcag gcaacgggtg gagcagtttg ccagggcctt ccccatgcct ggttttgatg 60
 agcattgaag gcacctggga aatgaggccc acagactcaa agttactctc cttcccccta 120
 cctggggcag tgaaatagaa agccttttcta ttttttgggt cgaggaggaa gacctctcac 180
 ttagggcaag agccaggtat agtctccctt cccagaattt gtaactgaga agatcttttc 240
 tttttccttt tttcggtaac aagacttaga aggaggcccc aggcacttcc tgtttgaacc 300
 cctgtcatga tcacagtgtc agagacgag 329

<210> 400
 <211> 451
 <212> DNA
 <213> Homo sapien

<400> 400
 ctggcttcac tgctcagggtg attatcctga accatccagg ccaaataagc gccggctatg 60
 cccctgtatt ggattgccac acggctcaca ttgcatgcaa gtttgctgag ctgaaggaaa 120
 agattgatcg cgtttctggt aaaaagctgg aagatggccc taaattcttg aagtctggtg 180
 atgctgccat tgttgatatg gttcctggga agcccatgtg tgttgagagc ttctcagact 240
 atccaccttt gggtcgcttt gctgttcgtg atatgagaca gacagttgag gtgggtgtca 300
 tcaaagcagt ggacaagaag ctgctggagc tggcaaggtc accaagtctg cccagaaagc 360
 tcagaagcta aatgaatatt atccctaata cctgccaccc cactcttaat cagtgggtgga 420
 agaacggctc agaactgttt gtttcaattg g 451

<210> 401
 <211> 180

<212> DNA
<213> Homo sapien

<400> 401
ccaggaagca ggccagggga ttggcagcac tgcccagcac cacagccagg ttgtaggcca 60
gacgcccgtg gggtaagcag gaaaagctct gcacggcagg cagcacgcca ttggtcagcg 120
cgttggtggc ggccaacagg cccagcaggc aggcactgcg ggctgataga agctgatagg 180

<210> 402
<211> 385
<212> DNA
<213> Homo sapien

<400> 402
ccaggccacc tgtgcggggc tcctcgatgt ggaagggttcg ggtgaggaga ttgtagaagg 60
agccgtagca cacggccacc acagtgcacg tgaggcagat cacgtttagg ggcattgctga 120
agtcgggtgt cggcaggttc accagcagcg gctccgtgta gagccgcaca aagtagttag 180
agccatcaga gactgggaac aggcctgttg agaggggact ctcttcccag tccactggct 240
tggctgctac catgctgggc acaagggcgc tgaggacaga tgggctgaca tagaagccat 300
ggtaggatc tggcgtgtac tcggctccact tcagcagcgc ccgctcaaac tggatggaaa 360
ccttgggtgac tgagttggcc ggcag 385

<210> 403
<211> 440
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(440)
<223> n = A,T,C or G

<400> 403
ctgtttaacc agnaaccg ggggtcaccc cccacagaat gtacatgaaa cactagagga 60
ctgcatgttt ttccctgaga gaagcgtaag acaaacagaa gtcaaaaagt agtcactggg 120
agcgcattcc ttctaagcaa atcctccctt tcccttttgg aggatttgcc cgaactacgt 180
agccagtcag cacttagacc acctgcctcc tccccccct ataaaccac cactccctc 240
ctcctttccc aaaccacttg ggggtgtccta agccctcact gcccgaagcc caaaatatca 300
gctaagatcc ttgtcagtat ttccacagtc atacctaata aattgggaag tggggccct 360
aaaaaccaat tcacatctat gcacttggtt ccactggatt tggcagacag gcttttttag 420
ttaccgtaac cagatcttaa 440

<210> 404
<211> 239
<212> DNA
<213> Homo sapien

<400> 404
cctacgaaaa actcccggcc ggtgaagaga acgtcagtgc catccagcgt cgcgttctcg 60
tctcctatct ccacaattcg gagccccagg tcttgacagg ctttgccggac tccatcgacc 120
tctggcctac gagcggggct ccaggccgc gtgattaggg ccgtgtcccc ttggatcacg 180
gccgtgtcgc caagcagcgg tcccagcggc aatgactcct cagggtggcag ttctagcag 239

<210> 405
<211> 261

<212> DNA

<213> Homo sapien

<400> 405

ctggagaggc agcccttcac cggatgcccc gctccgtgcc cctgcggggc ccagcacagt	60
ttaccttctc cccccacggc ggtcccatct actctgtgag ctgttcccc ttccacagga	120
atctcttccct gagcgtggg actgacgggc atgtccacct gtactccatg ctgcaggccc	180
ctcccttgac ttcgctgcag ctctccctca agtatctgtt tgctgtgccc tgggtccccag	240
tgcgggccctt ggtttttgca g	261

<210> 406

<211> 641

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(641)

<223> n = A,T,C or G

<400> 406

ctgctcccgg gcntgggtggc agcaagtaga catcgggcct gtgcagggcc acccccttgg	60
gccgggagat ggtctgcttc agtggcgagg gcaggtctgt gtgggtcacg gtgcacgtga	120
acctctcccc ggaattccag tcatctcgc agatgctggc ctcacccacg gcgctgaaag	180
tggcattggg gtggctctcg gagatgttgg tgtgggtttt cacagcttcg ccattctggc	240
gggtccagga gatggtcacg ctgtcatagg tggtcaggtc tgtgaccagg cagggtcaact	300
tgggtggactt ggtgaggaag atgctggcaa aggatggggg gatggcgaaag acccggatgg	360
ctgtgtcttg atcgggggaca cacatggagg acgcattctg ctggaaggtc agggccctgt	420
gatccacgag gcagggtgaac atgctctggc tgagccagtc gctctctttg atgggtcagtg	480
tgctgtgcac cttgtaggtc gtggggccag actctttggc ctcagcctgc acctggtccg	540
tgggtgacgc agacccacc tgcttccct cggcgagcca ggacacctga atctgccggg	600
gactgaaacc cgtggcctgg cagatgagct tggacttgcg g	641

<210> 407

<211> 173

<212> DNA

<213> Homo sapien

<400> 407

ccagggtactg gcacaatcat gtctggatgg ggggtgggtgt gtctgtagg cagagaaaca	60
ggaaattgtc gtagtcagta tcgagcagcg tggcctcgtt cgccaccgta tagttgatct	120
tgaacttctt tggattctca gtcttctctc caaggacctt cttctcaaca cag	173

<210> 408

<211> 165

<212> DNA

<213> Homo sapien

<400> 408

ccactgtctg cagccatggc agaaagtgt caaagtccag caccttcaca ttcattctcat	60
cactcttggg gttccccagg accttgagca cctcggcgtt ggtagggttc tggccaggg	120
ccctcatcac atccccacac tggctgtaca ggatcttgcc atcac	165

<210> 409

<211> 329

<212> DNA

<213> Homo sapien

<400> 409

ctgtagcttc	tgtgggactt	ccactgctca	ggcgtcaggc	tcagatagct	gctggccgcg	60
tacttggtgt	tgttttgtt	ggagggtgtg	gtggtctcca	ctccgcctt	gacggggctg	120
ctatctgcct	tccaggccac	tgtcacggct	cccgggtaga	agtcacctat	gagacacacc	180
agtgtggcct	tgttggttg	aagctcctca	gaggagggcg	ggaacagagt	gaccgagggg	240
gcagccttgg	gctgaccaag	gacggtcagc	ttggtccctc	cgccaaatac	cgccggataa	300
gcaccactgt	tgtctgctga	ttgacagaa				329

<210> 410

<211> 235

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(235)

<223> n = A,T,C or G

<400> 410

ccatcagnga	gaaaggtgtt	tgtcagttgt	ttcacaaacc	agattgagga	ggacaaactg	60
ctctgccaat	ttctggattt	ctttattttc	agcaaacact	ttctttaaag	cttgactgtg	120
tgggcactca	tccaagtgat	gaataatcat	caagggtttg	ttgcttgtct	tggatttata	180
tagagctttt	tcatatgtct	gagtccagat	gagttgggtca	ccccaacctc	tggag	235

<210> 411

<211> 294

<212> DNA

<213> Homo sapien

<400> 411

aattaaggga	agatgaagat	gataaaacag	ttttggatct	tgctgtgggt	ttgtttgaaa	60
cagcaacgct	tcgggtcagg	tatcttttac	cagacactaa	agcatatgga	gatagaatag	120
aaagaatgct	tcgcctcagt	ttgaacattg	accctgatgc	aaagggtggaa	gaagagcctg	180
aagaagaacc	tgaagagaca	gcagaagaca	caacagaaga	cacagagcaa	gacgaagatg	240
aagaaatgga	tgtgggaaca	gatgaagaag	aagaaacagc	aaaggaatct	acag	294

<210> 412

<211> 433

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(433)

<223> n = A,T,C or G

<400> 412

cctgagaagc	cagaggcagg	tggagagggg	gtggaaagtg	agcagcgggc	tgggctggag	60
ccgcacacgc	tctcctccca	tgttaaatag	cacctttaga	aaaattcaca	agtccccatc	120
cacaaaaaaa	aaaanaanaa	aaatttcagg	gantaaaaat	anactttgaa	caaaaaggaa	180
catttgntgg	cctggggggg	catctnantt	tntntagcnc	cagngattcc	ctccccnccc	240
cacccatcac	atanatgtaa	cacctttggt	ntaaaaatggg	gagccgtttc	cacctngccc	300

ccntccccgc ccccgaggcag ttgccccggn gacacntcaa gacaggancg aggtagtntt 360
 tcancancac agttncaaca ggaacagaac agtntctccc gcccgaccct gcggcacaag 420
 ggattgacac gcn 433

<210> 413
 <211> 494
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(494)
 <223> n = A,T,C or G

<400> 413
 ccttatttct cttgtcnctt cgtacagggg ggaatttgaa gtagatagaa accgacctgg 60
 attactccgg tctgaactca gatcacgtag gactttaatc gttgaacaaa cgaaccttta 120
 atagcggtcg caccatcggt atgtcctgat ccaacatcga ggtcgtaaac cctattgttg 180
 atatggactc tagaatagga ttgcgctgtt atccctaggg taacttgctc cgttggtcaa 240
 gttattggat caattgagta tagtagttcg ctttgactgg tgaagtctta gcatgtactg 300
 ctcgagggtt gggttctgct ccgagggtcg cccaaccgaa atttttaatg caggtttggt 360
 agtttaggac ctgtgggttt gttagggtact gtttgcatta ataaattaaa gctccatagg 420
 gtcttctcgt cttgctgtgt tatgcccgcc tcttcacggg cagggtcaatt tcaactggta 480
 aaagtaagag acag 494

<210> 414
 <211> 294
 <212> DNA
 <213> Homo sapien

<400> 414
 ctgggaggat agcaccgggc atatttttga atggatgagg tctggcacc tgagcagtcc 60
 agcgaggact tggctcttagt tgagcaattt ggctaggagg atagtatgca gcacggttct 120
 gagtctgtgg gatagctgcc atgaagtaac ctgaaggagg tgctggctgg taggggttga 180
 ttacagggtt gggaacagct cgtacacctg ccattctctg catatactgg ttagtgagggt 240
 gagcctggcg ctcttctttg cgctgagcta aagctacata caatggcctt gtgg 294

<210> 415
 <211> 421
 <212> DNA
 <213> Homo sapien

<400> 415
 ccttgccctt gccctccac gaatgggttaa tatatatgta gatatatatt ttagcagtga 60
 cattcccaga gagccccaga gctctcaagc tcctttctgt cagggtgggg gggttcagcct 120
 gtccctgtac ctctgagggt cctgctggca tcctctcccc catgcttact aatacatccc 180
 ctccccata gccatcaaaa ctggaccaac tggcctcttc ctttcccttg ggacaaaaat 240
 ttaggggctt cagtcctca ccgccatgcc ctggcctatt ctgtctctcc ttcttcccc 300
 tggcctgttc tgtctctgag ctctgtgtcc tccgttcatt ccatggctgg gagtcaactga 360
 tgctgcctct gccttctgat gctggactgg ccttgcttct acaagtatgc ttctcccaca 420
 g 421

<210> 416
 <211> 342
 <212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(342)

<223> n = A,T,C or G

<400> 416

ccactttctt	tcccacnctg	gaaggcggca	tctatgactt	cattggggag	ttcatgaagg	60
ccagcgtgga	tgtggcagac	ctgataggtc	taaaccttgt	catgtcccgg	aatgccggca	120
agggagagta	caagatcatg	gttgctgccc	tgggctgggc	actgctgag	cttattatgt	180
cccgtgcac	tcccctatgg	gtcggagccc	ggggcattga	gtttgactgg	aagtacatcc	240
agatgagcat	agactccaac	atcagtctgg	tccattacat	cgtcgcgtct	gctcaggtct	300
ggatgataac	acgctatgat	ctgtaccaca	ccttccggcc	gg		342

<210> 417

<211> 389

<212> DNA

<213> Homo sapien

<400> 417

tattaattag	gttcttaaga	catttagaac	accaatttgt	gaggataaat	tccattcgtc	60
agagcaaaca	cagatcgag	gtagccctgg	agctgaggaa	tagctttgat	ttttggtaaa	120
at ttgtgagt	ccacagcttt	ctgatcaatc	ttgcgctgct	ccgtaatctc	atat tttctt	180
ttttctgtgt	cgaagatctc	accttccctg	tgtctgggct	tccgcagctt	cttcttcttg	240
aagtaagcat	cagtaagatg	ttttgggatt	tttaccattgc	tgatattcgat	tttgggtgaa	300
gtggcaatga	caaatttctg	gtgtgttctt	cgtagaggaa	ctcgattgag	gaccagaggt	360
ccagtcacaa	gtaataagcc	actagccag				389

<210> 418

<211> 343

<212> DNA

<213> Homo sapien

<400> 418

gtgggagggg	gccaggttgg	gatggaggga	gtttacagga	agcagacagg	gccaacgtcg	60
aagccgaatt	cctggtctgg	ggcaccaacg	tccaaggggg	ccacatcgat	gatgggcagg	120
cgggaggtct	tgggtgtttt	gtattcaatc	actgtcttgc	cccaggctcc	gggtgtgactc	180
gtgcagccat	cgacagtgac	gctgtagggt	aagcggctgt	tgccctcggc	gcggatctcg	240
atctcgttgg	agccctggag	gagcagggcc	ttcttgagggt	tgccagtctg	ctgggtccatg	300
tagggcacgc	tgtttttgca	gtggtagggt	atgttctggg	agg		343

<210> 419

<211> 255

<212> DNA

<213> Homo sapien

<400> 419

cctagcaaga	gaatcaccaa	at ttatggag	agttaacagg	ggtttaacag	gaaggaagtg	60
ccttttagtaa	gttctcaagc	cagaggctgg	aggcagcagc	taaatcagag	gacagcatcc	120
tcagtgaag	tgagccattc	ggggtggcat	gtcactccag	gaataaacac	aacttagaaa	180
caaattgattt	cgtaggatag	cacagtgaca	tggtgcactg	tgaacctgag	gccactgtgt	240
caaactgtgc	actgg					255

<210> 420

141

<211> 261
 <212> DNA
 <213> Homo sapien

<400> 420
 cttctgatga taaccaaccc ctagctacca ctctgtattc atcaggggag gggataaac 60
 cccacatgca agaagaaccc ttgccccag tgtcaaatgg gatggggatg ctagagttat 120
 agtaaagggg aaaccctatg taagctgtta acagagttca caggggtagg gataaccct 180
 gttctccagc tcccaaatgt gctcactttc ccagcttctt catccgttca tcaatgctgg 240
 caaagtcccc ctcaactgtg g 261

<210> 421
 <211> 179
 <212> DNA
 <213> Homo sapien

<400> 421
 ccttcctggt gttgtttcaa atgctgcttg atttctcgta acagatctgc atctatgtaa 60
 tacctttctt cagatctgac tgctccaaaa tgattctgca tcctgatttg agacatcaat 120
 tcatttagtc ggcccttgaa ctgagtaggt gcatttagtt caccctgaat cgtatccag 179

<210> 422
 <211> 424
 <212> DNA
 <213> Homo sapien

<400> 422
 cgagggtccaa atctgatctg cagatgcaga agattcgaca gaagctgcag actaaacagg 60
 ctgccatgga gaggtctgga aaagctaagc aactgcgagc acttaggaaa tacgggaaga 120
 aggtgcaaac ggaggttctt cagaagaggc agcaggagaa agcccatatg atgaatgcta 180
 ttaagaaata tcagaaaggc ttctctgata aactggattt ccttgaggga gatcagaaac 240
 ctctggcaca gcacaagaag gcaggagcca aaggccagca gatgaggaag gggcccagtg 300
 ctaaacgacg gtataaaaac cagaagtttg gttttggtgg aaagaagaaa ggctcaaagt 360
 ggaacactcg ggagagctat gatgatgtat ctagcttccg ggccaagaca gctcatggca 420
 gagg 424

<210> 423
 <211> 256
 <212> DNA
 <213> Homo sapien

<400> 423
 ctgtggccta gggtacctc aagactcacc tcattccttac cgcacattta aggcgccatt 60
 gcttttggga gactggaaaa gggaaggtga ctgaaggctg tcaggattct tcaaggagaa 120
 tgaatactgg gaatcaagac aagactatac cttatccata ggcgaggtg cacaggggga 180
 ggccataaag atcaaacatg catggatggg tcctcacgca gacacacca cagaaggaca 240
 ctagcctgtg cacgca 256

<210> 424
 <211> 330
 <212> DNA
 <213> Homo sapien

<400> 424
 ccagccgcat gggagtggag gcagtcacg ccttgctaga ggccaccccg gacacccag 60

```

cttgcgctgt gtcactgaac gggaaccacg ccgtgcgccct gccgctgatg gagtgcgtgc      120
agatgactca ggatgtgcag aaggcgatgg acgagaggag atttcaagat gcggttcgac      180
tccgagggag gagctttgcg ggcaacctga acacctacaa gcgacttgcc atcaagctgc      240
cggatgatca gatcccaaag accaattgca acgtagctgt catcaacgtg ggggcacccg      300
cggctgggat gaacgcggcc gtacgctcag                                     330

```

```

<210> 425
<211> 333
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(333)
<223> n = A,T,C or G

```

```

<400> 425
ctgctccatg gntcaaaagt cagcaccacc cacaccacaca atgatcactg acatgggcag      60
gttcgaggca cgcaccacag cctcacgtgt ggcttcacaca tccgtcacag caccatcagt      120
cagnagaaac agnatgaagt attgngaggc antcccctga tgtgcagcct gggctgcaaa      180
cctggacctg cccgggaggc cgctcgaaaag ggcgaattcc agcacactgg cggccgttac      240
tagnggatnc aganctcggg acnaagcttg gcagtaatca tggtcatagc tgtttcctgt      300
gagcggntgg gatgaacgcg gccgtacgct cat                                     333

```

```

<210> 426
<211> 411
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(411)
<223> n = A,T,C or G

```

```

<400> 426
gggtgttcat catgaggatt gcttctgcca tggagctgat ggacgtgggc aggttgctga      60
gaaggtgggg tggaaagtga tgccgggggt ggggtgagtgc cctggctctg ttcatagggg      120
agcctttccc tagcagtgga acgctgtggt cattttctct agcatattcc ctggggaagt      180
ctagatttgc tattaatctg gctgagaatc taagttctgt gccttagaga cagtttgcac      240
tttcccatat tgtgcctggg acagccatat gatTTTTTTT cccaccaaac aagtatgcaa      300
acagaaacca gttcaaaggg ggatggtgta aaagatgagg cagtanaaat gcctttgaat      360
ggttttctgt agctaattct ctttaaattt tgtcctgctt tttttcttta t                                     411

```

```

<210> 427
<211> 450
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(450)
<223> n = A,T,C or G

```

```

<400> 427
acgtgtacaa gtttgaactg gatacctctg aaagaaagat tgaatttgac tctgectctg      60

```

```

gcacctacac tctctactta atcattggag atgccacttt gaagaaccca atcctctgga      120
atgtggctga tgtggncatc aagttccctg aggaagaagc tccctcgact gtcttgcccc      180
agaacctttt cactccaaaa caggaaattc agcacctgtt ccgcgagcct gagaagaggc      240
ccccaccgt ggtgtccaat acattcactg ccttgatcct ctccgccgtt cttctgtctct      300
tcgctctgtg gatccggatt ggtgccaatg tctccaactt cacttttgct cctagcacga      360
ttatatttca cctgggacat gctgctatgc tgggactcat gtatgtctac tggactcagc      420
tcaacatggt ccagaccttg aagtacctgg                                     450

```

```

<210> 428
<211> 377
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(377)
<223> n = A,T,C or G

```

```

<400> 428
cagggtata gtgcgctatg ttgatctggt gttcatgcta agttccgcat caatatggtg      60
acttcttggg agtgggggac caccagggtg cctaaggagg ggtgaacctg cctacgttgg      120
aaatagagct ggncaaaact cctgtgctca tcagtagtag aattgcacct gtgaatagcc      180
nccgccctcc agcatgggca acataacaag accctgcctc ttaaagataa aaattggaaa      240
acactngtag gaaaaaaagg gtgnnttggtc taaataaatn tggattgggn ataaatgacn      300
caaaactatc atgaatttga aagcntttct aatttcttga aagtctgaaa aaagttaaan      360
cncaatttta tctnaaa                                     377

```

```

<210> 429
<211> 206
<212> DNA
<213> Homo sapien

```

```

<400> 429
gttgctcctc caaagaaggt tggcttcaag gccgtgtcca gggacccacg agcagaggca      60
ctggggggca agggatctcc aagggggcaa gggatcccta aagggggtag ctcacaggtg      120
aggggggtta gggccctctc agggagcgcc tgaggccata cattcaagag tgctccctggt      180
gaggcccgag gaagagccag gactgg                                     206

```

```

<210> 430
<211> 473
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(473)
<223> n = A,T,C or G

```

```

<400> 430
ccttatttnt cttgtccttt cgtacagga ggaatttgaa gtagatagaa accgacctgg      60
attactccgg tctgaactca gatcacgtag gactttaatc gttgaacaaa cgaaccttta      120
atagcggtcg caccatcggt atgtcctgat ccaacatcga ggtcgtaaac cctattgttg      180
atatggactc tagaatagga ttgcgctggt atccctaggg taacttggtc cgttgggtcaa      240
gttattggat caattgagta tagtagttcg ctttgactgg tgaagtctta gcatgtactg      300
ctcggagggtt gggttctgct ccgaggtcnc cccanccgaa atttttaatg caggtttggg      360

```

agntnaggac ctgtgggttt gttaggtact ggggtgcatta ataaattaaa gctccatagg 420
gtcttctcgt ctgtgctgtg tatgcccncc tcttcacggg caggtcaatt tca 473

<210> 431
<211> 215
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(215)
<223> n = A,T,C or G

<400> 431
cctgtatnaa gctanaaaaa gactaccagc ccgggatcac cttcatcgtg gtgcagaaga 60
ggcaccacac ccggctcttc tgcactgaca agaacgagcg ggttgggaaa agtggaaaca 120
ttccagcagg cactgctgtg gacacgaaaa tcaccacccc caccgagttc gacttctacc 180
tgtgtagtca cgctggcatc caggggacaa gcagg 215

<210> 432
<211> 391
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(391)
<223> n = A,T,C or G

<400> 432
ccagcactgc cacaaacttt ttcagggcca ccaggcgctg cccttccagg accgggaacc 60
tgcccacttc tatccgcagg atgtagtga gtgcagattc caggtcagcc atgtagatcc 120
tggagcgatc tgccaatttc caaacagtgg gagctatctt gttagcagtg gttggtgcaa 180
ctgtggtctg ggcagcctcc ctggtgagcc cagagagtct ctgcaggtaa gcggtataga 240
aggacctgga ttccatgagc acggggactc gggagacgga gccattccgg aacagcaggt 300
agcaagaggg gaagtcggtg acaccaaact ttctcaccac attggcctct gtgttcagca 360
ccctgcgcac cgccacncc ttgtgctggg a 391

<210> 433
<211> 420
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(420)
<223> n = A,T,C or G

<400> 433
ctgtagcttc tgtgggactt ccactgctca ggcgtcaggc tcagatagct gctggctgcg 60
tacttgttgt tgctttgttt ggagggtgtg gtggtctcca ctccgcctt gacggggctg 120
ctatctgcct tccagggcac tgtcacggct ccgggtaga agtcacttat gagacacacc 180
agtgtggcct tgttggcttg aagctcctca gaggaggcg ggaacagagt gaccgagggg 240
gcagccttgg gctgacgtag gacggttagt ttggnccctc cgccgaatgc cgcanttcta 300
ctgtcccaca cctgacagta atagtcncc tcatcttcgg cttgggctct gctgatggtc 360

aggggtggccc gtgntccccc agttggagcc aggggaatcnc tcagggatcc canagggccn 420

<210> 434

<211> 239

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(239)

<223> n = A,T,C or G

<400> 434

ccaaccanga	gagaagggat	cgcttggtgc	ccaggggcca	ccaggagctc	caggccact	60
tgggattgct	gggatcactg	gagcacgggg	tcttgagga	ccaccaggca	tgccagggtcc	120
taggggaagc	cctggccctc	aggggtgtcaa	gggtgaaagt	gggaaaccag	gagctaacgg	180
tctcagtggg	gaacgtggnc	cccctggacc	ccagggtctt	cctgggtctg	ctggtnacg	239

<210> 435

<211> 415

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(415)

<223> n = A,T,C or G

<400> 435

ctgtccaatg	gcaacaggac	cctcactcta	ttcaatgtca	caagaaatga	cgcaagagcc	60
tatgtatgtg	gaatccanaa	ctcagtgagt	gcaaaccgca	gtgacccagt	caccctggat	120
gtcctctatg	ggccggacac	ccccatcatt	tcccccccag	actcgtctta	cctttcggga	180
gcaaacctca	acctctcctg	ccactcggcc	tctaaccat	ccccncanta	ttcttggcgt	240
atcaatggga	taccgcagca	acacacacaa	gttctnttta	tcgccaaaat	cacgccaaat	300
aataacggga	cctatgcctg	tttagggntn	taacttggnt	actggccgca	anaattccat	360
agtcaagagc	atcacagnct	ctgcatntgg	aacttctcct	ggctntcaga	cctgn	415

<210> 436

<211> 152

<212> DNA

<213> Homo sapien

<400> 436

ccaggattga	caggccatcc	attcacagcc	aggagatget	gggccagtcc	ctccaagagg	60
tctccgtcat	ggcagtgatg	aaaacctaac	aggggtggccc	cctgtgccag	ctcagggtgac	120
tgagagccga	gggcctgaca	ggttcccagc	ag			152

<210> 437

<211> 174

<212> DNA

<213> Homo sapien

<400> 437

ccagggtactg	gcacatcatg	ctctggatgg	gggtgggtgg	gtcctgtaag	cagagaaaca	60
ggaaattgtc	gtagtcagta	tcgagcagct	gtggcctcgt	tcgccaccgt	atagttgatc	120

ttgaacttct ttggattctc agtcttctct ccaaggacct tcttctcaac acag 174

<210> 438
 <211> 485
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(485)
 <223> n = A,T,C or G

<400> 438
 ccacggccct ctcggccctc tcgctgggag cggagcagcg aacagaatcc atcattcacc 60
 gggctctcta ctatgacttg atcagcagcc cagacatcca tggtagctat aaggagctcc 120
 ttgacacggg caccgcccc cagaagaacc tcaagagtgc ctcccgatc gtctttgaga 180
 agaagctgcg cataaaatcc agctttgtgg cacctctgga aaagtcatat gggaccaggc 240
 ccagagtctt gacgggcaac cctcgcttgg acctgcaaga gatcaacaac tgggtgcagg 300
 cgcagatgaa agggaagctc gccnggtcca caaaggaaat tcccgatgag atcagcattc 360
 tccttctcgg ngtggcgcac ttcaagggc agngggtaac aaagtttgac tncagaaang 420
 acttccctcg aggatttcta cttggatgaa gagaggaccg tgagggtccc catgatgtcg 480
 gacc 485

<210> 439
 <211> 317
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(317)
 <223> n = A,T,C or G

<400> 439
 gggccgtctt cccctccatc gtggggcgcc ccaggcacca gggcagtgat ggtgggcatg 60
 ggtcagaagg attcctatgt gggcgacgag gccagagca agagaggcat cctcacctg 120
 aagtacccca tcgagcacgg catcgnacc aactgggacg acatggagaa aatctggcac 180
 cacaccttct acaatgagct gcgtgtggct cccgaggagc acccgtgct gctgaccgag 240
 gccccctga accccaaggc caaccgcnag aagatgaccc agatcatggt tgagaccttc 300
 agcaccacag ccatgta 317

<210> 440
 <211> 338
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(338)
 <223> n = A,T,C or G

<400> 440
 ccanaaagac ttcccaggga agatgcttgg ctctctgctc caaggtgggc catggtatag 60
 ggccctcgaa gggcttgtgg ctgggtgat cccaggggac attgctcaaa gtgcacagga 120
 ggtggcagca ggtcaggcg agttcctggt ccaggagacat caggaggag ggtagaagcc 180

147

tagggagtgt gcgaggctgc tgggatgagg gagctcaggg gctaccagct aaccagcctc	240
agctcaatgg tttctccatc cttgggtctg tagtcagcaa taccttgcaa cagtgggggtg	300
ttgggggtctc ggagaagctg ccagaactcc ctttctcc	338

<210> 441
 <211> 505
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(505)
 <223> n = A,T,C or G

<400> 441	
ccacacagan tcaccaagcc acagacttgt cttccacaag cacgttctta tcttagccac	60
gaagtgacca agccacacgt actaaagggt gaactcaaag atatgtacag ggtattaaac	120
aaataccaag gggaacagtt aacttcaata caaggtcgaa atcagcaaca agttctacaa	180
tccagnctg atatcagata caagcttcaa ggacaatttc ttttcgaagg cttattccag	240
tttcgngagg ctatcatgag gtgtgtgcat ttgccagggg caaatttcta ttctcaatta	300
acccatgcag caaatgctac ncatgggtgcn gagtccgttt agaagcattt gcggtggacg	360
atggaggggc ccgactcgtc ttactcctgc ttgctaatec acnngngctg gaaggnggac	420
agtgaggcca cggatggagc caccnatcca caccgagtn cttgcgtctg ggggtgctg	480
natnttgatc ttcattggtg tgggc	505

<210> 442
 <211> 386
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(386)
 <223> n = A,T,C or G

<400> 442	
cgccaggtag tacctccgcc ggtgaccag gggctctgag acacaaggag tctgcatgct	60
taagtgctag acatgctcag ctttgtggat acgcggactt tgttgctgct tgcagtaacc	120
ttatgcctag caacatgcc atctttacaa gaggaaaccg taagaaaggg cccagccgga	180
gatagaggac cacgtggaga aaggggtcca ccaggccccc caggcagaga tggatgaagat	240
ggtcccacag gccctcctgg tccacctggg cctcctggcc cccctggtct cgatgggaac	300
tttgctgctc agtatgatgg aaaaggaggg nggacttggc cctggaccaaa tgggcttaat	360
gggacctana ggcccactg gtgcag	386

<210> 443
 <211> 404
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(404)
 <223> n = A,T,C or G

<400> 443

148

```

cctccctctc agagcttgcc ccaggggactc tctggccctc aggggttcaat gtattctgac      60
caaggccaag ctttcctggg gctcagggaa aatcacactt tgctaccga agctgatatcc      120
cctcagatgc caggaaggcc gtgatcatct gactccaccc tcctgagaca cattctctcc      180
ctgactgtcc tgttctaagt cagcggagca ccttaggatg gaggggtgga ggcgaggcca      240
ngatgcagcc tctgtgaaca ggtgcctgga ggctgggaaa tgacctgag agggcaggac      300
acagcnaccg ngggcttaag gtgagggngg agagcaagnt tggcccactt tacaattcta      360
gntcagagcc ancccctaac atggngggca tttattcatt tcgg                        404

```

<210> 444

<211> 318

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(318)

<223> n = A,T,C or G

<400> 444

```

catgggctat agtgcgctat gttgatctgg tgttcattgct aagttccgca tcaatatngc      60
gacttcttng gagtggggga ccaccangtt gcctaaggag ggggtgaacct gcctacgttg      120
gaaatagagc tgggtcaaaac tcctgtgctc atcagtagta gaattgcacc tgtgaatagc      180
caccgccctc cagcntgggc aacatagcaa gacctgcct cttaagataa aaattggaaa      240
acactggtan gaaaaaaagg ctgtttgggc taaanaagtc tggatngggg ataaatgaca      300
cnaancatc atgactnt                                     318

```

<210> 445

<211> 418

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(418)

<223> n = A,T,C or G

<400> 445

```

ccagtcacaac ctgctcctca ttattgtata aatgagcaga atcaatatgg cggaagccag      60
cttcaattgc caatttgggtg gcctctaaag ctttactttt aggaacctct gcaggcgcat      120
aggtgccaaa tcccaggaca ggcattgaagt gaccatcatt cagcttcaca cactgatatt      180
tcgaatccat ttctgtcact agcctggctg gcaaattgtt ctttcttcct ccctcacagg      240
ctataagagc aatgagctgg caacgcccct gagcacactg tctgctgntt aaccaatggc      300
atgtgagagg agggacagag gcagtcttac acaagctgtg ataaaaattg catncagttc      360
aaccagtttc ttacnttatt ctaatgnnga ggaagtgtgn gaagagcaca aagtcaga      418

```

<210> 446

<211> 361

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(361)

<223> n = A,T,C or G

<400> 446
ctgtccaatn acaacaggac cctcactcta ctcagtgtca caaggaatga tgtaggaccc 60
tatgagtgtg gaatccanaa cgaattaant gttgaccaca gcgacccagt catectgaat 120
gtcctctatg gcccagacga cccacacntt tccccctcat acacctatta ccgtccaggg 180
gtgaacctca gcntctcctg ncatgcagcc tctaaccacac ctgcacagta tccttggctg 240
attgatggga acntccagna acacnacaca agagctcttt atctccancn tnactganaa 300
gaacagcgcg actctatncc ttccaggggg ggggggtggg gnntgngggac cttncggggc 360
c 361

<210> 447
<211> 321
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(321)
<223> n = A,T,C or G

<400> 447
ccagganant ggttcccaa aggggacctc acccgccccg agctctggag ccgctgacgc 60
tcgcatccag gacatttgag atgggaatcc aaataggcta cttgnaaaag acgtgctgca 120
ngcagccctg gagagactca tggagttcat tgtacattac tccatctacc gaggcagcgc 180
atggcatgac tnaacggctt gnaacaaaca canaaattac caccacaaac attcaggaac 240
caaataat ctgctatggt cacaccacag acaatgcagg aagaggcttt ttattgctng 300
ngtnggtttt caaatcatgt t 321

<210> 448
<211> 325
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(325)
<223> n = A,T,C or G

<400> 448
ccagcttcaa ctttttagta tagaagatac aggatcacaa aaaggagact acgctttgca 60
aacatagcat caaaattcaa cttttctctt tgcagtttat ccatggngtc agcatacctt 120
gcaaggggaag ctacttacat caaataactt ttctatatac atttcctcat tgaccttttc 180
tcaaagaata tcttggtttt gccgaacaaa cataatatag gngtctgcca gatccattcc 240
tggtttctgt ngtgaaggaa aagcaggggg aacaaaataa tatcagggtc tcaatngtga 300
nattattatt taatcatacc ctgan 325

<210> 449
<211> 123
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(123)
<223> n = A,T,C or G

<400> 449
 cattaatntt ggaagcgatg gtgtggatta catcagtgtt agggcatggt gtggatatta 60
 ttacattann attggaagcg atggtgtgga ttacatcagt gatagggcac ggtgtggata 120
 tta 123

<210> 450

<211> 328

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (328)

<223> n = A,T,C or G

<400> 450
 ctggcaattt tgagctgccg gttatacacc aaaatgttct gttcagtacc tagctctgct 60
 cttttatatt gcttttaaatt tttaaagaaa ttatattgca tggatgtggt tatttgtgca 120
 tattttttta caatgcccaa tctgtatgaa taatgtaaac ttcgattttt ttttaaaaaa 180
 attagatttt agctggagct tttgactaat gtaaagtaaa tgccaaacta cgcacttgat 240
 ngggatgttt ttgtaangtt aattttctaa gactttttca catccaaagt gatgctttgc 300
 tttgggtttt aactgtttca acntnggn 328

<210> 451

<211> 209

<212> DNA

<213> Homo sapien

<400> 451
 ctgccttggt tcaacagaca tgcaaagatc ctaggagaca gtcccatag accttcagac 60
 attaaaaagg gagccgtaca gtttgtttga agcacttcgt cttaccatt tatgcagggg 120
 cccaggaata cttacacaca gccagaatga ggttcccaa ggacttacat taattatggc 180
 tcttgcttcc tttcacaat gagctgagg 209

<210> 452

<211> 457

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (457)

<223> n = A,T,C or G

<400> 452
 ctgtctantc ccttcaagag ctgtttatag aagcttgaga atggggtaaa aatttctgct 60
 agcaaaatca agttcttttt gaaattttat cagtaatcca gaatttagta gtccatgcct 120
 tctcactcag catttagaaa taaaaatgtg gtttcttaaa cgtatatcct ttcattgata 180
 tttccacatt tttgtgcttg gatataagat gtatttcttg tagtgaagt gttttgtaat 240
 ctactttgta tacattctaa ttatattatt tttctatgta ttttaaatgn atatggctgt 300
 ttaactcttg aagcattttg ggcttaagat tgccagcacc acacatcaga tgcagtcatt 360
 gttgctatca gtgtggaatc tgatagagtc tngactccgg ccacttgagg ttgtgnactc 420
 caaagctaag gacagtgatg aggaagatgg catgtgg 457

<210> 453

<211> 277
<212> DNA
<213> Homo sapien

<400> 453
ccaattgatt tgatggtaag ggagggatcg ttgacctcgt ctgttatgta aaggatgcgt 60
agggatggga gggcgatgag gactaggatg atggcgggca ggatagttca gacggtttct 120
atttcctgag cgtctgagat gttagtatta gttagttttg ttgtgagtgt taggaaaagg 180
gcatacagga ctaggaagca gataaggaaa atgactacga gggcgtgac atgaaagggtg 240
ataagctctt ctatgatagg ggaagtagcg tcttgta 277

<210> 454
<211> 198
<212> DNA
<213> Homo sapien

<400> 454
gttaaaagat agtaggggga tgatgctaata aatcaggctg tgggtggttg tgttgattca 60
aattatgtgt tttttggaga gtcattgctg tggtagtaata ataattgttg ggacgattag 120
tttttagcatt ggagtaggtt taggttatgt acgtagtcta ggccatatgt gttggagatt 180
gagactagta gggctagg 198

<210> 455
<211> 608
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)... (608)
<223> n = A,T,C or G

<400> 455
ctgagcaagc taaggaccag gggcaactag accctaataa tngtacttt tgaaaatgat 60
acaaactacc ttggttgtaa gaagtgcagg ttgaacactt taggagaaca gtcttcaaac 120
tggcaattca aaatttccca ttatatgtga ataaaattgg aaggatgtta aatgtccatg 180
gaaagtactt cttgtaagtt aggatgcctt atactgaggc tttanaatga aagtacactt 240
cacaaatgga atagtgaaca taaattacca gaagtcaaga taatagtcac actagtaagg 300
taagcaaggt aaattccctt atacacaaaa attattttga tgaccttttt caataatgaa 360
tctgaaatga agtggtttta aaagctccct aaacacaaaa cgaacataaa actgcttaat 420
aacttttagag ctcatgtaat attcttgctg aaaacagtta ctgaaattac cagcgaaatg 480
atggaatatc tttaaagcag gncactcngt ataactctgga ataatttcac ttgctaactt 540
ttaagaagta ttctctggac tataaatcnt gggcaaatag acttcactt tattattacc 600
ccaaatta 608

<210> 456
<211> 467
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)... (467)
<223> n = A,T,C or G

```

<400> 456
cctggacctg tgtaaacctt caaacactct tttttacatt aggtcgtgaa gttaaatttt    60
ttactgtttc tgtgctacag actcttcaaa gggaaatagt taagtcaatt tcaaagaaaa    120
tgaccagcac atttttaaaa cattagaaat gatttgactt tgactatcta ctgccaaaaa    180
aaggttaagg aatttgtaat gagaagctaa aaactttaag gaattttaag gaactcaaaa    240
caaaaactca ttaaattgtaa ttaaagttaa ttctacaaat aaagcctctt aatacatttc    300
tataatagtc acttaagact taaattcaaa cactagcaaa ccacaaaatc agactgtntg    360
actgacatcc aaaagataaa tataaatcaa aatccgaccc cagcattagc caaggggtag    420
gtgttcctct tgaggaaggc aggaattcct cttctgccac ctgttg    467

```

<210> 457

<211> 183

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (183)

<223> n = A,T,C or G

```

<400> 457
ccaaattttt tacttttaac actgaaaaca gaggaagtta ataaaaatth taacctataa    60
agtccccctg ttgttagtca ttaacagcag attgtcagat aagactggta aaatgatggc    120
tgctaagcat ttgatgatcc aggcgcagga tgatcaaact gcagcagatc atgcacgtga    180
cag    183

```

<210> 458

<211> 445

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (445)

<223> n = A,T,C or G

```

<400> 458
gaaaaatata aagccaaaaa ttggataaaa tagcactgaa aaaatgagga aattattggt    60
aaccaattta ttttaaaagc ccatcaattt aatttctggt ggtgcagaag ttagaaggta    120
aagcttgaga agatgagggt gtttacgtag accagaacca atttagaaga atacttgaag    180
ctagaagggg aagttgggta aaaatcacat caaaaagcta ctaaaaggac tgggtgtaatt    240
taaaaaaaac taaggcagaa gggttttgga agagttagaa gaatttgga ggccttaaat    300
atagtagctt agtttgaaaa atgngaagga ctttcgtaac ggaagtaatt caagatcaag    360
agtaattacc ancttaatgt ttttgcntt ggactntgag ttaagattat tttttaaatc    420
ctgaggacta ncattaatgg gacag    445

```

<210> 459

<211> 426

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (426)

<223> n = A,T,C or G

<400> 459
cctatgatan cttctctagc tatcatactc caatcagcaa aaaatgagaa aatgttgaga 60
aatagaagat aattcctcat ttaaggccac cttctagaat ttgtgcttaa gattctgctt 120
tcttctcatg ggccagcact tcggcaactg gcaaaaatta ggtgtacagg gatctaggta 180
atactgttta tttagagcaat aatatattgt gctaacgttc aggcaccta ttactgagaa 240
ataagggaaa atgagtgtaa agtacaacta agagtctcgg cgacagggaa aaataccatc 300
agttaaatat ccatagtcct agagcattta tgtaaaactg caatntgaat cctgcaatac 360
atnttggtt tttccctcag tgataccatg tgagggaagn ngctctgtca aggcgggccg 420
gataga 426

<210> 460

<211> 348

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (348)

<223> n = A,T,C or G

<400> 460
ccaaatttta aaatgttatt tttcatatca tttataacct tgtcacatc cacttaaaga 60
agtttggtta tatttctactg aaaattttct tccagagtag gttttttttc gtgggttggg 120
gggtaacttt actacaatta gtaagtntgg tgcagaatct catgcaaatg aggagtgcag 180
cagngtgata atttaaacad atntaaacaa aaacaaaaaa aatgaatgca caaacttgct 240
gctgcttaga tcaactgcagc ttctaggacc cggtttcttt tactgatnta aaancaaacc 300
aaaaaaanta annacnttgt gcctgaaatg aancttggtt ttttntna 348

<210> 461

<211> 378

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (378)

<223> n = A,T,C or G

<400> 461
ccactaagac agaacggaat ctagtagaag tgcaccaatg cttcagtcct tcctactcag 60
catggtgagc agtgggtcaat ctgtgccctg tggaaatgat ggcagataat tctggcatgt 120
gtaaataata ataaataatt cacttggtgc aggcagtatg tctatgaatt aaaacctagt 180
gtgtacacag tgccatcatg tgttacagcc ccacagtagg aatctacacc aaaatattta 240
ttagaaggaa tttggtccgt actacatcac gctttccgga gggtaaaaaa taaagtccat 300
ctatagacat ttcaccacag acccagagac tgagtctggc taaaacctgc aaaatgtcta 360
taacaaaagn ggatggct 378

<210> 462

<211> 197

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(197)

<223> n = A,T,C or G

<400> 462

gcgagggtcca cactattaaa agctgttggg taattgaagg tgatataaaa tgactgtcnt	60
catttggagt gngcagcaca nttacttcat gttgtcang tttanaacaa tntccctgn	120
aagttctcac acagatnggn agaaatcata cctantntg gtnaatcact atggcagccg	180
tngaagaatn taagaga	197

<210> 463

<211> 279

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(279)

<223> n = A,T,C or G

<400> 463

cataagtgat gangaggnaa aatcantnaa taagcctaca acntagaata cattaaaact	60
tgcacatata catgttcaca gcatgtatac aatgataatc cctacggttt aaccaagtta	120
tggttccctt ctacagcaga cacaaaacca aggtgaacta ggtnggcaga tgtanaggga	180
ataccaaaaa aagggtaatn ngntcactga ttctgaagna tntgactgan catactgagc	240
ttctgnactt tgggaatgca tnnagгнаac aatatcttg	279

<210> 464

<211> 552

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(552)

<223> n = A,T,C or G

<400> 464

gatgggttga taggtgcagc aaaccaccct ggcgcatgtt taccaatgta acaaacctgc	60
acatccttga cagggtactcc aaaactaaaa gtaaaaaat ctaaaagaaa aaagaaaaag	120
aattaaacc aaaatcactt ccccatctgg acttgattta gatgaaaagc ttctggactt	180
tgagctgatg ctatagtggg ttgaaaattt tggggtcttc agaaggggat gaggatatat	240
tgcagagag agcaacatga atcatngaga gccagagtat agagagnggt gggtagactg	300
taggagagcc ctcaatgatc ccggtgtct tgtattcgcg ttgcacttac ttgtataata	360
tggcagatgg gatgtgatgt cactttcaag attangttat aaatagacta tggcttcaat	420
cagagggttt tcttctctgt ctanctctct tttgggtagn ttcatctga gagaaagcca	480
nacctcngcc gcnaccacg ctaaggggcg antccagcn cactggcgcg cngttactag	540
tgatccgng ct	552

<210> 465

<211> 444

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(444)

<223> n = A,T,C or G

<400> 465

```

ccactcttgg tagaaacctt gaaactttca ccttgctggg ctttagcaaa gtttcctttt    60
acagttctgt ttatgagctt cagctactga taaagcactt cctgaacttc tctattatca    120
tagngaccct ctgaataacc tgagtgactg gctcggcaat tcgctttata accattctta    180
ttcccaaagt tggagcacat aaacatttag atgtcttttc ctgtaaaata ttctagacat    240
ttacccaaac tctagttcaa catatactca acttgcactg tatatctccc tgcttttttg    300
agacagagaa gaaattcagg aggtgnccca tctccagagt ttctctgttg gaaagcagcn    360
atcaagaanc ctttaaaaaa ttggtgtnaa gcntngccnc ctgcagaaat gcntngcccc    420
acattattct tctgggnaa agna                                           444

```

<210> 466

<211> 381

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(381)

<223> n = A,T,C or G

<400> 466

```

cctactatgg gtgttaattt ttactctctt ctacaagggt ttttcctagt gtccaaagag    60
ctgttcctct ttggactaac agttaaatat acaaggggat ttagagggtt ctgtgggcaa    120
atttaaagtt gaactaagat tctatcttgg acaaccagct atcaccaggc tcggtaggtt    180
tgctgcctct acctataaat cttcccacta ttttgctaca tagacgggtg tgctctttta    240
gctgttctta ggtagctcgt ctggnttcgg gggctcttagc tttggctctc cttgcaaagt    300
tatttctagt taattcatta tgcannaggt ataggggnta gtccttgcta tattatgctt    360
ggttataatt tttcatcttt c                                           381

```

<210> 467

<211> 95

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(95)

<223> n = A,T,C or G

<400> 467

```

cctatanatt ntggnttgta tactgggtcc tgaaaaccct cttgngctc tgtttttaag    60
gagctgaanc caanganccg caataataat actttt                               95

```

<210> 468

<211> 224

<212> DNA

<213> Homo sapien

<400> 468

```

cagtgggtct ctgatgcctt gcctgcagca gaaggaggga gcagagatca agaggaagga    60
aaaaatcata tgtacttatt tgaaggtaaa gattattcta aagagcccag taaggaagac    120
agaaaaatcat ttgaacaact ggtaaacctt cagaaaaccc ttttggagaa agctagtaaa    180

```

gagggccgat cactccgaaa taaaggcagt gttctcatcc cagg 224

<210> 469
 <211> 416
 <212> DNA
 <213> Homo sapien

<400> 469
 ctgagttcta gttcaaaagc tttatcctta acttcgcat gtactatgta aattctagaa 60
 tagaaaaggg aaaggtaaga ttttggtaac ctccaaacat tgaagtagtt cacagacca 120
 aagtcagtac aaattagaat gtccatccat aataaaagta tctataaaat tacacagaca 180
 cattctacat agtatttaac attagagaag acaaattaca cagggactga aataaaatga 240
 aacatctact ctcccacaaa atgttgaata tacctaatac acccaagttc agtttatttt 300
 tgcacattgc tttagagata taacttggct gggcacagtg gctcacacct gtaatcccaa 360
 cactttggga gaccaaggcg gatggatcac ttgaggtcag ttcgagacta gcctgg 416

<210> 470
 <211> 376
 <212> DNA
 <213> Homo sapien

<400> 470
 caccttttaa ctgtatcaca aagtctgttg ctgtggttac agcctttgtt tccagtgatg 60
 ttttgtccat gctttccccc aacccttaac aatgggtact caaaagaatg aaataatgag 120
 tcatctatc gggaatatgt taaaatatcc ctctttatca ttacatttca ctgcttagaa 180
 actaggctgt aattcaaggc aacagttaag tctgagaact gttaaaaaaa tctttgattt 240
 tttttcattt ttaagaaaaa cctgcctatt taattgttca gacttgtaag aggttcttca 300
 attacatcct ttttggttaa tgtattattt ctggaacaag tagataaaat tctacgcagt 360
 aagcataata aaaatc 376

<210> 471
 <211> 357
 <212> DNA
 <213> Homo sapien

<400> 471
 ggcttcgtat aatggttctt ttgtcacccc tgcacgacga tttcgtacc cgtacaactc 60
 tgacaaggga acgaaatgct tctgtgtatt cacctagtgg tctgtgaac agaagaacaa 120
 caactccacc ggatagtgga gtactgtttg aagggttagg catttcaaca agacctagag 180
 atgttgaaat tcctcagttt atgagacaga ttgcagtaag gaggccaaact acggcagatg 240
 aaagatcttt gcggaaaatt caagaacaag atattattaa ttttagacga actctttacc 300
 gtgctggtgc tcgagttaga aatattgaag atggtggccg ctacagggat atttcag 357

<210> 472
 <211> 557
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (557)
 <223> n = A,T,C or G

<400> 472
 cngagatgac atttacaatc tcttgaaang cagcagatgg cactctggtg cttcctatga 60

agcaacatgc	ttgaaatcaa	gggccaacaa	ttgttgtagg	aaagcaaaat	atacctctaa	120
cacctacgtt	taccaaaaaa	gctgacatct	caaactctga	gttggtgaga	ctcaaatttc	180
tcatcccaa	agaagcctat	tacggtagtg	tgntggatgc	tttttgatc	tctgataggc	240
aggcactata	atggggggaa	atacttctga	ataaaaacat	tggctgtctt	gcaactgtgc	300
atataatgtc	tattcaaggg	ggcagtgtgc	ctagcatgat	cctgaaatgt	tgagataaaa	360
ggaagtgtgc	attaaagcac	tatttgtctt	atatgaaaag	agtgactcta	tcttccagta	420
aacaagantt	cctgcaatga	aaaagaaatt	tttctcttca	ttatctataa	actatacaaa	480
ataaccttcc	tttttaacct	aagactcaaa	cattnatatt	tgattttatt	ctatttgata	540
ccaattggta	tgtccag					557

<210> 473

<211> 264

<212> DNA

<213> Homo sapien

<400> 473

cctccatcaa	cagaaaggat	aaagaccctt	tcgggtctcc	tcattaattc	tgaactggaa	60
aagccccaga	aagtccggaa	agacaaggaa	ggaacacctc	cacttacaaa	agaagataag	120
acagttgtca	gacaaagccc	tcgaaggatt	aagccagtta	ggattattcc	ttcttcaaaa	180
aggacagatg	caaccattgc	taagcaactc	ttacagaggg	caaaaaaggg	ggctcaaaaag	240
aaaattgaaa	aagaagcagc	tcag				264

<210> 474

<211> 165

<212> DNA

<213> Homo sapien

<400> 474

aattcagctt	ccagaggccc	ttattagtcc	ttgttgacag	aaacatagat	ttggcaactc	60
ctttacatca	tacttggaca	tatcaagcat	tgggtgcacga	tgtactggat	ttccatttaa	120
acagggttaa	tttgaagaa	tcttcaggag	tggaaaactc	tccag		165

<210> 475

<211> 417

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(417)

<223> n = A,T,C or G

<400> 475

aagttctctt	cttgttttta	acacattcct	gataacttct	aaagatgacc	aaaataaaaac	60
agaatatcta	cagagatcat	tttctgaatt	ttttgtacat	ccaaggataa	caacataaaa	120
aaaataaaaac	tggacagcat	tccacatcca	agtgacacaga	accatttttg	caagattaaa	180
taatgtaaac	attgggaaca	gccaaatcag	cgaagaatgc	caacacctca	aaacacctgg	240
tggtgcgcgt	tcattaagtg	gttcaaaatc	cagatctata	attgcgcaat	attcaccgta	300
tataaaaaga	aatggatatt	aatttttgaca	aatagctgca	actgagactt	ctttttattt	360
ctttatatgn	gnatatagtg	aattttttatt	atttttaaaa	ttttatttat	tttttta	417

<210> 476

<211> 321

<212> DNA

<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(321)
<223> n = A,T,C or G

<400> 476
catttaataa caaaaacaac ctgtacggaa aaccnaagg caaccacata gcatatgtaa 60
aatgtgcaaa tacactttaa aatgcangtt attctatagc anttgcaaga tagaatttca 120
ctgtaattag ggaatctagc tcatcctaac ttaatagnct tttgcatgtn tagacaatgc 180
aattctacaa ggnacnactc agcgttgatg cttaaagtatg aaacacatcc tcagattatt 240
catccgaaaa tattaaaata gcntcatggt ttattattct ttaatgagtc ntgagctcat 300
ttctaaagct tcataaagca t 321

<210> 477
<211> 546
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(546)
<223> n = A,T,C or G

<400> 477
gctgtgggta tattgtaaat gaagcatcta acatgtgcac aacttgcaac aaaaactcct 60
tggactttaa atctgtcttt ctcagtttcc atgtgtgat tgacttgact gatcacacag 120
gcacccttca ttctgtagt ctcacaggaa gtgttgctga ggagactttg ggctgcacgg 180
tacatgagtt tcttgcaatg acaaatgaac agaaaacagc attaaagtgg caattcctct 240
tggaaagaag caaaatttat ttaaaattcg ttctatcaca cagagcaagg agtggattga 300
aaattagtgt actctcgtgc aagcttgacg atcctactga ggcaagcaga aacttgctctg 360
gacaaagaca tgtttaaaac ggtctatcat ttggaactct ggaaaagtat aagagtttta 420
actcccttta aaatggaata ttaatttgaa aattatgggg aaaattgcat tttgtttaca 480
tgtggtgaac atgtttctag aaattggtat ggcgggaagg gggctgggtg agtctgaagg 540
acctcn 546

<210> 478
<211> 100
<212> DNA
<213> Homo sapien

<400> 478
aagaaaagtg gtaaaatcaa gtcttcttac aagagggagt gtataaacct tggttgtgat 60
gttgactttg attttgctgg acctgcaatc catgggttcag 100

<210> 479
<211> 508
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(508)
<223> n = A,T,C or G

<400> 479
 gnnttcctaaa ttcttctaac tcttccaaaa gccttctgcc ttagtttttt ttaaattaca 60
 ccagtccttt tagtagcttt ttgatgtgat ttttaaccaa ctcccccttc tagcttcaag 120
 tattcttcta aattggctct ggtctacgta aacacctca tcttctcaag ctttaccttc 180
 taacttctgc accaccagaa attaaattga tgggctttta aaataaattg gttaccaata 240
 atttcctcat ttttctcagt ctattttatc caatttttgg ctttatattt ttctatcttc 300
 tatacttctc caatacttgt cttagcttgt ttttcatttt ctatctgaaa ctcttgacaa 360
 tatcttctaa tttccctatc ttctctattc ttttcttcgc ctccccgtac ttctgcttcc 420
 agntttccac ttcaaacttc tatcttctcc aaattgttca tcttaccact cccaataatc 480
 tttccatttt cgtgtagcac ctggncag 508

<210> 480
 <211> 81
 <212> DNA
 <213> Homo sapien

<400> 480
 ggtgcccttt tctaactact cacaacaaaa ctaactaata ctaacatctc agacgctcag 60
 gaaatagata agggaaatga c 81

<210> 481
 <211> 306
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)... (306)
 <223> n = A,T,C or G

<400> 481
 tcgccttcgg ccgccgggca ggtaggggn acaagacgct acttccccta tcatagaaga 60
 gcttatcacc ttcatgatc acgccctcat agtcattttc cttatctgct tctagtcct 120
 gtatgccctt ttctaacac tcacaacaaa actaactaat actaacatct cagacgctca 180
 gggaatagaa accgtctgaa ctatcttgcc cgccatcatc ctagtcttca tcgcctccc 240
 atccctacgc atcctttaca taacagacga ggtcaacgat ccctccctta ccatcaaac 300
 aattgg 306

<210> 482
 <211> 582
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)... (582)
 <223> n = A,T,C or G

<400> 482
 ggggggaaca gtcattatac attatttaga ctcattcctt cttccagtgc cttatgatt 60
 atttcctacc ttaccattg atcttaaaact gngcaggcta aaaagaggaa ccagaactcc 120
 cttaagcact tttaagacta tttaaaaaat aaagntttgt tggcattgaa gagtaagctg 180
 cttaaggagc tgaatgaaaa gatagtaccc tttgtggctg tatgaagaga gaaactgaat 240
 ttctatccaa gagaccttaa tntagcctat tagggaatta tcttcccaa aagtacaagt 300
 aattttgcac tgcaggagaa ggataagtag atttgattta catcacattt tatacacacc 360

```

tttcaagang gagaaatctg cttcataaat agnaggaatc tatgettaaa ctnaacattt 420
aatggtgacn tcttacaaca gccttgaaaa nnattggaan tcngacntga nggnggaaac 480
tggaanaaag aatatctttc tcttctgcat cctttinatcc tcaaacttag catggattca 540
cacgctgagg aaangttngg tnacnaccng aacattttaga ta 582

```

<210> 483

<211> 275

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (275)

<223> n = A,T,C or G

<400> 483

```

gcctcactaa aataacagat ttcagtatag ccaagttcat cagaaagacc caaatggaat 60
gatttacaaa atagaacact ttaaaccagg tcagtcctat cttttttag tagaaggcta 120
tcagtcataa cacaatttcg cgtacacctc tgctcattat ggaattacac ttaaaacgaa 180
tctcaagagg gtgaccattg ttgtttcaga taccatccct aaggagagt gttaacagga 240
agattgccag ngttactgat ggaaagaagc gcttg 275

```

<210> 484

<211> 434

<212> DNA

<213> Homo sapien

<400> 484

```

catatttcca caggccaatt tctttctggt tttctgctaa gctatttcag catttttagct 60
tttctctctt gctttgttta ctcatgattg ccagatggct acgttacctc taagcatcag 120
atcctcacia attaatggtt aaatgtaagg gagggatttt actctcttgc attaaaaaaa 180
agctttattg agatataatt tactgtaaca ttgactcatt taaagtatgc tagtcaatag 240
accaaactct gaataaactc ccattcacia ttgctacaaa gggaataaaa tagctgggaa 300
tatagctaac aagggagtg aagggcctct tcaaggagaa ctacaaacca ctgctcaaga 360
aataagagag gatacaaaca aatggaaaaa cattccatgc tcatgaatag gaagaatcaa 420
tatcgtgaaa atgg 434

```

<210> 485

<211> 291

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (291)

<223> n = A,T,C or G

<400> 485

```

ncaccactgc agccctacat acagttgaaa aaaaattcca ttctgttaac atttgtttta 60
taagttttca cgcaatacac aaaaaacccc tctgcacttc ttgtaaagaa caaaaaagat 120
acacaacagt taagcgtaaa gatcacaggc aatagcattc aaacatggat gtgggtagag 180
aaaggagtac ctggcatgag tacctgctta gtttgactga atccttgatt tttaatattg 240
cttttcatgg gccgctcaca acaccaacgc tgtgtgaggt atggtagtca g 291

```

<210> 486

<211> 274
<212> DNA
<213> Homo sapien

<400> 486
ctgtaatat gtagttgctc cagaatgtca agggcagctt acggagatgt cactggagca 60
gcacgctcag agacagtga ctagcatttg aatacacaag tccaagtcta ctgtgttgc 120
aggggtgcag aaccggtttc tttgtatgag agaggtcaaa gggttggttt cctgggagaa 180
attagttttg cattaaagta ggagtagtgc atgttttctt ctgttatccc cctgattggt 240
ctgtaactag ttgctctcat ttttaatttca ctgg 274

<210> 487
<211> 184
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(184)
<223> n = A,T,C or G

<400> 487
tggcaccaag attctcagct caccgtacca gcatctgatt gtcggactac ctgctgcttt 60
ccctgatatt tatacatgat attcgnaaaa tgtaaagaag ctattattca tacagacatc 120
tagagaagga gngaagnntt taaaaaata aaaaaatact tatttcaagc tttagctgtg 180
ttct 184

<210> 488
<211> 393
<212> DNA
<213> Homo sapien

<400> 488
ctgcattttt attgcatct gcagatgaac tggaaaatct catthttacaa cagaactggg 60
acagacgacc accatattca ctgaggtcta aatttgcagt ttccactaat gacattttga 120
tttcccaaca gagatacttc tggcttact gcacagtctt ttaagagaaa tacttccatt 180
atgccacatt gtccttgatc cgtaagtgat gtgttaaggt gcttcaaagg aactctgacc 240
tctgaagta ttgagctact ttagtatgtc cagcctattg ctttttgttt tagtgtgtca 300
ccataaatat caggggcata aaaggctatc tattcttaat tcaaggataa aacagaagaa 360
gcttgtggta taaaacaata gttcaagatc cag 393

<210> 489
<211> 607
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(607)
<223> n = A,T,C or G

<400> 489
gtgcttatgt acttaagggg aactactcta actgggtgaa gaggatgatg aagcatccat 60
gtccctacaa aggatatgaa ctcattcttt ttatggctg catagtattc catgggtgat 120
atatgccaca ttttcttaat ccagctatc atcgatggat atttgggttg gttccaagtc 180

```

tttgctattg tgaatagtgt cgcaatgaac atacatgtgc atgtgtcttt atagcagcat      240
gatttataat cctttgggta tatacccagn aatgggatag ctgggtcaaa tggattttct      300
agttctagat ccttgtggaa ttgccacact gtcttccaca atgggtgaac tagtttacag      360
tcccaccaac agtgtaaaag tggtcctatt tctccacatc atctccagca cctgttggtt      420
cctgactttt taatgattgn cattccaact ggtgtgagat ggtatatcac cgtgggtttg      480
atttgcatth cctgatggc cagtgatgat gaacnttttt tcatgtggtt tttggctgca      540
taaattggcct gcctttnta cttctataaa atttttcann tcttattatt attcctgggg      600
gnttaag                                           607

```

<210> 490

<211> 179

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (179)

<223> n = A,T,C or G

<400> 490

```

cttctaggaa tactagtata tcgctcacac ctcatacct ccctactatg cctagaagga      60
ataatactat cactgntcat tatagctact cccataaccc tnaacacca ctccctctta      120
gccaatattg ngcctattgc catactagtc tttgccgcct gcgaagcanc ggtaggacc      179

```

<210> 491

<211> 399

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (399)

<223> n = A,T,C or G

<400> 491

```

cctctacctg taatcacatt aatttttcta aagacagggg nggtgttttg aagataaatg      60
tcattagtct atgataatag catcatagga caattagcca ttttagactt gaccatattt      120
tctcttttta gcatatagcc atcttgatat ttagngggga gactactcca atggagcaac      180
agtttcattt tacatgattg gatttagaaa ttacaaatt ttaaactcat aagaattcta      240
aataatttga aaatggaaac atttgaccca cagtctagca gcataaatac atttataaaa      300
tacttcattg ttgatcttag gtcattgatt taaaacagaa tttggtgact atgggcaggt      360
ggagggggcc ngtgaggaag gtataaaaga gaaatcttt                                           399

```

<210> 492

<211> 482

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (482)

<223> n = A,T,C or G

<400> 492

```

ctccacctta ctaccagaca gccttagcca aaccatttnc ccaaataaag tataggcgat      60

```

163

```

agaaattgaa acctggcgca atagatatag taccgcaagg gaaagatgaa aaattataac 120
caagcataat atagcaagga ctaaccctta taccttctgc ataatgaatt aactagaaat 180
aactttgcaa ggggagccaa agctaagacc cccgaaacca gacgagctac ctaagaacag 240
ctaaaagagc acaccgtct atgtagcaaa atagtgggaa gatttatagg tagaggcgac 300
aaacctaccg agcctggtga tagctggttg tccaagatag aatcttagtt caactttaa 360
tttgcccaca gaacctcta aatccccttg taaatttaac tgttagtcca aagaggaaca 420
gctccttgga cactaggaaa aaaccttgta gagagagtaa aaaatttaac acctatagta 480
gg 482

```

<210> 493

<211> 207

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(207)

<223> n = A,T,C or G

<400> 493

```

cataaatatt atactagcat ttaccatctc acttngngga atgctagtat atcgctcaca 60
cctcatatcc tccctactat gcctagaagg aataatacta tcactgttca ttatagctac 120
tctcataacc ctcaacaccc actccctctt agccaatatt gtgcctattg ccatactagt 180
ctttgccgcc tgccaagcag cggtagg 207

```

<210> 494

<211> 283

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(283)

<223> n = A,T,C or G

<400> 494

```

ccaattgatt tgatggtaag ggagggatcg ttgacctngt ctgttatgta aaggatgcgt 60
agggatggga gggcgatgag gactaggatg atggcgggca ggatagttca gacggtttct 120
atttcctgag cgtctgagat gttagtatta gttagttttg ttgtgagtgt taggaaaagg 180
gcatacagga ctaggaagca gataaggaaa atgactatga gggcgatgac atgaaagggtg 240
ataagctctt ctatgatagg ggaagtagcg tcttgtagac cta 283

```

<210> 495

<211> 590

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(590)

<223> n = A,T,C or G

<400> 495

```

tatgtatata attttcttag ttactagcat agagaaatta ctgattttaa aaaacatttc 60
aaattctagc atgttgtagg attctattgc cttttctaaa aagtacatct tgcttatccg 120

```

```

atttctaaca aaactattta atttgaagaa gggagaatga atttggataa aaagcaaaaa 180
tttaaaggta ctcaaattta ggcaaaccat taaagcaatc ttagtttaca gttaattggg 240
tagaatggtc aacactttct tcaggttagt tcatggagtg gatatgcatt gatagaacaa 300
cttagagatg cttttacagt tgagaaagct cattatatat gttatcttta agaatcagct 360
tatttatttc atatgtttgt tctttaagaa gaccaaagag ccctgcaaat gaatgttgat 420
ttgttttttt gtttgtttta tatttttgta gagataagat ctcactttgt tatgttgccc 480
aggctggctc caaactctca acttgaagtg atctgcccac ctcagcctcc caaagtgggtg 540
ggattacagg catgagccac cgcacctgga cctgcccggg cggncgctcg 590

```

<210> 496

<211> 307

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (307)

<223> n = A,T,C or G

<400> 496

```

ggagattagt atagagaggn anacnttttt tcnggatatt tggtcacatg gataagtggc 60
gctggcttgc catgattgtg aggggtagga gccaggtagt tagtattagg aggggggngn 120
ttaggggggc tgaggagaag gttggggaac agctnaatag gttgttngnt gatttgnta 180
aaaaacanta gggggatgat nctaataatt antgctgtgg gtggttgtgn tgattcaaat 240
tatngccttt ttcggagann catgtcangt ggtagtaaata ataattgttg ggaccattan 300
ttcttan 307

```

<210> 497

<211> 216

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (216)

<223> n = A,T,C or G

<400> 497

```

cattttcttc ttggtttctt cagttaagtc aaanngncac gttcctcttt ccccatatat 60
tcatatattt ttgctcgta gtgtatttct tgagctgttt tcatgttgtt tatttctgt 120
ctnggaaatg gtgttttttt ttgttgttgn tggttttttt tttttttttt aaactnggna 180
ccncnaantt gaaaaaatgn ttntttttcc ctnaca 216

```

<210> 498

<211> 375

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (375)

<223> n = A,T,C or G

<400> 498

```

gaatttcctg gcaccttttc tcgctagaga agattnngtg tgactggggt gcctataagc 60

```

```

catatagata caaactttta tctctaatac caagtcttag agggatatat taatagatct 120
aataaattta ttcttagact tattgtttca tgggntagt agtctttgct actggagaca 180
atacagactt gtcagttttt ttaaaaaaaa aaaatttgcc aagctancac attaaaaana 240
tntcctaagg ctntcatttt atgaggatga ttataaacnt ttntgngata aatatcacca 300
taataaactg ttaagtacaa ctgcnggccc cccttanagn gaattcctnc agttanaaat 360
ttatTTTTTTT gccaa 375

```

<210> 499

<211> 215

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(215)

<223> n = A,T,C or G

<400> 499

```

ccacnaaagc agaagcttaa agcatagtag taaagaggnn aaaaagaagg acgaaaataa 60
atcagatgac aggatggta aagaagttga cagtagtcat gaaaaggcca gaggtaatag 120
ttcactcatg gaaaagaaat taagtagaag gttgtgcgaa aatcggagag gaagcttgtc 180
acaaaaaaaa aaaaaaaaaa aaaaaaaaaa gtttt 215

```

<210> 500

<211> 489

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(489)

<223> n = A,T,C or G

<400> 500

```

ccactacgat aagcaggtag ctgggttttg tagtgagntt gtcctttaag ttacaggaac 60
tctccttata atagacactt cattttccta gtccatccct catgaaaaat gactgaccac 120
tgctgggcag caggagggat gatgaccaac taattcccaa accccagtct cattggtacc 180
agccttgagg aaccacctac acttgagcca caattgggtt tgaagtgcac ttacaaggnt 240
tgtctacttt cagttcttta ctttttacat gctgacacat acatacactg cctaaataga 300
tctctttcag aaacaatcct cagataacgc atagcaaaat ggagatggag acatgatctc 360
tcatgcaaca gcttctctaa ttatacctta gaaatgttct cctttttatc atcaaatctg 420
ctcaagaagg gctttttata gtagaataat atcagtggat gaaaacagct taacatttta 480
ccatgctta 489

```

<210> 501

<211> 286

<212> DNA

<213> Homo sapien

<400> 501

```

aaaaacactc aaacacagcc ttggaggagg gagtcagttt taaaagactc ttataaaagt 60
aatatactgc tagctctgaa gaatcggagg ctaaaatcat ctcttcaagt cccagggaa 120
tcccaaagaa ctccagggga aggtgggatg ggccagagag ctctggaagc ttccaggtct 180
gttgcaagcc tcacctggtc cacagtaggc tcttccaggt ctgtcaggaa cccaggagcc 240
tcccctagca cacagtaggc tcacaaaaag ggagcactgc tgctgg 286

```

<210> 502
 <211> 168
 <212> DNA
 <213> Homo sapien
 :
 <220>
 <221> misc_feature
 <222> (1)...(168)
 <223> n = A,T,C or G

<400> 502
 cctatgattg tgggggcaat gaatgaagcg aacagagntt cgttcatttt ggttctcaga 60
 gtttggtata attttttatt tttatgggct ttggtgaggg aggtaagtgg tagtttgtgt 120
 ttaatatatt tagttgggtg atgaggaata gtgtaaggag tatggggg 168

<210> 503
 <211> 173
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(173)
 <223> n = A,T,C or G

<400> 503
 cctttataat aaattaggca aaaggttcag tgcnnnggcta tantggacaa catgaaactc 60
 cataaaaatg actggatagg gggactgctt gagacttttc ttttgggcat tactaacaga 120
 attcaaagaa attccaacca cgcttatattt tccaaattct actgaaatga gag 173

<210> 504
 <211> 310
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(310)
 <223> n = A,T,C or G

<400> 504
 tagtattcta tttaaaaatt aagttttggg gtctgtaaaa tatacaggac aatgactttt 60
 ttaaaatgta agttaatacc tcctcctcac ttgtcttaat tgaacttagg tgtttattct 120
 taaaggngga ccttgatgaa aatgttgaga tgggaagtgt tattaggcaa aacttggtat 180
 agattttctca tataactctt aattgaccct tagaatttta acaaccgcgc ctggccaat 240
 agactgtttt ttagagtant tttaggctct cancaaaatt gaggggaaaa tacagggtgt 300
 tcccattaaa 310

<210> 505
 <211> 530
 <212> DNA
 <213> Homo sapien
 <220>

<221> misc_feature
 <222> (1)...(530)
 <223> n = A,T,C or G

<400> 505
 cctcaggga cttacaatta tggcaaaagg ggaaggggaa gcaagcacct tcttcacaag 60
 gcatcaggag agagagagaa agagagtagg ggaaactacc ccttttaaac catcatatcc 120
 tgtgagaact ccctcagtat tagaagagca tgagggaaac cgcctccata atccaatcac 180
 ctcccaccag gaccatccct caatacatgg ggggttacaat tcaagatgag gttcgggtgg 240
 ggatacagat ttaaaccata tcagaatggg taatgatatt gttgtatatt accaactata 300
 atcttcttag tggtatagta caataatgta aaaaattgag taaatttggt ttctatatta 360
 ttctgttttt ggaaaacatg tatatagtca gggctgtttg tctcaagaaa atatggtaaa 420
 ctctgctgtt ttggctactg gtgcctagaa tttggggatg tacattgggt ttgattcaca 480
 tgcacatttc cttctagttc acagtaacta tttctaacta tttcccnata 530

<210> 506
 <211> 352
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(352)
 <223> n = A,T,C or G

<400> 506
 cttgaacgct ttcttaattg gtggctgctt ttaggcggta ctatgggtgn taaatttttt 60
 actctctcta caagggtttt tcctagtgtc caaagagctg ttctcttttg gactaacagt 120
 taaatttaca aggggattta gagggttctg tgggcaaatt taaagttgaa ctaanattct 180
 atcttgga accagctatc accaggctcg gtagggtttg cgcctctacc tataaatctt 240
 cccactattt tgctacatag acgggtgtgc tcttttagct gttcttaggt agctcgtctg 300
 gtttcggggg tcttagcttt ggctctcctt gcaaanntat ttctagttaa tt 352

<210> 507
 <211> 370
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(370)
 <223> n = A,T,C or G

<400> 507
 cctaactaga tcttatcaga atagggggga agggngtcgg ttcctcctta ttgagtgtta 60
 atgaccctgt aagatgtaat ttcttttatt tcattctgtt acctagaaaa tctatcacag 120
 cctttagta ttgattgctc aatctataaa gagctcagtt tacagcatga ctgttagtaa 180
 cagggnattt ttaatgagtg actcttcaac acctcagagt ttcactaaat tccaacccat 240
 cagcccagta gtctaacatt aagggtctta ggaaatgaga acttatcacc tttccttatc 300
 atgaaaaggt aacctccagg taaccaaaaa tagaacttcc tctgtgttcg ttttttatag 360
 aaattactgg 370

<210> 508
 <211> 129
 <212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(129)

<223> n = A,T,C or G

<400> 508

ctgttaaaag aacaaactta gcaatatata acagttnngt aacaggattt ttgactattc	60
actttgggag ttatttttaa aaatccactt ttttactgag ttttactaca taccaggcac	120
tgtacttgg	129

<210> 509

<211> 422

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(422)

<223> n = A,T,C or G

<400> 509

ntgggaagtc gtgacatcca tgggaaccca gcgctgtgat gctgggtgtt gngttctccg	60
cgagaagtga ccattgttgg agcaccatcc agagctagtg accantncag tggacagtta	120
gtgggagaat caaaaatcct ttccagaatg tctgtttctc actacntgca ccgggngatt	180
acaggcacca gtgcagngat gattgtactt atttgacaca tactccccgt cntcctggnt	240
nttgttctcg anaanggtgg gtaaatattc caggaaaaan aatgcacatt gaatggatgt	300
gagagaccac attgcctctc ccactgcttt ggggagcact ttcctgtcat ttctaactta	360
ccacntgctt ggtgtactat atgtatgttg tgcctcatat gttgcaaaga actaangtga	420
gt	422

<210> 510

<211> 238

<212> DNA

<213> Homo sapien

<400> 510

ccacctatga attggtggtt tacctactca atggatagca gcacgaggac tgctgtactg	60
cacaaaaaga agacaaaaag attacagtgg accatgggat acagaagcca gcatggcaga	120
cagaagaaaa atagtttggg aacatgtaac tatcctaagt ggaagttttg ttgtaggaaat	180
tatagtaatc acaccacatt acttggcctt tcggtaatgt gaaaaaaaaa aaaaatcc	238

<210> 511

<211> 254

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(254)

<223> n = A,T,C or G

<400> 511

ccnattgatt tgatggtaag ggagggatcg ttgnngctcg tctgttatgt aaaggatgcg	60
---	----


```

tacggatggg agggcgatga ggactaggat gatggcgggc aggatagttc agacggtttc      120
tatttcctga gcgtctgaga tgtagtatt agttagtttt gttgtaagng ttaggaaaag      180
ggcatacagg actaggaagc acgataagga aaatgactat gagggcgnga tcatgaaagg      240
tgataagctc ttct                                                         254

```

<210> 512

<211> 269

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(269)

<223> n = A,T,C or G

<400> 512

```

cctacctgta aactacagta ctttatatat ctatgggntt aataaaaaana aaatccacaa      60
atcttaaaaa ggaacttta atgcagggct atattgaatt ggnaaactgc aacacaaact      120
ggcgcaacat aggtaaatga ataccaatct cactctatgt gatgcaagca tgctactttc      180
ccactaattt aaattacttt caaccactat gagccagaat gcatgcctga accttaaaact      240
gcactttaaa aagtaacatc ttggcctaa                                         269

```

<210> 513

<211> 266

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(266)

<223> n = A,T,C or G

<400> 513

```

ggaggggggt tgtagggggg tcggaggaga aggntgggga acagctaaat aggttggtgt      60
tgatttggtt aaaaaatant agggggatga tgctaataat taggctgtgg gtgggtgtgt      120
tgattcaaat tatgtgnttt ttggagagnc atgncantgg tagtaatata attgttgaga      180
cgattagttt tagcattgga gtaggtttag gttatgnacc gtactctagg ccatatgtgt      240
tgganattga nactagtagg gctagg                                             266

```

<210> 514

<211> 271

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(271)

<223> n = A,T,C or G

<400> 514

```

acatgcaana aatcgagaat cttaaaaaac annacgaanc tgccttgaa nncttactgg      60
nntangatat ttatnttgcg gctgagatac ttgaacaact tcggatcnga antagacaan      120
aanggnant tntatactgc nncagagggt acacagntca ttgtattaga gangaacana      180
tgggtctggt gttcacacat tggggggaan atgggcgtnn acangagagg nnganaaacn      240
anganagcct ncctggttng cataanaaaa a                                         271

```

<210> 515
<211> 328
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(328)
<223> n = A,T,C or G

<400> 515
ccaatgaggg gcaaagtgag cgncnagaag angttttgac tgaaataaat caaacacaaa 60
aatntaagtt cacagtgaca gtttaaacaa aatccaaaca aactaacaac anaaacaccc 120
cttgntttgc ctctagtgga aggtgggana acacaanctc gtcctaaaaa ttgactagta 180
aaggggaaaa cccggtcatt tncctactct ttccangaaa tatctaatac aagaaagaac 240
ttctnctcat tatacngaag gaatttngaa aaatgatgta tttttggaac acctaantga 300
aatactggaa cctgggcaag ttcaccac 328

<210> 516
<211> 220
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(220)
<223> n = A,T,C or G

<400> 516
ncctnagttg aaggacccca tgtacatata ggccagggga gcagtactag gntaactaga 60
aggatctcat ccccatatgt gggctcattt caagtctatg gatgactacc ttcattgntg 120
tgtgcgagat ggtttcaccc ctgaaaata tgggcacttc ancataanat agcnaaatct 180
ttataatgat caatncatcc tacctccttt tacatgcatg 220

<210> 517
<211> 296
<212> DNA
<213> Homo sapien

<400> 517
tgcgatttct tccttggtgt ttgctttggt ctgtgttcaa tccagagagc ttaaattgtc 60
attatttttg gaagaaaacc tgtatttttg ttagtttaca atattatgaa atttcacttc 120
aggagaaact gctgggcttc ctgtggcttt gttttcttag tttctttttc cgtgccgtgt 180
atTTTTaat tgatttttct tcttttactt gaaaagaaag tgttttattt tcaaactctg 240
tccatattta cattctagtt cagagccaag ccttaaactg tacagaattt ccactg 296

<210> 518
<211> 299
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(299)

<223> n = A,T,C or G

<400> 518

gaagatagaa	aaatataaag	ccaaaaattg	gataanatag	cactgaaaaa	atgaggaaat	60
tattggtaac	caatttattt	taaaagcccg	tcaatttaat	ttctgggtgg	gcagaagtta	120
gaaggtaaa	cttgagaaga	tgagggtggt	tacgtagacc	agaaccaatt	tagaagaata	180
cttgaagcta	gaaggggaag	ttggttaaaa	atcacatcaa	aaagctacta	aaaggactgg	240
tgtaatttaa	aaaaaactaa	ggcagaaggc	ttttggaaga	gttagaagaa	tttggaagg	299

<210> 519

<211> 464

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(464)

<223> n = A,T,C or G

<400> 519

gctgcacatc	ggaggaaaac	tcggtaaagc	agaatgaggt	tgatatgttg	aatgtatttg	60
attttgaaaa	ggctgggaat	tcagaaccaa	atgaattaaa	aaatgaaagt	gaagtaacaa	120
ttcagcagga	acgtcaacaa	tacaaaaagg	ctttggatat	gttattgtcg	gcaccaaagg	180
atgagaacga	gatattccct	tcaccaactg	aatttttcat	gcctatttat	aaatcaaagc	240
attcagaagg	ggttataatt	caacagggtga	atgatgaaac	aaatcttgaa	acttcaactt	300
tggaatgaaa	tcattccagg	atttcataca	gtttaacaga	tcgggaaact	tctgtgaatg	360
tcattgaagg	tgatagtgc	cctgaaaagg	ttgagatttc	aaatggatta	tgtggtctta	420
acacatcacc	ctcccaatct	gttcagttct	ccagngtcaa	aggc		464

<210> 520

<211> 221

<212> DNA

<213> Homo sapien

<400> 520

ctgatatcta	cttatttaac	acaagtctct	aatacaatac	aattttatta	attttattcc	60
acatgcccc	cattagatct	ctagactcat	tcatectaca	tacctacttt	gtatcctttg	120
acctacatct	ccctacttcc	tcctccagtc	cccaccccc	acccactggg	gctaaccact	180
gtttcattcc	ctttttcatt	ctacatatgt	gagatcatgc	t		221

<210> 521

<211> 312

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(312)

<223> n = A,T,C or G

<400> 521

ctgatagctt	tctcttcgcc	tagattaata	tcttctnnct	tcccattcac	agccccacc	60
gacatcaaag	ctttgctgtt	ttatctgtca	aaaatgtctt	cacacttttc	attcttaaat	120
aaaagtgtcg	agtaaggaca	ttttcacaac	aaatttttat	tttacaaaac	ttacaatgat	180
ttgaatccaa	aacaactttc	attatttaac	tgtaaagtaa	atatataatt	tattagngnt	240

gtcttagttc attttgtgct gctttaacag tgtatccttg tgatagttgt ggggtggggg 300
 aggggggaag ga 312

<210> 522
 <211> 336
 <212> DNA
 <213> Homo sapien

<400> 522
 ccttctttcc ccactcaatt cttcctgccc tgttattaat taagatatct tcagcttgta 60
 gtcagaccca atcagaatca cagaaaaatc ctgcctaagg caaagaaata taagacaaga 120
 ctatgatatc aatgaatgtg gggttaagtaa tagatttcca gctaaattgg tctaaaaaag 180
 aatattaagt gtggacagac ctatttcaaa ggagcttaat tgatctcact tgttttagtt 240
 ctgatccagg gagatcaccc ctctaattat ttctgaactt ggtaataaaa agtttataag 300
 atttttatga agcagccact gtatgatatt tttaag 336

<210> 523
 <211> 172
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (172)
 <223> n = A,T,C or G

<400> 523
 ngaenggcnc ntggctatgt ntatagatag ggctttaacc actatctgng aagcangagn 60
 gacannattc ttgctctcac atnccacngg anacgtattt ctcttctctt acnagcgaag 120
 aaccatctnt ttctaaagcc cccattctat tgccttgct tttctctggc tt 172

<210> 524
 <211> 471
 <212> DNA
 <213> Homo sapien

<400> 524
 ccagacctgc agaaaaactt agcacagctc aatctgctgt tttgatggct acagggttta 60
 tttgggtcaag atactcactt gtaactattc caaaaaattg gagtctgttt gctgttaatt 120
 tctttgtggg ggcagcagga gcctctcagc tttttcgtat ttggagatat aaccaagaac 180
 taaaagctaa agcacacaaa taaaagagtt cctgatcacc tgaacaatct agatgtggac 240
 aaaaccattg ggacctagtt tattatttgg ttattgataa agcaaagcta actgtgtgtt 300
 tagaaggcac tgtaactggt agctagttct tgattcaata agaaaaatgc agcaaacctt 360
 taataacagt ctctctacat gacttaagga acttatctat ggatattagt aacatttttc 420
 taccatttgt ccgtaataaa ccatacttgc tcaaaaaaaa aaaaaacctt c 471

<210> 525
 <211> 332
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (332)
 <223> n = A,T,C or G

<400> 525
 cccnctgta ttccagcctg ggtgacccca tctcanggae gaaaagtac cagatgtcgn 60
 gggtaaagggt tgggtcttcaa gtggcctcat aagttgtctt gcattttaa tcaagggaatt 120
 cattggacca ataggttaca ttttcgttcc ttttttgggt tggttcatct gtttaagcagt 180
 ggggggcctaa ttactgctcc tttgtaaaaa cacattttcc caaagaacac tgaattaccg 240
 ttcaaactgg ttgttgatgg gtaataaggg ctgtttttgc tgcccaaaaa gggcttaaca 300
 atttaggcgg atagtttact taaaaaaaaa aa 332

<210> 526

<211> 440

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(440)

<223> n = A,T,C or G

<400> 526
 ccaggttacc tcccctaaca gatgtggtgt tctganggggt tggttaagtgc cccgaggaaa 60
 ataggcctta actgttaaca tctacagaga agaaagcatg gtcacactgg caaggagtaa 120
 gaagggattg ggtaaaaagaa aatgggagag aaaagggaaa aaagttttgg caagacaatt 180
 gtccctgctc aagaagctgc aggggtgaaag ctttcctttc ttctattttt gtttttaatg 240
 nctgtctctc tgatcagngg aaaagtgaag atttctagta tctagcacta acgtatgacc 300
 caactttgag ggatcacaaag ctagaacaag ttgaggattt aaaatcctgg ataattatat 360
 acttaaagtt catgagcata aagctcactt gaccatgcag aaatgctggg aagcagggtg 420
 catggcatgg gaatacatct 440

<210> 527

<211> 124

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(124)

<223> n = A,T,C or G

<400> 527
 tttccatag tctgttgggt gcataaatgn cttcttctga gaagtgtctg ttcctatcct 60
 ttgccccctt tttgaggact taaatgtag acctaagacc ataaaaacc tagaagaaaa 120
 ccta 124

<210> 528

<211> 162

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(162)

<223> n = A,T,C or G

<400> 528

174

```

ctgcgggaga aatatgggga caagatgttg cgcangcaga aaggtagccc acaagtctat    60
gaagaacttt tcagttactc ctgccccaaag ttcctgtcgc ctgtagtgcc caactatgat    120
aatgtgcacc ccaactacca caaagagccc ttcctgcagc ag                               162

```

<210> 529

<211> 409

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(409)

<223> n = A,T,C or G

<400> 529

```

cctttaaaat atagcttata aaatgtatac tatnngccag gagagctcac atttttctgc    60
agttttccag tggacctgcc tatggaatac tgtaaagaaa aatctgcaaa aatattccta    120
gcaattgaat cagtgtcttt aaataaaaga agtggagagg ggcttggtta aattattctg    180
acaagttttc ttgctagtgg ttgccaaaat taaggatatt tgaagtgtcc tatcacccaa    240
atttggtctt aagaaaaagc tatattctgn gtctataggg tgaagcccac actatctgtg    300
ctgcattctc aatgatacaa tacctatctg gaaactttcc tgttttgcca atgggtgcac    360
aaatctaaaa cattttatca caaaagggtac ttgaatttaa atttctttt                409

```

<210> 530

<211> 325

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(325)

<223> n = A,T,C or G

<400> 530

```

ccgccagtgt gatggatata tgcagaattc gccctttcna gatttgngcc cgggcaggtc    60
catggctagg attatagata gttgggtggg tggggnaaat gagtgaggca ggagtcagag    120
gaggttagtt gtggcaataa aaatgattaa ggatactagt ataagagatc aggttcgtcc    180
tttagtggtg tgtatggcta tcatttgttt tgaggtagt ttgattagtc attgttgggt    240
ggtaattagt cggntgttga tganatattt ggagggtggg atcaatagag ggggaaatag    300
aatgatcagt actgcggcgg gtagg                               325

```

<210> 531

<211> 173

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(173)

<223> n = A,T,C or G

<400> 531

```

ccaattgatt tgatggtaag ggagggatcg ttgaccncgt ctgttatgta aaggatgcgt    60
agggatggga gggcgatgag gactaggatg atggcgggca ggatagttca gacggtttct    120
atttcctgag cgtctgagat gttagtatta gttagttttg ttgtgagtgt tag           173

```

<210> 532
 <211> 395
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(395)
 <223> n = A,T,C or G

<400> 532
 caggctcctac tatgggtggt aaatttttta ctctctctac nggggttttt cctagtgtcc 60
 aaagagctgt tcctctttgg actaacagtt aaatttacaa ggggatttag aggggtctgt 120
 gggcaaattt aaagttgaac taagattcta tcttgacaa ccagctatca ccaggctcgg 180
 taggtttgtc gcctctacct ataaatcttc ccactatttt gctacataga cgggtgtgct 240
 ctttttagctg ttcttaggta gctcgtctgg ttctgggggt cttagctttg gctctccttg 300
 caaagttatt tctagttaat tcattatgca naaggatatag gggntagtcc ttgctatatt 360
 atgcttggtt ataatttttc atctttccct tgcgg 395

<210> 533
 <211> 290
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(290)
 <223> n = A,T,C or G

<400> 533
 ctgaaccatt atgggataaa ctgggtgcaa ttctttgcct tctctacttc tcaactgattg 60
 aacataagct tccagggtc cctgaaaac caaaatgaaa acaatgtcaa aatattagat 120
 aaatcacata aaacagttaa ggggatacca atatataaaa attattaggt aagctcattt 180
 ctggaactgt taatgctcgg ttccacaatc caagngacc aacagccttc actcagntac 240
 tggnaagtnt actatggtta ctacngntac taccttttagt gtnaaaaact 290

<210> 534
 <211> 334
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(334)
 <223> n = A,T,C or G

<400> 534
 ccgccagtgt gatggatatt tgcagaattc gcccttagcg agnnagccgg gcagggtccat 60
 ggctaggttt atagatagtt ggggtggttg tggggnatga gtgaggcagg agtccgagga 120
 ggttantttg tggcaataaa aatgattaag gatactagta taagagatca gggtcgtcct 180
 ttagtggtgc gtatggctat catttgtttt gagggtagnt tgattagnca ttgttgggng 240
 gtaattantc ggctgttgat ganatatatt gaggtgggga tcaatanagg gggaaatana 300
 atgatcagtn ctgcggcngg tnnacctcn gcc 334

<210> 535
 <211> 557
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(557)
 <223> n = A,T,C or G

<400> 535
 nccataagct tcagtgcgca aaaggccaag gccagtggtta atttggttatt tcttaaataa 60
 ctttcccttt cattttttaa ttataaattt aacttctaac atgttttatg gttaaaattg 120
 tacttttttc ctttagcgac attcaaatgc atcacatca ctttgtgaaa ttgttcgcct 180
 gagcagagac cagatgttac aaattcagaa cagtacagag cccgaccccc tgcttgccac 240
 tctagaaaag tatgtgtaaa actctgttct tgttcttctt tcatattgat gctgttccat 300
 gtgttaccat tgtgagtggg tggtaagtgt tccttatgtg ggaatcatgt gccttgaaaa 360
 taaccttggg tgggtgagaa ggtagggaag cctgcttctt ttatctcaag taaaagtttt 420
 ggcagggtta agaagataaa tgacatttat atctagactt ttgagttttc caattatttg 480
 gtaaaaatgg gaaattctgt agaagccctt ccttaaaaat gggggaagtc catttnanaa 540
 aattaactgg taggtca 557

<210> 536
 <211> 372
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(372)
 <223> n = A,T,C or G

<400> 536
 gtccaacct tcatttctga aactgttcta gagcacngtg tctttctcgt agttcataac 60
 ttacccttc agtctagaat tagaattaca ttatctgttt tactacttta ctagactgta 120
 agctcctaga agataaggac tagggagttc atctctgtat tccaccagaa ggtacagtga 180
 ctcatatcta gagtctttag atgaaactta ctgagttgaa taacttaata tatttctgtt 240
 ttcatccca agggaggcca tgtctggaga tagaccttga atttaataaa ttttaggcac 300
 tataccattt cagtggagaa aattgttggg aaatttgggg ggatggatat ataaggggga 360
 ggaagtcact gg 372

<210> 537
 <211> 284
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(284)
 <223> n = A,T,C or G

<400> 537
 ccttctgatg caaacagaaa ggaaatgttg tttggangcc ttgctagacc tggacatcct 60
 atgggaaaat ttttttgggg aaatgctgag acgctcaagc atgagccaag aaagaataat 120
 attgatacac atgctagatt gagagaattc tggatgcggt actactcttc tcattacatg 180

acttttagtgg ttcaatccaa agaaacactg gatacttttg aaaagtgggt gactgaaatc 240
ttctctcaga taccaaacaa tgggttaccc agaccaaact ttgg 284

<210> 538
<211> 293
<212> DNA
<213> Homo sapien

<400> 538
gtacatagta ggtgtatata tttatgggct atataagatg ttttgataca ggcatgtaat 60
gtgaaacaag cacatcaaca agaatggggg atccatcccc taaaacattt gtcctttggg 120
ctacatgtca tttcctaag taaagaaaat ggacagacag aaccaacatt gatttgactg 180
ggtgaaaaag tccatttgag ttgggagcag gggttggtt cctggatttg ggttgtagg 240
acagtgtaaa aaggcttcac aggggaacat tcttttctga taaaggaaag cag 293

<210> 539
<211> 468
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1) ... (468)
<223> n = A,T,C or G

<400> 539
tttcnataaa ctttattttt agagcagttt taagnnggta gcaaaattga ttagaaggna 60
cagagatgtc ccatacacct cctactccca cacatgcaca gccttcccca ttatcaatag 120
ccccaacag agggatacat ttgttaacaa ctgacgaacc tacatatcat tatcacccaa 180
agtccacagt ttatattatt ccttctggag aattttcaaa tacagaaatt cctctaccag 240
gaataaacta ncaatttcct ctcggtcttc tataaattta attattattt cagaaattag 300
cctatcttta caggagaaaa tgttataaac catgaaaaga ctatcaaata cacaaggaag 360
tgaatgntat ataaaaaatg taccatctcc taaacaacta cctgcattcc cttcttgtg 420
gtaagttata atttgnnata gttctgatca tctgtttaat taatttgc 468

<210> 540
<211> 397
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1) ... (397)
<223> n = A,T,C or G

<400> 540
ctgttttatt aattccccca tttgcagcac acttntctct tccaacattc atcagtcaga 60
tcagagtcca cggctctttc aaaatttaga taaactggct tacattttgt aatgatgtcc 120
ccagacaaca cccactcca acccattctg tttgttacta ttagtttaca acatgcattg 180
gcctttactt tcattttcat agtatttaaa aatggaaggg cactcccaa tttactttaa 240
cccctttaat aatctctctc ctccgtctct ctctggctcc ccagacaact gttgatttac 300
tttcctttat gatggattag tttgcatttt ctagaatttt atatgactga catataaagn 360
ttttatgttt ctcccctttg gggttcttca tgtggca 397

<210> 541

<211> 248
<212> DNA
<213> Homo sapien

<400> 541
cctagatagg ggattgtgcg gtgtgtgatg ctagggtaga atccgagtat gttggagaaa 60
taaaatgtgc atagtggggg ttttatttta agtttgttgg ttaggtagtt gaggtctagg 120
gctgttagaa gtcctaggaa agtgacagcg agggctgtga gtttttaggtg gagggggatt 180
gttgtttgga aggggggatgc gggggaaatg ttgttagcaa tgagaaatcc tgcgaatagg 240
cttccggc 248

<210> 542
<211> 366
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1) ... (366)
<223> n = A,T,C or G

<400> 542
aatcggccct ctatagcat gctcgagcgg ccgccagtgt gatggatatc tgcagaattc 60
gcccttgagc gatancgcgg gcaggtccaa ttgatttgat ggtaaggag gagtcgttga 120
ccncgtctgt tatgtaaagg atgcgtaggg atgggagggc gatgaggact aggatgatgg 180
cgggcaggat agttcagacg gtttctatct cctgagcgtc tgagatgtta gtattagtta 240
gttttgttgt gagtgttagg aaaagggcat acaggactag gaagcagata aggaaaatga 300
ctatgagggc gtgatcatga aaggtgataa gctcttctat gataggggaa gtacgcgtctt 360
gtanac 366

<210> 543
<211> 460
<212> DNA
<213> Homo sapien

<400> 543
cctactatgg gtgttaaatt ttttactctc tctacaaggt tttttcctag tgtccaaaga 60
gctgttcctc ttggactaa cagttaaatt tacaagggga tttagagggt tctgtgggca 120
aatttaaagt tgaactaaga ttctatcttg ggcaaccagc tatcaccagg ctcggtaggt 180
ttgtcgccct tacctataaa tcttccact attttgctac atagacgggt gtgctctttt 240
agctgttctt aggtagctcg tctggtttcg ggggtcttag ctttggctct ccttgcaaag 300
ttatttctag ttaattcatt atgcagaagg tataggggtt agtccttgct atattatgct 360
tggttataat ttttcatctt tcccttgagg tactatatct attgcgccag gtttcaattt 420
ctatcgccct tactttatctt gggtaaattg tttggctaag 460

<210> 544
<211> 116
<212> DNA
<213> Homo sapien

<220>
<221> misc_featur
<222> (1) ... (116)
<223> n = A,T,C or G

<400> 544
 ccgccagtgt gatggatatt tgcagaattc gccctttgga gngctngcgc ccgggcaggt 60
 ctgtttcagc agctctcct tcttcttccc gcgangatct cgagccttga tcttgg 116

<210> 545
 <211> 380
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(380)
 <223> n = A,T,C or G

<400> 545
 cgacggatcg atnagctnga tatcgaattc ggacgagcat ggcgtattgc tgcagatatg 60
 gattcttcag aatgctccat gacaaatgta ctgacgggaa gncnatctaa aggaggcatt 120
 gtnatgagag aaaggtctcg agctccagat aaagagagat acagagttct tgggaattgga 180
 gttgcagaaa cagtaagaca atcgattgtg ggggaagcgtt cttttagaga atctttggcc 240
 ttcactccaa agcgttggtt ttcataata ataagtagct cgtgccgaat tcctgcagcc 300
 cgggggatcc actagttcta gagcggccgc caccgcggag gagctccagc ttttgttccc 360
 tttagtgagg gttaatttcg 380

<210> 546
 <211> 418
 <212> DNA
 <213> Homo sapien

<400> 546
 ccagggaat taggcaggag aaggaaataa agggatttca attaggaaaa gaggaagtca 60
 aattgtccct gtttgcggat gacatgattg tatatctaga aaacccatt gtctcagccc 120
 aaaatctcct taagctgata agcaacttca gcaaagtttc aggatacaaa atcaatgtac 180
 aaaaatcaca agcattctta tacaccaata acagaccaac agagagccaa attatgagtg 240
 aactcccatt cacaattgct tcagagaata aaatacctgg gaatccaact tacaagggat 300
 gtgaaggacc tcttcaagga gaactacaaa ccactgctca aggaaataaa agaggatata 360
 aacaaatgga agaacattcc atgctcatgg gtaggaagaa tcaatatcat gaaaatgg 418

<210> 547
 <211> 172
 <212> DNA
 <213> Homo sapien

<400> 547
 cctgaggttg ggagaaattt tgtccatttc tttagaacca aaattggcaa ccagagagta 60
 tttgatgtt acacaaaata tctagtttcc ctttctagcc taaattgggt tgtttatagc 120
 acccgtctct ccatctgaga aaaatgggta ggatgctggt gcagggatga gg 172

<210> 548
 <211> 367
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(367)

<223> n = A,T,C or G

<400> 548

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ggctctgactt aagagaaaca atggaaggca agaggcagta gaataatata ttcaaaagat      60
gcaaaggaaa aaaacctctc agccacgaat tccttatcca gcaattatctt ttcaaaaatg      120
aaaataacac aaagaccttag ccagataaac agaaacatta actgaagttg ttgctggcag      180
acctaccata taaaaataaa aaactctaaa aaaattccta tggctaaaag caagttacag      240
aagacagtca cttgaatcca cattttaaaa aaagcactga tatacgtaat attgacatta      300
taaaagacag taaaaatgca tttcttcttt ataataaatn gcttattaaa taacatgtgt      360
ataatgg                                           367

```

<210> 549

<211> 418

<212> DNA

<213> Homo sapien

<400> 549

```

ccaaatcaga acctagagtg agcattctat aaactcacct ttgctttgat ccttgaagat      60
cacaagtttt gatactgttg aaatctctac tctttcaaca ctttaattaa atggcattta      120
gaatttcata tacttctgtt gttgtttcca caatcttaaa ctggatttag aaatacttat      180
aatgtaaatg caagagcttt aacttagtaa ccgtatttcc tattttttgt tgtttttctt      240
ttgccagaat ttctgtttgt ctacaataaa gtccagcgaa atacagtatt tggtagggtt      300
acttgttaac ataaaatttt atcatttgta gagtttttac ttaaccttcc tattctctag      360
tctctataat ctttcaatga agataaccag ttacgaatat ctcctatacc atattagg      418

```

<210> 550

<211> 234

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(234)

<223> n = A,T,C or G

<400> 550

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cctaccgccc gcagnactga tcattctatt tccccctcta ttgatcccca cctccaaata      60
tctcatcaac aaccgactaa ttaccacca acactcacia caaaactaac taatactaac      120
atctcagacg ctcaggaaat agaaaccgtc tgaactatcc tgcccgccat catcctagtc      180
ctcatcgccc tcccatccct acgcatcctt tacataacag acgagggtcaa cgat          234

```

<210> 551

<211> 542

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(542)

<223> n = A,T,C or G

<400> 551

```

caccctacc ccnntcctca taaaagttnc tctccctgga tcctcttttt ccctcatgag      60
tgcccgggtg cccaagtcaa aaacctggga gtgatataaa ctccccacac atccagtcag      120
tcactcatca actctattga ttctgtctgc taaatatatn tcaattgtat taacttaaac      180

```

```
atatgcatan ggcactttct tcttcactgc atttttgtgg gctgcactta cctttcaggt 240
aacgacaaca ctggcccttc ttgcccttct agtcagaagt gccaaaatga tgagagctag 300
ccatgacaaa cccacagcca acattacact gaatgtgcaa aactggaagg gcatccaaac 360
agaggagggg agagaggaat agacaggaag tcaaactgtc tctgtttaca gatgacatgt 420
ttctatatct ataaagcccc atagtcttgg ccccaaagct tcttctgctg ataaacttta 480
gcaaagtctt agcatacaaa atcaatgtgc aaaaattact aacagtccta tacatcaagt 540
ca 542
```

<210> 552

<211> 411

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (411)

<223> n = A,T,C or G

<400> 552

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cctggntgac aaggaggtgc ctgtnatgtg aagatttgag gaaagagcat tccaggcagg 60
gggaaggcct gatgcaaagg gtctactgca ggcattagct gagcttattt aaagatcaga 120
atgaaggcca ttgtggctag aacagagtgg acaggaagga atgggtaccag gcaaagctga 180
agaagtgggc aggattgagc tctcataant catggcaaag agttcccat tcatgtttg 240
acggaaataa attggaaggt cttaagtagg agaagatttg attagattta cattttacga 300
agaagcactc tggatgttat gtgaagaaat ggcctttgca gggcaagggt ggaaacaaag 360
agatcagtta ggaaattatt ggagtagctg aggattggat gaggggatgt g 411
```

<210> 553

<211> 631

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (631)

<223> n = A,T,C or G

<400> 553

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ccgggattag aactaaaaca agtgagatca cccctctaata ttttctgaa cttggttaat 60
aaaagtttat aagattttta tgaagcagcc actgtatgat attttaagca aatatgttat 120
ttaaataatt gatccttccc ttggaccacc ttcattgttag ttgggtatta taaataagag 180
atacaaccat gaatatatta tgtttataca aaatcaatct gaacacaatt cataaagatt 240
tctcttttat accttctca ctggccccct ccacctgccc atagtcacca aattctgttt 300
taaatcaatg acctaagatc aacaatgaag tattttataa atgtatttat gctgctagac 360
tgtgggtcaa atgtttccat tttcaaatta tttanaattc ttatgagttt aaaatttgta 420
aatttctaaa tccaatcatg taaaatgaaa ctgttgctcc attggagtag tctcccacct 480
aaatatcaag atggctatat gctaaaaaga gaaaatatgg tcaagtctaa aatggctaata 540
tgtcctatga tgctattatc atagactaac gacntttatc ttcaaaacac caaattgtct 600
ttagaaaaat taatgtgatt acaggtagag g 631
```

<210> 554

<211> 558

<212> DNA

<213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(558)
 <223> n = A,T,C or G

<400> 554
 ccaggntagt ctccaactcc tgaccttagc tgatccaccc acctcggcct cccaaagtgc 60
 tgggattaca ggcattgagcc actgcgcccg gccaaacttg atatgcattt ttaaataagt 120
 taatacatta ttcattggttt agtctcatta tatattctat ggtccacttt gaaatttcat 180
 ctaacaaaaa tcatcttcat cctgcaattt gaggtttgga cacaatgggg attgatcagt 240
 aattttcttca tatgcccttt ctcaaggaaa tagtttctta tgaaaaaaaaa gtcctatgtt 300
 ttcatgtaag ttctcttttt ggagaagaaa aggagacatt cttacttagc actctcagtt 360
 ttacaaaacg ctgccaacct taaaatttgt ctattgattc ccaaggcaca caaccaatag 420
 tctgtcaata acccggaata acatttcttt aaggccccag taactttcac atgtttgggt 480
 tccaatcctc acctagaatc ttgttaagaa aagtaaacca ttcactcctc tagaaactct 540
 aaggttgctt cttagggg 558

<210> 555
 <211> 212
 <212> DNA
 <213> Homo sapien

<400> 555
 ccagggtatct gcataatggc ttttcttctg ttgcctttgt tcctttgtgg ccccagctaa 60
 ttgcctgaga gtgccactgt tagttttcaa ctctttctga tagaaaccct gtgtactaac 120
 atggaaatct taggtaatct gctttttcaa agcacaatgc agaatttatt ggcggtgggt 180
 taactttaag aatatccgag aagccaccaa gg 212

<210> 556
 <211> 219
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(219)
 <223> n = A,T,C or G

<400> 556
 ccatgtgtct atctggagag aaggggaaac agcaagtgca aaggccctga gatggaacat 60
 atctggagaa ttcgaagaat ggtaagaagg ccagagtgga gcagaacaag tgtgggagag 120
 agttgtagga gatgagatca aaggctagga atgaagtgtg aggccatgtc atgtgacctt 180
 gtatgtcctt gtaaggcttt tttttttttt ttttancct 219

<210> 557
 <211> 482
 <212> DNA
 <213> Homo sapien

<400> 557
 cctactatgg gtgttaaatt ttttactctc tctacaaggt tttttcctag tgtccaaaga 60
 gctgttcttc tttggactaa cagttaaatt tacaagggga ttttagagggt tctgtgggca 120
 aatttaaagt tgaactaaga ttctatcttg gacaaccagc tatcaccagg ctcggtaggt 180
 ttgtcgcttc tacctataaa tcttccactc attttgctac atagacgggt gtgctctttt 240
 agctgttctt aggtagctcg tctggtttcg ggggtcttag ctttggctct ccttgcaag 300

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ttatttctag ttaattcatt atgcagaagg tataggggtt agtccttgct atattatgct 360
tggttataat ttttcattt tcccttgccg tactatatct attgcgccag gtttcaattt 420
ccatcgcccta tactttattt gggtaaatgg tttggctaag gttgtctggt agtaagggtg 480
ag 482

```

<210> 558

<211> 679

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (679)

<223> n = A,T,C or G

<400> 558

```

ctgtnaaaat tctgaaccta tccccaaaag aaaaaccgtg aaatacaagt tttaggaggt 60
ggagcaaaaga aaagccaagt tattttaaac caataaacac aagagacaat tctgctggag 120
aatctacttt ctccaaaaca tcaaatggac tttaaagcag aagaccacat tttatgagaa 180
agttatgtca ctgaaaagct tcatgtaaag tgactttgta aatggaatat ttttaaata 240
taaaaagaaa ataacttttc caggaatcct ttggagaggc tgataaccag atattaaatt 300
atcaattttg ccaaagtgga cttttaaaaa atgtgttact tttaaaaact aacttgaaag 360
aatctatgag gcaatctatc tgagtatgtt tattgttgct ccattggctt tcaggatttt 420
ggtcatttca ctgttaactc ttacatcaga gaataaagaa aagaaaatga aactttgtta 480
ggaactggga tggaaaatgt agtcccagac agatctactg acctcgactg agtttcagaa 540
atatcccagg attttggtta ttcatgcctt tcttttggtga ctttctttca aattagccaa 600
ttaagatac cccttcaatc accggtgaca tcagtacaac agtttttcaa cagttttctc 660
tctcctgacc aaacagttt 679

```

<210> 559

<211> 488

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (488)

<223> n = A,T,C or G

<400> 559

```

ccccactgta ctccagcctg ggtgacccca tctcaaagaa gaaaagttag cagatgtcat 60
gggtaaagggt tggcttcaa gtggcctcat aagttgtctt gcattttaa ttagggaatt 120
cattggacca ataggttaca ttttcgttcc ttttttggtt tggttcatct gtttagcagt 180
gggggcctaa ttactgctcc tttgtaaaaa cacattttcc caaagaacac tgaattaccg 240
ttcaaactgg ttgttgatgg gtaacaaggg ctgtttttgc tgccccaaaa gggcttaaca 300
atttaggcgg atagtttact taaaaaaaaa aatcctttgg agacatactg aaaatgcaaa 360
ctagtttcta aattatcaat tccctacatg aanaagcagt ttgccanagt ttagtctcan 420
aaaatgactg gttggctcta tttaaatcan aaccaattt ctacgcacct gccggcccg 480
ccaagggc 488

```

<210> 560

<211> 602

<212> DNA

<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(602)
<223> n = A,T,C or G

<400> 560
cctantttaag aattccttgc cttagtgggtg aacaaggact aaacacagac aatgggtgaa 60
acacagacgc taattcacat aacagagagt aggaacacctt aagaatgaat tgatgcagac 120
tcctatagaa ttcctctgtt atgactgggt tcttattttc tcctccttgt atgtagtga 180
aatttcacat ttatgaatag ttccttggt ctttttttaa agttgtgaat gcgagtgtt 240
ggctttgtaa tacaactttt tagtatccag aagataacca gtgctctacc aataaagatc 300
ttttgataca aagggtttta acttctgcca gtcttactc attttttca ggttttttat 360
acatttctta aacaacacat acattatgta aaatataaga attaattgtac attctcaagg 420
ccagattcag tgacaaaatg cactacccga atctagtaac acatttactc cttgctgcat 480
ataagtggcg tgtaagaaat acagggtata ttgttttggt atccatgcag taaatgttca 540
caaatatcag gcaaacaaact agacgntctt cagctactaa aattaactgt cccagtcaca 600
aa 602

<210> 561
<211> 683
<212> DNA
<213> Homo sapien

<400> 561
gtctatTTTTT aaaaagaaag aaaaaaacca cttttttata gtccctagct ttgccatatg 60
cccgcccttaa gtggaaggaa agttaatcac ttaactatgt tttataaaaa gaaaaaagg 120
cttggaaatgc tattactgtt cacacaaagt atgattctgt ttgaataagg caaatgtccc 180
tttttttaaa aaaagacatt actgtaatat caaaaaccgt ggcagtttgt atacaactct 240
gggcttgatt ttttttaaaa aaacagaatg aattgatgtc ttattttata aatgttctat 300
atttattagg agaaaacttt atattgcctt ttttatcaat catgtaacag gcttatagct 360
ttccaacaga gctgcttgcc aaacaatttt ttttgtttat taaacagtgc tgaaacaaac 420
aggatcagca tttacttaag atgttaagaa tgaggacttt taatcagccg aaccaagata 480
ttgttacctg tatgcattcc caaagtctag atgctcagta tgttcagtca tatctttcag 540
aatcagtgaa ccgattaccc tttttttggt attcactcta catctgccaa cctagttcac 600
cttgggtttg tgtctgctgt agaagggaac cataacttgg ttaaaccgta gggattatca 660
ttgtatacat gctgtgaaca tgt 683

<210> 562
<211> 420
<212> DNA
<213> Homo sapien

<400> 562
gcactttttt tccagtaagg attcatctct tgctctccta tatggtcatt atattttata 60
ttttacatat ttataaacat gacatatgta tttatgttcc acaaagggtc ttgaatagaa 120
tttacacata gagttccctg ggttgatgtg tttatcaaaa tggaagataa agtgaattaa 180
ttactttaat atttaacact attgaataga aataatttcc ccaatattgc ttcattgatt 240
agacagtcta ttaaatgttt aagcaaggca ctagactaag tttattaaga caaattttgg 300
aatatgtgca gaaatatgac ctggctaata gtacagagtc aaagctgggt gaatggtgtt 360
atatagtgga ttcagattga tgtggcagtg gtggttacac taggggcact aaggttatcc 420

<210> 563
<211> 482
<212> DNA
<213> Homo sapien

<400> 563
ctccacctta ctaccagaca accttagcca aaccatttac ccaaataaag tataggcgat 60
agaaattgaa acctggcgca atagatatag taccgcaagg gaaagatgaa aaattataac 120
caagcataat atagcaagga ctaaccctta taccttctgc ataatgaatt aactagaaat 180
aactttgcaa ggagagccaa agctaagacc cccgaaacca gacgagctac ctaagaacag 240
ctaaaagagc acaccctct atgtagcaaa atagtgggaa gatttatagg tagaggcgac 300
aaacctaccg ggcctggtga tagctggttg tccaagatag aatcttagtt caactttaac 360
tttgcccaca gaaccctcta aatcccttg taaatttaac tgtagtcca aagaggaaaca 420
gctctttgga cactaggaaa aaaccttgta gagagagtaa aaaatttaac acctatagta 480
gg 482

<210> 564
<211> 302
<212> DNA
<213> Homo sapien

<400> 564
ctggaagtga aggtactaat atacaaatgg ctcttgtttc tgaatatgtg atataatttg 60
tgaatctttg gaaactgaat ttttctatg gagtgc aaat atagaaggtt tattttacaa 120
tggttggtgt gaaaagaatt cactttgtaa acaactatta aggctggaag tttagtgaag 180
gtgcatagtt ttgaaagcta cacagtgtaa aaatcaaact tattgtttgt aattttgctg 240
ttacatgtta agttactttg acagcaattt tctaatagata atgtgattta tgatttaaaa 300
gg 302

<210> 565
<211> 554
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(554)
<223> n = A,T,C or G

<400> 565
ccanngtgac atcatggcaa tacagcaaga attctgnnat ttatttagaa gcctcaagga 60
gaaggatcct ggagcccctg aatgagagtt tcttctccat gcctctcccc agtcaaaata 120
catggaaata ttcatagaag cattgtaccc agcatgataa ggaaggatgg agaatggttc 180
cttatatctc tgttcacaag acatcaacac tcttaagtaa ctgtatgaaa taaattctct 240
gctgaaagca aataaaccat ctgaaaggtc ttctgggttac ttacacagat ttcctagaga 300
atctgaaatc agcctaacag ggaagattaa tttttaaatg aatccaagtt aatgaaagca 360
aagaactctt atacagaaat acattttcct attataaagc aggactacct tccctaattt 420
ctgatagacc taggacaatt tgaatgggca ttgaaattct tttgggtgaa ttacgcaaac 480
aagcaaagga aaagtctcaa ttattattgg aaaatttggg gagagattat tatctcttga 540
tctcctagtn natt 554

<210> 566
<211> 631
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(631)

<223> n = A,T,C or G

<400> 566

```

ncgaagctgt gaannccattc acacggaatc tgganggtat tactgtaact tcttataata    60
cataatataa aagtttttga aagatataga cacaattaac ccctaaacaa cacactatct    120
gatttctcaa agcaatggct atttaacaag atgtaaaagg acaataacat atcaaagaac    180
tttcacacac ctaaagatag catttagcag caagttagtc agacaaaaca aacataaata    240
tcttcacatt tcctatgttt gtttttaact ttacttcata aagccactga taattgaggt    300
ttctttcaag tataagattt ctaaaattaa aaactgtttt tgacatatatt ttataaagaa    360
ataaaaagca aaacgcaatc caactattta tatgagtcct tcttctccaa cagctttaga    420
tgtttttctg agtacttttt acacagaata tttttattaa aatcagttct aattcattta    480
tgcagattag gggaaaatga ttcataataa attaacctta aaattacctt ctatctgctt    540
ctacctctat ccccccata ccaccaaatc tgttgctaca gtgaactgta gccaatgtct    600
gtttgagggg gcccaaagca tctggttaatc t

```

<210> 567

<211> 510

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(510)

<223> n = A,T,C or G

<400> 567

```

cctatnatag cttctctagc tatcatactc caatcagcna aaaatgagaa aatgttgaga    60
aatagaagat aattcctcat ttaaggncac cttctanaat ttgtgcttaa nantctgttt    120
tcttctcatg ggccagcact tcggcaactg ggaaaaatta nngtacagg gatctaggna    180
atactgttta tttgagcaat aatatattgn gctaactgtc aggcaccta ttactgagaa    240
ataagggaaa atgagtgtaa agtacaacta agagtctcgg ctacagggaa aaataccatc    300
agttaaatat ccatagtcct agagcattta tgtaaaactg caatttgaat cctgcaatac    360
atthttggctt tttcctcagt gataccatgt gtgggaagtt gttctgtcaa ggtgggtcgg    420
ataatttgcc ctggaaagga cggatagtga ctttcctgac atgtaaaaca tttgatcctg    480
aagacacaag tcaagaaata ggcattggtg

```

<210> 568

<211> 180

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(180)

<223> n = A,T,C or G

<400> 568

```

ttaatntgac ncacgcttat gcggaggaga atgntttcat gttacttata ctaacattag    60
ttcttctata gggatgata ttggtccaat tgggtgtgag gagttcagtt atatgtttgg    120
gatttttttag gtagtgggtg ttgagcttga acgctttctt aattggtggc tgcttttagg    180

```

<210> 569

<211> 237

<212> DNA

<213> Homo sapien

<400> 569
 ccaattgatt tgatggtaag ggagggatcg ttgacctcgt ctgttatgta aaggatgcgt 60
 agggatggga gggcgatgag gactaggatg atggcgggca ggatagttca gacggtttct 120
 atttcctgag cgtctgagat gttagtatta gttagttttg ttgtgagtgt caggaaaagg 180
 gcatacagga ctaggaagca gataaggaaa atgactatga gggcgtgatc atgaaag 237

<210> 570
 <211> 352
 <212> DNA
 <213> Homo sapien

<400> 570
 ctgtctctcc atttagagcc ccagttggtc ctgacctctt acaaatttgg tgttttctact 60
 ttgatgttta tgaaccgatt gcattaaaaa tgcaggataa tgattcaggg ttagagaaac 120
 tattatttat acaaattgtg ttaacacctc atcattttta attggctgtg ctaataatgc 180
 tcattgtgct cttcagggtt atgtgtgtgt gtgtgtgtgt gttttgcctg aatctgcaac 240
 ctacatttgc tctggcagta tgttgagtat atgctagaat agaattggacc taggcaactc 300
 taaggtccta caactaaata cacttactta ggaaacctcc taaataagta gg 352

<210> 571
 <211> 402
 <212> DNA
 <213> Homo sapien

<400> 571
 ctgattttta caataactac tgtgttctct gcaatagtgt gttctgatta gaaatgacca 60
 atattatact aagaaaagat acgactttat tttctggtag atagaaataa atagctatat 120
 ccattgtact tagtttttct tcaacatcaa tgttcattgt aatgttactg atcatgcatt 180
 gttgaggtgg tctgaatggt ctgacattaa cagttttcca tgaaaacggt ttattgtgtt 240
 tttaatttat ttattaagat ggattctcag atatttatat ttttatttta ttgttttcta 300
 ccttgaggtc ttttgacatg tggaaagtga atttgaatga aaaatttaag cattgtttgc 360
 ttattgttcc aagacattgt caataaaagc atttaagttg aa 402

<210> 572
 <211> 70
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(70)
 <223> n = A,T,C or G

<400> 572
 tggatccgag ctcggtacca agcttggcgt aatcatggtc atagctgttt cctgtgntcg 60
 ttttacaacg 70

<210> 573
 <211> 423
 <212> DNA
 <213> Homo sapien

<400> 573
 ccaatggttt cttagtgaag gagtacacta gctctgaatg caatgccctc agaaagatat 60

```

cattcataga gacatacaaa gcacatggca acatgacatt ggaatacacg attctgagca 120
tcttcattca tgaccaacct ggctatagat ttcagatgtc ctcttggtc gaaggatatac 180
tgggatatcc atgctcactt gcattccttt ccctttaatt tcattttcta agtccttctt 240
gtattgtttc taaaagaaca gaaaataatc ttggagcttt gcttaagctt taatagcgat 300
gttgaaattt acatgtttga atctcaaagc caccatgtg gaaagaaaac ttatgctctt 360
tccagctatg attcacggca tttattttaa actttgtatc ttgctgctgt cttacctggc 420
tgg 423

```

```

<210> 574
<211> 129
<212> DNA
<213> Homo sapien

```

```

<400> 574
ctgttaaaag aacaaactta gcaatatata acagtttgct aacaggattt ttgactattc 60
actttgcgag ttatttttta aaatccactt ttttactgag tcttactaca taccaggcac 120
tgtacttgg 129

```

```

<210> 575
<211> 684
<212> DNA
<213> Homo sapien
.
<220>
<221> misc_feature
<222> (1)...(684)
<223> n = A,T,C or G

```

```

<400> 575
ccagatntga cttttcaaaa ctactcacat tgtgaaaaan gcaggaacaa atctagtttc 60
aagttcagca tgccgttccc tgtttaattc ataaaacaca actggcagaa gtattacttg 120
aagcaaaaca aaagtaacgt gggaacttgc ttatttgcta agccacaatg tatttttcca 180
ggaatagcat aaatttgcca tctttcttgt gtctatggaa aaggggttta gaattgtttc 240
actaaaaatt aaatttctat attgtcaaac atgattgtat actcaaattt taaaatgtga 300
agggaaacact tactaagcat ttctgggta tgccactata ttaagtccta gtaatatgat 360
atagtttatt tcaatttttt ttcaactcat acttccttta aaatagcact gaccaaaaga 420
aagttaacat gagcttcattg tacaattttt aatctttttg cagaaaaata aactgagaaa 480
ggctaaaatt gttttattta agccactata ccaagacata ttgatttcac caatataaaa 540
attgagatag tttacatttt ttggtacatc tttaaaatct ggtatgtatt tttatactga 600
cagcacatct caatttggac aagctacatt tccagggtc aatagtcacc atgaatctca 660
attgtaatca aagaggttgg cctg 684

```

```

<210> 576
<211> 134
<212> DNA
<213> Homo sapien

```

```

<400> 576
ccttatttct cttgtccttt cgtacagggg ggaatttgaa gtagatagaa accgacctgg 60
attactccgg tctgaactca gatcacgtag gactttaatc gttgaacaaa cgaaccttta 120
atagcggctg cacc 134

```

```

<210> 577
<211> 133
<212> DNA

```

189

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(133)

<223> n = A,T,C or G

<400> 577

ctgtctctcc attnagaagc cccantnggt cctnacctct tacaaatttg gtgttttcac	60
tttgatgttt atgaaccgat tgcattaaaa atgcaggata atgattcagg gttaganaaa	120
ctattattta tac	133

<210> 578

<211> 200

<212> DNA

<213> Homo sapien

<400> 578

cctcaaactc atcttcaaag gtgaccagc aatcagtgct aatgccttta ctgtagttaa	60
cctggtaatt tcattcttta gtctctccaa gaaaatctga agtgtattag gcaagtcaga	120
acccaaattg tctccaagggt tgcaaataat ttgtcccata caggaaatag ccctttcctt	180
gacttcctga tcaatgtcag	200

<210> 579

<211> 402

<212> DNA

<213> Homo sapien

<400> 579

ctgattttta caataactac tgtgttcctg gcaatagtgt gttctgatta gaaatgacca	60
atattatact aagaaaagat acgactttat tttctggtag atagaaataa atagctatat	120
ccatgtactg tagtttttct tcaacatcaa tgttcattgt aatgttactg atcatgcatt	180
gttgaggtgg tctgaatgtt ctgacattaa cagttttcca tgaaaacgtt ttattgtgtt	240
tttaatttat ttattaagat ggattctcag atatttatat ttttatttta tttgtttcta	300
ccttgaggtc ttttgacatg tggaaagtga atttgaatga aaaatttaag cattgtttgc	360
ttattgttcc aagacattgt caataaaagc atttaagttg aa	402

<210> 580

<211> 245

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(245)

<223> n = A,T,C or G

<400> 580

ccaattgatt tgatggtaag ggaggggatcg ttgacctcgt ctgttatgta aaggatgcgt	60
agggatggga gggcgatgan gactaagatg atggcgggca ggatagtcca gacngtttct	120
atttcctgag cgtctgagat gttagtatta gttagttttg ttgtgagtgt taggaaaagg	180
gcatacagga ctaggaagca gataaagaaa atgactntta gggcgtgatc atnaaanggg	240
ataaa	245

<210> 581

<211> 294
 <212> DNA
 <213> Homo sapien

<400> 581
 tgcagcgcaa gtaggtctac aagacgctac ttccccctatc atagaagagc ttatcacctt 60
 tcatgatcac gccctcatag tcatttttctt tatctgcttc ctatgcctgt atgccctttt 120
 cctaacactc acaacaaaac taactaatac taacatctca gacgctcagg aaatagaaac 180
 cgtctgaact atcctgcccg ccatcatcct agtcctcatc gccctcccat ccctacgcat 240
 cctttacata acagacgagg tcaacgatcc ctcccttacc atcaaatcaa ttgg 294

<210> 582
 <211> 230
 <212> DNA
 <213> Homo sapien

<400> 582
 gaggtcgccc tcatagtcac tttccttacc tgcttcttag tctgtatgc ccttttccta 60
 acactcacia caaaactaac taatactaac atctcagacg ctccaggaaat agaaaccgctc 120
 tgaactatcc tgcccggcat catcctagtc ctcatcgccc tcccatccct acgcatcctt 180
 tacataacag acgaggtcaa cgatccctcc cttaccatca aatcaattgg 230

<210> 583
 <211> 481
 <212> DNA
 <213> Homo sapien

<400> 583
 ccaaggggtg tctgcctgcc tcagcctccc aaagtgcctg gattacaggt gtgagccact 60
 gtgcctgacc acaggaaaac ttatttaaata gagagatttg actcgaaaga tcccgttttt 120
 ttaaggctct tagttcttaa aagcggcaca taatagaatt agtataatcc caaataaatt 180
 ttcagtagat ttttggtgta acttgagaag atgattctgt catttttagt gacaatttaa 240
 aagacctgaa attgtctaca gccatagaaa gtgaactact gatagttgtt tctgtaaaagt 300
 tttattggaa cacaaccaca cctatttggt catctgtatt gtctttgggt actttgtgca 360
 gagaccatgg ccacaaaacc taaaacattc actttctagc tctttaagaa ataattggcc 420
 cactgacacc ctgggtctaa ggtctagacc aattatttct caagagtatt agctgaatca 480
 g 481

<210> 584
 <211> 306
 <212> DNA
 <213> Homo sapien

<400> 584
 ccaattaaga gctaaattta caaaataatc tctatcagga ggctttaagg tttaatgtct 60
 ctaaagtccc tatggatata agaggcttga atgtactgaa ttcaaatttg gtttttaaat 120
 gttataatag tttaggcccg agagccacat atttctgtct aagaatagaa agcatagcta 180
 gctgccca cagaatatc atatagaggt ggggggcaag aacaaaattt attcatttga 240
 tacatagaaa tgggactact tagaatagac tcataataga aagcatcatc tggtttctca 300
 tctcag 306

<210> 585
 <211> 308
 <212> DNA
 <213> Homo sapien

<400> 585
 ccagaatggt acagagtgga ggggtgttctg ctaatgactt cagagaagta ttttaagaaaa 60
 acatagaaaa acgtgtgcgg agtttgccag aaatagatgg cttgagcaaa gagacggtgt 120
 tgagctcatg gatagccaaa tatgatgcca ttacagagg tgaagaggac ttgtgcaaac 180
 agccaaatag aatggcccta agtgcagtgt ctgaacttat tctgagcaag gaacaactct 240
 atgaaatggt tcagcagatt ctgggtatta aaaaactaga acaccagctc ctttataatg 300
 catgtcag 308

<210> 586

<211> 416

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (416)

<223> n = A,T,C or G

<400> 586
 cctgtctttg aatggatgaa atagggttaat aaaaaacatc actgttttaa aactagaaca 60
 ctgaaaaatt ctaggaaagc ttattttccc ttatatTTTT atggnacttt caacacttna 120
 caacactatt tnaattaann tttnttctag agtttatann atatcagtac attcttttct 180
 gtggatgcaa taatatagaa tcttatttnc aatcttactg gcaggntctn ttaaatttct 240
 caacgngtgn catagtgatt aaccaaaatt agttatgatt tctgcctatc tgtgtgagaa 300
 cttacagggg aaattgttct aaacctgagg aacatgaagt aactgtactg cacactccaa 360
 atgatgacag tcattttata tcaccttcaa ttacccaaca gcttttaata gtctgg 416

<210> 587

<211> 382

<212> DNA

<213> Homo sapien

<400> 587
 cctactatgg gtgttaaatt ttttactctc tctacaaggt tttttcctag tgtccaaaga 60
 gctgttcttc tttggactaa cagttaaatt tacaagggga ttttagagggt tctgtgggca 120
 aatttaaagt tgaactaaga ttctatcttg gacaaccagc tatcaccagg ctcggtagggt 180
 ttgtcgctc tacctataaa tcttcccact attttgctac atagacgggt gtgctctttt 240
 agctgttctt aggtagctcg tctggtttcg ggggtcttag ctttggtctt ccttgcaaag 300
 ttatttctag ttaattcatt atgcagaagg tataggggtt agtccttgct atattatgct 360
 tggttataat ttttcatctt tc 382

<210> 588

<211> 307

<212> DNA

<213> Homo sapien

<400> 588
 cctactcttc tccgtccatt gtactatctg cccgtgggtg ggatggcagt aggatcatat 60
 ttgatgactt ccgagaagca tattattggc ttcgtcataa tactccagag gatgcgaagg 120
 tcatgtcctg gtgggattat ggctatcaga ttacagctat ggcaaaccga acaatttttag 180
 tggacaataa cacatgggact aatacccata tttctcgagt agggcaggca atggcggtcca 240
 cagaggaaaa agcctatgag atcatgaggg agctcgatgt cagctatgtg ctgggtcattt 300
 ttggagg 307

<210> 589
 <211> 89
 <212> DNA
 <213> Homo sapien

<400> 589
 cctgggtgat tgaggatgca atgagctgtg attgtgccac cacactccag cctgggcaat 60
 acagcaagac tgtctcaaaa aaaaaaaaaa 89

<210> 590
 <211> 456
 <212> DNA
 <213> Homo sapien

<400> 590
 cctcagttct tgattgtggt tgacggggcg tcacatgaa ggagcccat tagtataaag 60
 cttccaacct tttctcttaa tcgtttcttt aatcttttaa accatcttca agtgcataagg 120
 ggagttttccg atgccagagg atgaaagcaa gtgctctctc caccctctcc tcccagagtg 180
 aaaacaaatc cttttgctga tacttgtttc aaaagcatcc attgtaaagc ttctcagtga 240
 cacaaaatac tgagaggtaa ctttttatca atcaaaccac atacccaat ttaacacctt 300
 tcaatgctct gaattcaact gacagactaa aggggtgttc ctgtaacagt ctgaaatatt 360
 aagtgttttt tttgttttgt ttttaaatct tatttcagaa aacttcctct tggggtagga 420
 aagtacacat gaagcagcaa agtaacgaag aaaaac 456

<210> 591
 <211> 289
 <212> DNA
 <213> Homo sapien

<400> 591
 ccaattgatt tgatggtaag ggaggggatcg ttgacctcgt ctgttatgta aaggatgcgt 60
 agggatggga gggcgatgag gactaggatg atggcgggca ggatagttca gacggtttct 120
 atttcctgag cgtctgagat gttagtatta gttagttttg ttgtgagtgt taggaaaagg 180
 gcatacagga ctaggaagca gataaggaaa atgactatga gggcgtgatc atgaaagggtg 240
 ataagctctt ctatgatagg ggaagtagcg tcttgtagac ctacttgcg 289

<210> 592
 <211> 435
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(435)
 <223> n = A,T,C or G

<400> 592
 cgcgttagat gcgccttttc cggcctgtgc gtctgctctg gttcctctca ggcagcaaag 60
 ctggggaagg aagctcaggc aggagcctcc ccgacaccac agcggcacaa gcagcagcta 120
 aagcaccgca ctttgctctg ctaacctttt acttaaatga ggttttgcca aatccacatc 180
 tggaaccgca tcacacccat ttgcaaggat gtttgttctt tgatgaaact gcattctctac 240
 tgcacatgan ggctttcatt gtaggacaag aggagagttc gtttattttt gtaactgttt 300
 tacatgttcc gattanttaa tcggnagctt atgtcatttg ctatgcctgt tgtcttctaa 360
 tctctcctta ctaaaacatt acttcaaatt tnaattgacc cttgtttata atttatttaa 420
 cgggatttgn gtgtc 435

<210> 593
 <211> 633
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(633)
 <223> n = A,T,C or G

<400> 593
 ctgttttagtc agataattgt gtccgaattg attangaaaa taatagacca gccataaaagc 60
 agcataaaaat attatgaaac tattccagaa gtccagtaat atcttttggga cctgtctcata 120
 gcccaagttt tgtgaatact tttgtagtta aaaaaaattt ttactttacc agggcattgc 180
 aattcttttc catcagtgaa tttcattcta cagacttttc agagcatctc ataatcagtc 240
 aacaaatcta tttcaaatgt gtttgttact aagcaacggg tgctaagagc ttctgtaatt 300
 aagatgaaag ttccaaggta acaatgcccc aacacagcac catttttcacc attttctgat 360
 aatgcaggag taggatggct aaaagtgaag gaagaatcta ctctatggaa agcatggcac 420
 ctgaaatttc tgaagatatt ggctgtcctc tagcttatat gagagagagt gtttgtgctt 480
 tactaatcaa ccagtcattt ttttcttggt tggtgaaat gtacattcca gacatgaaca 540
 ggtagagtat gtgttggggg cagggttata ctgcatgggt gtgctgagac agggccacgt 600
 ggtgatgtaa atgatgctgn ctgacacgtg cag 633

<210> 594
 <211> 501
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(501)
 <223> n = A,T,C or G

<400> 594
 cctttacaag atgctgggtac cttgatcttg gacngggcag gctccaagat ggaaagaaaag 60
 tgagcatctg ctttttaggg attatccagt ctatactact ctgttctagc cacacaaaac 120
 aggttaagac agaaattggg accaagagtg ggggtgttact acagcaaata cctgaaaatg 180
 tagaagaggc tttgaaatgt ggtaattgga agaagctggg agaatttgga ggagtaggct 240
 agaaaatgtc tgtattttca tgaatggagc attaagaata attccgggtga ggccataggg 300
 aaagtctaaa acttttcaga aattatgtaa gcgattgtga ttagtagggt ggtagaaaata 360
 tagacagtaa aagcaattct gatgtggttt cagaggaaaa tgaaaaatat tagaaactga 420
 aggaaggggc atccttgcta taaactggca aagaacttgg ctgaaatgtc tccatgtcca 480
 agagatttat ggcagaaatg t 501

<210> 595
 <211> 383
 <212> DNA
 <213> Homo sapien

<400> 595
 ctggtcacca tcatcccttt aatcaactca cacctgttta aagagtgttt ctgatttgac 60
 cttcatccct tagtttactg gcgttaaaaa aagtctcagc aattttcatt atttctcgtg 120
 ggtctcatta tcaaaccttt acttatttcg gcataatttc tctgggcttc ttctagtctc 180
 tgccttacaa gcaatgctgt tctgtaaacc tattgaaacc tctggaacat ttcacattta 240

```
gagatggagg atggaaggat tggtagcaga agaggggctaa gatacgtttt ctgtcttgag 300
ctgaaagcac agtctactct ccttcgtttt gtcgatgaga aagttgaggc cagaggggag 360
gtgacatggt tagagtcacc cag 383
```

```
<210> 596
<211> 266
<212> DNA
<213> Homo sapien
```

```
<400> 596
ccatggctag gtttatagat agttgggtgg ttggggtaaa tgagtgaggc aggagtccga 60
ggagggttagt tgtggcaata aaaatgatta aggatactag tataagagat cagggttcgtc 120
cttttagtggt gtgtatggct atcatttggt ttgagggttag tttgattagt cattgttggg 180
tggttaattag tcggttggtg atgagatatt tggagggtggg gatcaataga gggggaaata 240
gaatgatcag tactgcggcg ggtagg 266
```

```
<210> 597
<211> 383
<212> DNA
<213> Homo sapien
```

```
<220>
<221> misc_feature
<222> (1)...(383)
<223> n = A,T,C or G
```

```
<400> 597
ctgggtacca tcatcccttt aatcaactca cacengttta aagagtgttt ctgatttgac 60
cttcacccct tagtttactg gcgttaaaaa aagtctcagc aattttcatt atttctcgtg 120
gggtctcatta tcaaaccttt acttatttcg gcataatttc tctgggcttc ttctagtctc 180
tgcccttaca gcaatgctgt tctgtaaatt tattgaaacc tctggaacat ttcaccttta 240
gagatggagg atggaaggat tggtagcaga agaggggctaa gatacgtttt ctgtcttgag 300
ctgaaagcac agtctactct ccttcgtttt gtcgatgaga aagttgaggc cagaggggag 360
gtgacatggt tagagtcacc cag 383
```

```
<210> 598
<211> 266
<212> DNA
<213> Homo sapien
```

```
<400> 598
ccatggctag gtttatagat agttgggtgg ttgggtgtaaa tgagtgaggc aggagtccga 60
ggagggttagt tgtggcaata aaaatgatta aggatactag tataagagat cagggttcgtc 120
cttttagtggt gtgtatggct atcatttggt ttgagggttag tttgattagt cattgttggg 180
tggttaattag tcggttggtg atgagatatt tggagggtggg gatcaataga gggggaaata 240
gaatgatcag tactgcggcg ggtagg 266
```

```
<210> 599
<211> 294
<212> DNA
<213> Homo sapien
```

```
<220>
<221> misc_feature
<222> (1)...(294)
```

<223> n = A,T,C or G

<400> 599

ccaattgatt	tgatggtaag	ggagggatcg	ttgaccacgt	ctgttatgta	aaggatgcgt	60
agggatggga	gggcgatgag	gactaggatg	atggcgggca	ggatagttca	gacggtttct	120
atttcctgag	cgtctgagat	gttagtatta	gttagttttg	ttgtgagtgt	taggaaaagg	180
gcatacagga	ctaggaagca	nataaggaaa	atgactatga	gggcgtgatc	atgaaagggtg	240
ataagctctt	ctatgatagg	ggaagtagcg	tcttgtagac	ctacttgccg	tgca	294

<210> 600

<211> 213

<212> DNA

<213> Homo sapien

<400> 600

agatattggg	ctgttaattg	tcagttcagt	gttttaattct	gacgcaggct	tatgcggagg	60
agaatgtttt	catgttactt	atactaaca	tagttcttct	atagggatg	agattgggtcc	120
aattgggtgt	gaggagtcca	gttatatgtt	tgggattttt	taggtagtgg	gtgttgagct	180
tgaacgcttt	cttaattggg	ggctgccttt	agg			213

<210> 601

<211> 471

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(471)

<223> n = A,T,C or G

<400> 601

ncctactatg	ggtgttaa	tttttactct	ctctacaagg	ttttttccta	gtgtccaaag	60
agctgttcct	ctttggacta	acagttaa	ttacaagg	atttagagg	ttctgtgggc	120
aaatttaaag	ttgaactaag	attctatctt	ggacaaccag	ctatcaccag	gctcggtagg	180
tttgctgcct	ctacctataa	atcttcccac	tattttgcta	catagacggg	tgtgctcttt	240
tagctgttct	taggtagctc	gtctggtttc	gggggtctta	gctttggctc	tccttgcaaa	300
gttatttcta	gttaattcat	tatgcagaag	gtataggggt	tagtccttgc	tatattatgc	360
ttggttataa	tttttcatct	ttcccttgcg	gtactatatac	tattgcgcca	ggtttcaatt	420
tctatcgcct	atactttatt	tgggtaaatg	gtttggctaa	ggttgtctgg	t	471

<210> 602

<211> 482

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(482)

<223> n = A,T,C or G

<400> 602

tgagcataca	gcaataaaaa	taacataatt	tntatgtgta	caatatttat	ggaatacgtt	60
actggaacag	ataaataatt	tagttaataa	catgacaaag	aacagaaatt	gtatacacta	120
tacagcatag	taatagaata	atgaatgatt	aaagttatta	atattaggta	gaaaatgaag	180
ggatctcttg	agagcagaac	tcaaggaagc	aagcaatttg	ccttatgagg	aaagagttac	240

```

ctgtggataa aggagaaact gaaaaattta caagtcaaga ctttttgagc aaaaacaaaa 300
atatgactat gagtcaccaa ttcagtacag tgaaaaaaaaa gttgaagaga tatcttggaa 360
gtaaaccatg ttgtggaaga gcagggtttt gataatcatg ggattattct gaatgaattt 420
taaattgcgat aggaatatat gagataattt caccagagaa taatatgatc atgtttgcat 480
tt 482

```

```

<210> 603
<211> 372
<212> DNA
<213> Homo sapien

```

```

<400> 603
gttccaacct tcatttctga aactgttcta gagcactttg tctttctcgt agttcataac 60
ttacccttct agtctagaat tagaattaca ttatctgttt tactacttta ctagactgta 120
agctcctaga agataaggac tagggagttc atctctgtat tccaccagaa ggtacagtga 180
ctcataacta gagtctttag atgaaactta ctgagttgaa taacttaata tatttctgtt 240
ttcattccca agggaggcca tgtctggaga tagaccttga atttaataaa ttttaggcac 300
tataccattt cagtggagaa aattgttggg aaatttgggg ggatggatat ataaggggga 360
ggaagtcact gg 372

```

```

<210> 604
<211> 468
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1) ... (468)
<223> n = A,T,C or G

```

```

<400> 604
gcngttttga gtgagtttct taatcctgag ttctggnttg attgcactgt ggtctgagag 60
atagtttgtt ataatttctg ttcttttaca ctactgagg agagctttac ttccaagtat. 120
gtggctcgatt ttggaatagg tgtggtgtcg tgcagaaaag aatgtatatt ctgttgattt 180
gggggtggaga gttctgtana tgtctattag gtccgcttgg tgcagagttg agttcaattc 240
ctggatagcc ttgttaactt tctgtctcgt tgatctgtct aatgttgaca gtgggggtgg 300
aaagtctccc attattattg tgtgggagtc taagtctctt tgtaggtcac taaggacttg 360
ctttatgaat ctgggtgctc ctgcattggg tgcacatata tttaggacag cnagctcttc 420
ttgttgaatt gatcccttta ccattatgta atggccttgn ctcttttg 468

```

```

<210> 605
<211> 288
<212> DNA
<213> Homo sapien

```

```

<400> 605
ccaattgatt tgatggtaag ggagggatcg ttgacctcgt ctgcttatgta aaggatgcgt 60
agggatggga gggcgatgag gactaggatg atggcgggca ggatagttca gacggtttct 120
atttcctgag cgtctgagat gtagtatta gttagttttg ttgtgagtgt taggaaaagg 180
gcatacagga ctaggaagca gataaggaaa atgactatga gggcgtgatc atgaaagggtg 240
ataagctctt ctatgatagg ggaagtagcg tctttagtagc ctacttgc 288

```

```

<210> 606
<211> 572
<212> DNA

```

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(572)

<223> n = A,T,C or G

<400> 606

gaatnaaatg aatgaaatag aaaatataat tgagagcttc aacaacagac tataccaaat	60
ggaggaaaaa atttctgaac ttgaagatag atcttttgaa ataacacaag cagtggcaaa	120
aatgaattaa aaagaataag gaaagcctaa aggatttatg agatatcatt aagcaagcaa	180
atattcatac tatgggcatt ccagatggaa aaaagaaggg taaaggtag gaaatcatat	240
ttaatgaaat aatagcagaa aatttcgga gtcttgggag agagatgagc atttaggtcc	300
agggagctca aagaacccca aacagattca acccaaacag gtcctctctg gagcccaaca	360
tagtcaaatt gtaataagta aaagacaaag aattccaana agcattcaag agaaaagagt	420
caagtcatat ataagggaat ctccattagg ctaacagcag atatctcagc agaaagctta	480
cangccanga gagaatggga tgatatattc aaagtacttg aaagcagggg tnggggaaac	540
cctgctagct aaaaatatta tacccttgca aa	572

<210> 607

<211> 178

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(178)

<223> n = A,T,C or G

<400> 607

ctcggggtaa tctcccagca agaggtcagg tcctggntgt gcgtcccagg gtgtcagtga	60
aattggctgc tcccctgacc cagggcacct tcatgcgtct tcacagcagg actactgtga	120
ccaaggccag acctttcatc tttcaaaaga ctttgactaa aaatgcttta aaaaagca	178

<210> 608

<211> 416

<212> DNA

<213> Homo sapien

<400> 608

cctgtctttg aatggatgaa ataggttaat aaagaacatc actgtttaaa aactagaaca	60
ctgaaaaatt ctaggaaagc ttattttccc ttatatTTTT atgggtacttt caacacttaa	120
taacactatt tcaattaagt tttctcctag agtttatagt atatcagtac attcctttct	180
gtggatgcaa taatatagaa tcttattcca aatcttactg gcagggtctc ttaaattctt	240
caacggctgt catagtgatt aaccaaaatt agttatgatt tctgcctatc tgtgtgagaa	300
cttacagggg aaattgttct aaacctgagg aacatgaagt aactgtactg cacactccaa	360
atgatgacag tcattttata tcaccttcaa ttacccaaca gcttttaata gtctgg	416

<210> 609

<211> 648

<212> DNA

<213> Homo sapien

<400> 609

ctgatctctc agcagaaact cttcaaacca gaagagagtg ggggccaata ttcaacattc	60
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```

ttaaagaaaa taattttcaa cccagaatct catatccagc caaactaacc ttcacaagtg 120
aaggagaaat aaaatccttt acagacaagc aaatgctgag agattttatc accaccaggc 180
ctaccctaaa agagttcctg aaggaagcac taaacatgga aaggaacaac cagtaccatc 240
gaggctagga agaaaccgca tcaactaagg agcaaaaataa ccagctaaca tcataatgac 300
aggatcagat tcacacataa cgatattaac tttaaagtga aatggactaa atgctccaat 360
taaaagacac agactggcaa attggataaa gagtcaagac ccatcagggt gctgtattca 420
ggaaacccat ctcaccgtgc agagacacac atagggtcaa aataaagggc tggaggaaga 480
tctaccaagc aaatggaaaa caaaaaaagg caggggttgc aatcctagtc tctgataaaa 540
cagactttta accaacaag atcagaagag acaagaagg ccattacata atggtaaagg 600
gatcaattca acaagaagag ctaactatcc taaatatata ttgcaccc 648

```

<210> 610

<211> 310

<212> DNA

<213> Homo sapien

<400> 610

```

ccagctcttc tctgtcacat tcctatttct gacttctgcc tggctttcag tttctgcccc 60
accttggtct tttcccagct tgaacctaat agaactccag agtttggggg gaggccagc 120
cctttgtttt ctgctcttga agcatattca cacataaaaa gttgtattct cttacacaaa 180
ctgttttgag gctcttaccg tagtcgaagg tatcttagat cttccttagt gatctcata 240
agaatatccg aaagtgtata accctcttca acaatctgaa acaaagatca gatccttaag 300
agctgagcag 310

```

<210> 611

<211> 254

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(254)

<223> n = A,T,C or G

<400> 611

```

ctgtttttac atctaaagca atagactaga actgaattnt cttctacata gtaaaatcac 60
aattgtggaa ttacaggaat tctggtgata ttaaggtgaa acaacaaaac acaaaaggcc 120
ctatttttaac agttgatgtg acagtaagtt ttaatagaac ctgtaacttc attttggaaa 180
tgctttctcca ccaaataagg cctttttccc ctatttaagg agccagatgg attgaaagat 240
gtggaaatag gcag 254

```

<210> 612

<211> 225

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(225)

<223> n = A,T,C or G

<400> 612

```

ctgactatat catgtcacca tcatagccaa tacaacattn ttgccatact tcctaaaaac 60
cttttcgcat acactgatca tgctacttat cagcacttcc taacatcctg accaaacaga 120
caccacacac tcttatagag tacactgtga gagaataaca tggacttgat atggcatcac 180

```

acttgtttta aagcaaaaaa aaaagaaaaa gaaaagaaaa aaaaa 225

<210> 613
 <211> 471
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(471)
 <223> n = A,T,C or G

<400> 613
 ccacagact tcttggtgc ctggctatat tcaatgtgaa gtaaaaaata tcccaagtct 60
 tacacaaaa tagaggctct gacttagaag tatgctttta gctttctttt taaataagac 120
 attctggaag aaaaaaaaaa aaaaaggaaa gaaaatcaag tttgaaacac agttaacact 180
 tattttggca agaaagcaac caaaatctaa aaagcataaa ctatgngtcc aaatgnaaaa 240
 ggnattacag aacaaactgc aagaggggaa aattaaagcc nactgaacg aaaaaataca 300
 gtatgtctaa cattttggaa ttgnaattta aaccctaagg gcaaaagctg aaaaatcatg 360
 cttanacctn ggncngnacc acnctaaggc cgaattccan cactactggcg gncgttacta 420
 gtggatccna nctcgggtacc aagcttggcg taatcctngg catagctgtt t 471

<210> 614
 <211> 421
 <212> DNA
 <213> Homo sapien

<400> 614
 gttatttttt agaatggctc tcccactcttg agtatgtgtg atgtttcctc atgtatgaat 60
 gaagcatata catctttgtc agaagtatcc cagaagcaat tctgtactct cctcattatg 120
 ttctattggg tgggccatgg tttttgattt gtctcattac tgatgatggg tacttttatt 180
 atttgataaa gggtgtatat aacttatcta ttatggcata atacattagc taaaaccttg 240
 gcgggtgtaaa acagcagata cttacgtttc tcataggaat ggctctattg agtacctctg 300
 tctcaaggct tctcaagagt ttgtagctac cttgttggct ggggttgcg tctgacctaa 360
 aggccttagt aggggggtgg agaaatcttc catatgttct ttgctacgtg gacctcacag 420
 g 421

<210> 615
 <211> 242
 <212> DNA
 <213> Homo sapien

<400> 615
 cctcctattt attctagcca cctctagcct agccgtttac tcaatcctct gatcaggatg 60
 agcatcaaac tcaaaactacg ccctgacgga cgcactgcga gcagtagccc aaacaatctc 120
 atatgaagtc accctagcca tcattctact atcaacatta ctaataagtg gctcctttaa 180
 cctctccacc cttatcacaa cacaagaaca cctctgatta ctctgccat catgaccctt 240
 gg 242

<210> 616
 <211> 392
 <212> DNA
 <213> Homo sapien

<220>

200

<221> misc_feature
 <222> (1) ... (392)
 <223> n = A,T,C or G

<400> 616
 cctaatttgt agattgtgaa agcagctttt agtttaactt atttacagac cccttataat 60
 taccatgttt tttttttnt tcctaaatct ntgggttcag cttgngaattt ttacgtgccc 120
 gtaaagtngg gatgttgaat nggcccttnt ttgttctggc agngagtcaa gngtccanca 180
 ttttttcata agngtttttt aaaatngttc tccancattt tatggctcct ccctcccatg 240
 tcctcaaacc cagcaaaagc gtanaggcan aattanagga ccnccccggg cggccgntaa 300
 gggcnaattc cagcncactg gcggccgtta ctagnggatc cnagctcggn nccaagctng 360
 gcgtaatcat ggncatagct gtttcctgtg an 392

<210> 617
 <211> 215
 <212> DNA
 <213> Homo sapien

<400> 617
 cctactatgg gtgttaaatt ttttactctc tctacaaggt tttttcctag tgtccaaaga 60
 gctgttcctc tttggactac cagttaaatt tacaagggga tttagagggg tctgtgggca 120
 aattttaaagt tgaactaaga ttctatcttg gacaaccagc tatcaccagg ctcggtaggt 180
 ttgtcgcctc tacctataaa tcttcccact atttt 215

<210> 618
 <211> 433
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (433)
 <223> n = A,T,C or G

<400> 618
 cttttgtntg cctgttttgt ggactggctg gctctgttag aactctgtcc aaaaagtgca 60
 tggaatataa cttgtaaaagc ttcccacaat tgacaatata tatgcatgtg tttaaaccac 120
 atccagaaag cttaaaccaat agagctgcat aatagtattt attaaagaat cacaactgta 180
 aacatgagaa taacttaagg attctagttt agttttttgt aattgcaaatt tatatttttg 240
 ctgctgatat attagaataa tttttaaatg tcatcttgaa atagaaatat gtattttaag 300
 cactcacgca aaggtaaatg aacacgtttt aaatgtgtgt gttgctaatt ttttccataa 360
 gaattgtaaa cattgaactg aacaaattac ccataatgga tttggttaatt gacttatgag 420
 caagctgggt tgg 433

<210> 619
 <211> 259
 <212> DNA
 <213> Homo sapien

<400> 619
 ctgcagtgtc cctttttata tcatgctagt gttgagacat acttgactaa cttgggaaca 60
 gttcgatata ttgacaaccg tcaacttaag aaaatcaaca gcttttggcc ccagcgtcca 120
 agtgaacttt tcatggagtg cagaatctca aatggacaaa atactttgtc tttttaaata 180
 ctgaaaattt aattattagt actatgactg aaagattctt catggctaaa aagctctgca 240
 tcaaactcaa ttcaggagg 259

201

<210> 620
<211> 393
<212> DNA
<213> Homo sapien

<400> 620
ccaccaaagc cacacggaga ttctgtcagg cgctgagaca ccacagcctt ttcaatctta 60
gggaaagaaa tcaagtcata taaattaata tcaacaggta aggtcattga gcaattgtct 120
ttcaactgtc taagacttta tcacttaaga tcataaacac agaagcaggt cataaaaaata 180
gcttttctta aggttttagga gaattttagg gggcacttac ttgataatct gaattttctta 240
gtcagaagtt taaataccac cttttaaaaa cataaaattt aatttgtaac aagttattaa 300
caaagcagta ttgtcgaaag ttttaagctt tctcccaata atttaattac attaatataa 360
tttttaccat tctaattggtt acaaagtaac cag 393

<210> 621
<211> 563
<212> DNA
<213> Homo sapien

<400> 621
ctgacaatga taaaattatc tctatatggg caaacgcgtg ctctttgtcg aagaagaaag 60
cttcagcttc atgttccagg tgagttaatt aggcaatgta tgaatgctaa tatctctttc 120
acatattttg cttaagatct gtcttaggac tctcgtctgg cccatattgg tttccaaggg 180
cagaagggcc tctttttgat gagaggcagt tttcagtaac tcttaaagtg ataacagcaa 240
aggagaggag agagaagagt aagacaaatc gaaacattct tcaattgctt cttggccttt 300
tggttaagct caagctcaaa acaggtcttc aaggagaaaa tacatcacia agaaaaggat 360
gtttttattc ttaccttgct ctagaaaaat ttccataaac tctattggct taattctgta 420
aacttgacca atatcagagt gcttcctacc aaggagggtg gctgatgagc gtgacctggg 480
tacatcctag aagaatgtgt gatgaagaag ctttcaccgt gtaaaagagt tgaaaattat 540
tcaaggagac attatggtct tgg 563

<210> 622
<211> 505
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1) ... (505)
<223> n = A,T,C or G

<400> 622
tcttaagtgt gtttaataga taaagtaaac tttcctagtc aagggttaga tttttattat 60
ctcttggtgt cggactttct acttttcaac ttgtgaacttc aaaaaaacat tactttgctt 120
atccttttga ctttgatcag gttgtttaga attgtagatc aaaccattct ttgatcattt 180
tattgtttta atgnntagtt ccatttataa tttttatagc caactctcgg ttattttctgt 240
cttttgagat tgcaattcag aagctgtatg tcgaagtaat ttatgagttg actttttatac 300
ttaggcttct ttaaatacta atagtcaaga attctagagc atctaataaa aaattaacct 360
tcagatcatt gggaatctgt cctcatttaa atatgtgtaa atgcatttcc acagcaaatt 420
gcttcatgcc ctttgnctat aaggaaatta ttccttgtag ctaatacatt tttcattttg 480
cagnccaaat cttttttgag aaagg 505

<210> 623
<211> 489

<212> DNA

<213> Homo sapien

<400> 623

cctactatgg	gtgttaaatt	ttttactctc	tctacaaggt	tttttcctag	tgtccaaaga	60
gctgttcctc	tttggactaa	cagttaaatt	tacaagggga	tttagagggt	tctgtgggca	120
aatttaaagt	tgaactaaga	ttctatcttg	gacaaccagc	tatcaccagg	ctcggtaggt	180
ttgtcgcttc	tacctataaa	tcttcccact	atthtgcctac	atagacgggt	gtgctctttt	240
agctgttctt	aggtagctcg	tctggtttcg	ggggctcttag	ctttggctct	ccttgcaaaag	300
ttattttctag	ttaattcatt	atgcagaagg	tataggggtt	agtccttgct	atattatgct	360
tggttataat	ttttcatctt	tcccttgccg	tactatatct	attgcgccag	gtttcaattt	420
ctatcgctat	actttatttg	ggtaaatggg	ttggctaagg	ttgtctggta	gtaagggtga	480
gtgggtttg						489

<210> 624

<211> 233

<212> DNA

<213> Homo sapien

<400> 624

gttggggaac	agctaaatag	gttgtgtgtg	atttggttaa	aaaatagtag	ggggatgatg	60
ctaataatta	ggctgtgggt	ggttgtgttg	attcaaatta	tgtgtttttt	ggagagtcac	120
gtcagtggta	gtaataaat	tgttgggacg	attagtttta	gcattggagt	agggttaggt	180
tatgtacgta	gtctaggcca	tatgtgttgg	agattgagac	tagtagggct	agg	233

<210> 625

<211> 459

<212> DNA

<213> Homo sapien

<400> 625

ttcgagaaca	tttttaataa	ataatgtgac	aaaattactt	ttctgattat	tggattttca	60
gtatgcaaaa	ttatggctaa	aaataagggg	cttcttacat	gaacataatg	aaaacattaa	120
tcacatggat	tggtccctta	gtactgcacg	ccttttctat	ggaacttttt	caaattatct	180
aaatgaacaa	gtttggtttt	ggatgaacac	agcctttttt	tttgtgggtc	agttttgttt	240
ggctttgtct	tccactgggg	tcagacctga	tacttatcta	tctatgaata	aatgtacatt	300
tttttcttca	aatagcacca	attataaaat	caatgatatt	cataaaatga	caaaaaagga	360
tcatagaat	ctactagtca	gagggcacat	tttgtcaatt	gaaagcaagt	aatgcctcta	420
ttagagattt	taaggaaatc	ttgtaggttt	cgacattgg			459

<210> 626

<211> 458

<212> DNA

<213> Homo sapien

<400> 626

cctgatgatt	gttttaaaaca	gtagaaaggg	ttcagctaag	aactacagtc	cactctcagc	60
cctgtcatgt	actataggac	aagtcttcat	tcacaacaaa	tggatagcaa	caccaatctc	120
gtaacactgg	gaaaactgca	tacaatat	agaaggaaca	ctaatacagc	agaatctgca	180
cacaacggag	tcaaagatct	gaggccaaat	cctactacac	tttacgactt	tgagttggtc	240
acttttctga	accttagctt	ctccatcagt	gtaaaactga	tgtaaaataa	tataaagcta	300
tatgaaagct	gatgtgat	acttgtgaaa	tagtatgtgc	aaaaggactt	tgtaaaatgt	360
aaagcactat	gctggttatt	gtgatatctg	agatatattt	aaagttgcaa	ttcaattcaa	420
caagcattca	tttagagtca	tgtgcaaggc	actgtgct			458

<210> 627
 <211> 393
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(393)
 <223> n = A,T,C or G

<400> 627
 ccatnngaac gcactcagga ggtgggttgt tctggatgca gaaaccagag atctagtttc 60
 tatccacaca gacgggaatg aacagctctc tgtgatgcgc tactcaatag atggtagctt 120
 cctggctgta ggatctcatg acaactttat ttacctctat gtagtctctg aaaatggaag 180
 aaaatatagc agatatggaa ggtgcactgg acattccagc tacatcacac accttgactg 240
 gtccccagac aacaagtata taatgtctaa ctgaggagac tatgaaatat tgtactggga 300
 cattccaaat ggctgcaaac taatcaggaa tcgatcggat tgtaaggaca tttgattgga 360
 ccgacatata cctgtgggct aggacttcca gga 393

<210> 628
 <211> 233
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(233)
 <223> n = A,T,C or G

<400> 628
 ctggatttat aaaatagttg aatgacaaaa gaagnntggt ttgacagtaa aaaaaagaca 60
 ttatggacaa aatatgcaa atgtgcaaag aaaaaataaa tttgcattag aaaggtgggc 120
 atttgatctc tgagccctgt gccatgtaac attgccatgt tctttcactg ttgtttgaat 180
 gttgtacccc ancccttgac tctggactta aggcaagcta tgactggctt tgg 233

<210> 629
 <211> 450
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(450)
 <223> n = A,T,C or G

<400> 629
 ccnggacaat ntaggcagga gaaggaaata aagggtattc aattaggaaa agaggaagtc 60
 aaattgtccc tgtttgcaga tgacatgatt gtatatctag aaaaccccat tgcctcagcc 120
 caaaatctcc ttaagctgat aagcaactcc agcaaagtcg caggatacaa aatcaatgga 180
 cacaaatcac aaacattctt atacaccaat aacagacaaa cagaggccaa atcacgagtn 240
 gaactctatt ccaattgctt tcaagaaaat taaaatacct agggatccaa cttacaaggg 300
 acatgaagga cctcttcaag gagaaactac aaaccactgc tcaatgaaat aaaagaggat 360
 acaaagaaat ggaagaacat tccatgctca ttggtagctt gatggggatg gcattgaatc 420
 tataaattac cttgggcagt atggacctca 450

<210> 630
<211> 486
<212> DNA
<213> Homo sapien

<400> 630
cctactatgg gtgttaaatt ttttactctc tctacaaggt tttttcctag tgtccaaaga 60
gctgttcctc ttggactaa cagttaaatt tacaagggga ttagaggggt tctgtgggca 120
aatttaaagt tgaactaaga ttctatcttg gacaaccagc tatcaccagg ctcggtagggt 180
ttgtgcctc tacctataaa tcttcccact attttgctac atagacgggt gtgctctttt 240
agctgttctt aggtagctcg tctggtttcg ggggtcttag ctttggctct ccttgcaaag 300
ttatttctag ttaattcatt atgcagaagg tataggggtt agtccttgct atattatgct 360
tggttataat ttttcatctt tcccttgctg tactatatct attgcgccag gtttcaattt 420
ctatcgccca tactttattt gggtaaatgg tttggctaag gttgtctggt agtaagggtg 480
agtggg 486

<210> 631
<211> 211
<212> DNA
<213> Homo sapien

<400> 631
tttacataaa tattatacta gcatttacca tctcacttct aggaatacta gtatatcgct 60
cacacctcat atcctcccta ctatgcctag aaggaataat actatcactg ttcattatag 120
ctactctcat aacctcaac acccactccc tcttagccaa tattgtgcct attgccatac 180
tagtctttgc cgcctgcgat gcagcggtag g 211

<210> 632
<211> 293
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(293)
<223> n = A,T,C or G

<400> 632
cagcgcaagt aggtctacaa gacgctactt cccctatcat agaagagctt atcacctttc 60
atgatcacgc cctcatagtc atttttcctt atctgcttcc tagtctgtga tgcccttttc 120
ctaacactca caacaaaact aactaatact aacatctcag acgctcagga aatagaaacc 180
gtctgaacta ngctgcccgc catcatacta gtctcatcg cctcccatc cctacgcac 240
ctttacataa cagacgaggt cnacgatccc tcccttacca tcaaatcaat tgg 293

<210> 633
<211> 263
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(263)
<223> n = A,T,C or G

<400> 633

nggtctgcag	tgtccctttt	tatatcatgc	tagtggtgag	acatacttga	ctaacttggg	60
aacagttcga	tatattgaca	accgtcaact	taagaaaatc	aacagctttt	ggccccagcg	120
tccaagtga	cttttcatgg	agtgacagaat	ctcaaatgga	caaaatactt	tgtcttttta	180
aatactgaaa	attnaattat	tagtactatg	actgaaagat	tcttcatggc	taaaaagctc	240
tgcacaaac	tcaattcagg	agg				263

<210> 634
 <211> 491
 <212> DNA
 <213> Homo sapien

<400> 634						
cctactatgg	gtgttaaatt	ttttactctc	tctacaaggt	tttttcctag	tgtccaaaga	60
gctgttcctc	tttggactaa	cagttaaatt	tgcaagggga	tttagagggt	tctgtgggca	120
aattttaaagt	tgaactaaga	ttctatcttg	gacaaccagc	tatcaccagg	ctcggtaggt	180
ttgtcgcttc	tacctataaa	tcttcccact	attttgctac	atagacgggt	gtgctctttt	240
agctgttctt	aggtagctcg	tctggtttcg	ggggtcttag	ctttggctct	ccttgcaaaag	300
ttatttctag	ttaattcatt	atgcagaagg	tataggggtt	agtccttgct	atattatgct	360
tggttataat	ttttcatctt	tcccttgccg	tactatatct	attgcgccag	gtttcaattt	420
ctatcgctta	tactttattt	gggtaaatgg	tttggctaag	gttgtctggg	agtaaggtgg	480
agtgggtttg	g					491

<210> 635
 <211> 270
 <212> DNA
 <213> Homo sapien

<400> 635						
ccaattgatt	tgatggtaag	ggagggatcg	ttgacctcgt	ctgttatgta	aaggatgcgt	60
agggatggga	gggcgatgag	gactaggatg	atggcgggca	ggatagttca	gacggtttct	120
atttcctgag	cgtctgagat	gttagtatta	gttagttttg	ttgtgagtgt	taggaaaagg	180
gcatacagga	ctaggaagca	gataaggaaa	atgactatga	gggcgtgatc	atgaaagggtg	240
ataagctctt	ctatgatagg	ggaagtagcg				270

<210> 636
 <211> 383
 <212> DNA
 <213> Homo sapien

<400> 636						
cctactatgg	gtgttaaatt	ttttactctc	tctacaaggt	tttttcctag	tgtccaaaga	60
gctgttcctc	tttggactaa	cagttaaatt	tacaagggga	tttagagggt	tctgtgggca	120
aattttaaagt	tgaactaaga	ttctatcttg	gacaaccagc	tatcaccagg	ctcggtaggt	180
ttgtcgcttc	tacctataaa	tcttcccact	attttgctac	atagacgggt	gtgctctttt	240
agctgttctt	aggtagctcg	tctggtttcg	ggggtcttag	ctttggctct	ccttgcaaaag	300
ttatttctag	ttaattcatt	atgcagaagg	tataggggtt	agtccttgct	atattatgct	360
tggttataat	ttttcatctt	tcc				383

<210> 637
 <211> 537
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature

<222> (1) ... (537)

<223> n = A,T,C or G

<400> 637

ttttaatcct	ggggtatata	ggcagnactt	taaattgcaa	agtcttccgg	gcctattttc	60
ctctacattt	ttgtaattaa	ctctgggggc	ttacttggtt	tggcagtact	gaaatcaaag	120
gagctgggtc	ttcttttctc	ccaattattt	tcatatgaaa	gcacctacaa	ttagcctggt	180
agtcctattc	agatacatca	aatatcagtg	aatgctttac	tattcgcaca	tttaagcatc	240
tttgttttac	ataaaattag	agtatgaaaa	ccagtgttca	attttttatc	ttggtgagct	300
tgtaaaatgc	cagcaattta	aaactaggac	ttttccccc	ataagccaag	gaggtagaat	360
tactaataca	agggttaaag	aaggtagatt	ttgttttcaa	tatttggtta	atattagaaa	420
gattcttccc	acagggaaga	actagcaagt	gtcccaattt	tttccaaacg	ttggggaggg	480
gaaaattcac	tgtatcatga	aaccctaagg	gtttgngtgc	acttcctgct	ttttagg	537

<210> 638

<211> 445

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (445)

<223> n = A,T,C or G

<400> 638

ccagcagaac	acagnagtga	tttgggtccc	tttgttcccc	agtgggggat	ctatecttgt	60
gcagggcaca	agcctacatg	gtggctctgg	tcatatcatt	agaaaataga	cagaaatggg	120
ctgcacacca	gaatgaatga	attgaattga	aaggggaggag	tgatggtgga	aaaaaaaaaca	180
agtcaattca	tttagactgg	tagaaccaga	accactgtgt	agtacatcca	aacgggttaa	240
attccctgga	agatgttaca	taatcctatc	atggtgttta	tttatggaaa	tctatttttaa	300
aaattttatg	taatactgca	cagtctgttt	gcatgatgcc	ttgtacgtag	tagcaactca	360
gtaaatactt	tttgaatgaa	ctagtatagt	attttaatta	gctagtcttc	gtgtactggt	420
acaaaagaac	agtgtcatct	tacag				445

<210> 639

<211> 584

<212> DNA

<213> Homo sapien

<400> 639

gcttgagtat	tctatagtgt	cacctaaata	gcttggcgta	atcatggtca	tagctgtttc	60
ctgtgtgaaa	ttgttatccg	ctcacaaatc	cacacaacat	acgagccgga	agcataaagt	120
gtaaagcctg	gggtgcctaa	tgagtgagct	aactcacatt	aattgcgttg	cgctcactgc	180
ccgctttcca	gtcgggaaac	ctgtcgtgcc	agctgcatta	atgaatcggc	caacgcgcgg	240
ggagaggcgg	tttgcgtatt	gggcgctctt	ccgcttcttc	gctcactgac	tcgctgcgct	300
cggtcgttcg	gctgcggcga	gcggtatcag	ctcactcaaa	ggcggtaata	cggttatcca	360
cagaatcagg	ggataacgca	ggaaagaaca	tgtgagcaaa	aggccagcaa	aaggccagga	420
accgtaaaaa	ggccgcgttg	ctggcgtttt	tccataggct	ccgccccctc	gacgagcatc	480
acaaaaatcg	acgctcaagt	caagaggtgg	cgaaaccgga	caggactata	aagataccag	540
gcgtttcccc	ctggaagctc	cctcgtgcgc	tctcctgttc	cgac		584

<210> 640

<211> 404

<212> DNA

<213> Homo sapien

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<400> 640
ccataggaac gcactcaggc aggtgggttg ttctggatgc agaaaccaga gatctagttt    60
ctatccacac agacgggaat gaacagctct ctgtgatgcg ctactcaata gatggtacct    120
tcctggctgt aggatctcat gacaacttta tttacctcta tgtagtctct gaaaatggaa    180
gaaaatatag gagatatgga aggtgcactg gacattccag ctacatcaca caccttgact    240
gggtcccaga caacaagtat ataatgtcta actcgggaga ctatgaaata ttgtactggg    300
acattccaaa tggctgcaaa ctaatcagga atcgatcgga ttgtaaggac attgattgga    360
cgacatatac ctgtgtgcta ggatttcaag tatttggtgt ctgg                    404

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<210> 641

<211> 138

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (138)

<223> n = A,T,C or G

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<400> 641
ctgtgacagg aacattacct gaagtgcagg gtggttacct gcacaaagtc ccatttccaa    60
aaatttctgt gtaattcacc agaaattttg gatggaataa ttagaaaaaa aaaaagaggt    120
taaaacntgt aactcaaa                    138

```

<210> 642

<211> 381

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (381)

<223> n = A,T,C or G

```

<400> 642
ctgtaggtgg aatttttacc cagaaaagat aggccctaga agcctcattt cttttctcca    60
tggaaaagga cagccctctg ctgcagcggt caacttggtg gtttactgac agagtgaact    120
acagaaatag cttttcttcc taaaggggat tgttctacat tttgaagtta ttttttaata    180
aaattgaatt atgttggtga ttgtgcttcc taataggaaa tgcattattg gactgttttt    240
gtaacatcct gtttattgca aatagctagt atcgttcaaa aactgtataa aatacttttg    300
tacatattag caatgtctaa tttgtataca cttcagttaa atttccttaa aacttgaaag    360
gggaccttgt anaaattaaa a                    381

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<210> 643

<211> 403

<212> DNA

<213> Homo sapien

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<400> 643
ccttcctaaa aaatagtggg gagctggagg ctacttccgc cttcttagcg tctggtcaga    60
gagctgatgg atatccatt tggccccgac aagatgacat agatttgcaa aaagatgatg    120
aggataccag agaggcattg gtcaaaaaat ttggtgctca gaatgtagct cggaggattg    180
aatttcgaaa gaaataattg gcaagataat gagaaaagaa aaaagtcatg gtagggtagg    240
tggttaaaaa aaattgtgac caatgaactt tagagaggtc ttgcattgga actggcactt    300

```

atcttctgac catcgctgct gttgctctgt gagtcctaga tttttgtagc caagcagagt 360
tgtagagggg gataaaaaga aaagaaattg gatgtattta cag 403

<210> 644

<211> 688

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(688)

<223> n = A,T,C or G

<400> 644

cctatttatt tgttttgccc ctggatcttt cctaatacaca attatatttc tttatttttg 60
cctttgagca gtttcattta tctttgtggg caggaagat taaatatgaa attcagtcca 120
gtcattttgc tactggtag ctttagttg aggcaagtaa aaatttttga ttaaaattag 180
tttcttaaaa ttatgccctt gctttaccaa ataatacaat tggctaaaaa ataagggtat 240
gtaactttgc attttgaaga acaaaccaat aatttttcat gagccctact cgatcttctt 300
taaagaagac cttcctaaga gacaattagg gatgagttg attaattgga aatagctcta 360
ggttagatta ttttaaattc catacaccaa gtgatttaac cacagtggca gtggcagctt 420
ctgaaccgtc aagtatgaac atcacttaaa aattaaaaga tgcttaataa taaactctta 480
attttcatta agccaatctg taattcagaa gaaaagcata tgtctgccat gggactattg 540
cagtgcgtct ccatcagtgt taacacagga gagatatgtt attttatgtg tatgtcttag 600
tttgggatat gtggtagtaa gaacatgtca agagtgtctt tcttcaaacc tgnacagctca 660
actgangaaa gacaggtact tccattgc 688

<210> 645

<211> 484

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(484)

<223> n = A,T,C or G

<400> 645

ccaaatgtgt ctccagccca cacttccagg tggcagagcg agctctctat tactggaata 60
atgaatacat catgagtta atcagtgaca acgcagcgaa gattctgccc atcatgtttc 120
cttccttgta ccgcaactca aagaccatt ggaacaagac aatacatggc ttgatataca 180
acgccctgaa gctcttcatg gagatgaacc aaaagctatt tgatgactgt acacaacagt 240
tcaaagcaga gaaactaaaa gagaagctaa aaatgaaaga acgggaagaa gcatgggtta 300
aaatagaaaa tctagccaaa gccaatcccc aggtactaaa aaagagaata acatgaaac 360
gcccagggtt acttgaatgt ttttataaga taggaatata tgtcttcacc atgggggggg 420
gtctcggatt tcactaacgt tgtatatgaa aatgggtgcn ataaaaagta cttttaaac 480
ttgt 484

<210> 646

<211> 447

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (447)

<223> n = A,T,C or G

<400> 646

```

gggtcgcgctt gaacaacttg gttcaagatg gtgggggcat ttttagagcg gcaataattg      60
aaaaaaaaagg cgaactctgc cttggagagg tagatgataa gaaataaaaa ggtgtttata      120
actattttgt attataaagt gggccttaga gataggaaga agaattgatg attccttttg      180
gatcaatcag aaaggaaaca cgaaagaaaa gtcaggaagg tagagagaga aaaagggagg      240
gaaggagaaa gaatgggaat aaaataagga ggtaagagat actatttttg ctgagcaacc      300
agtgtgtttc aggatgatac aaagaaaaat atagaataga aataagtgca ggcttggaa      360
cagctacaaa tcctaaagat ggggtgtgtg tggatgtgtg tgtgtgtgtg tgnacaccat      420
tgtgtgtttg taaaatgtgt atgtccc                                     447

```

<210> 647

<211> 388

<212> DNA

<213> Homo sapien

<400> 647

```

gaagggtgata taaaatgact gtcatcattt ggagtgtgca gtacagttac ttcattgttcc      60
tcagggtttag aacaatttcc cctgcaagtt ctcacacaga taggcagaaa tcataactaa      120
ttttggttaa tcactatggc agccgttgaa gaatttaaga gaacctgcca gtaagatttg      180
gaataagatt ctatattatt gcatccacag aaaagaatgt actgatatac tataaactct      240
aggagaaaac ttaattgaaa tagtgttatt aagtgttgaa agtaccataa aaatataagg      300
gaaaataagc tttcctagaa tttttcagtg ttctagtttt taaacagtga tgttttttat      360
taacctattt catccattca aagacagg                                     388

```

<210> 648

<211> 632

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (632)

<223> n = A,T,C or G

<400> 648

```

cctggctggg cntttgacct gcgnttttaa atnactcaca gaggggtggga caggaggaag      60
agtgaaggaa aaggtcaaac ctgttttaag ggcaacctgc ctttgttctg aattggtctt      120
aagaacatta ccagctccag gtttaaattg ttcagtttca tgcagttcca atagctgac      180
attgttgaga tgaggacaaa atcctttgtc ctactagtt tgctttacat ttttgaaaag      240
tattattttt gtccaagtgc ttatcaacta aaccttgtgt taggtaagaa tggaaatttat      300
taagtgaatc agtgtgaccc ttcttgatcat aagattatct taaagctgaa gccaaaatat      360
gcttcaaaag aagaggactt tattgttcat ttagttcat acattcaaag catctgaact      420
gtagtttcta tagcaagcca attacatcca taagtggaga aggaaataga tagatgtcaa      480
agnatgattg gtggaggagg caaggttgaa gataatctgg gggtgaaatt ttctagtnt      540
cattccgtac attttttagt agacatcaga tttgaaatat taatgttacc tcctcaatgg      600
ggtggtatca gacctgcccg ggcgncggnn tc                                     632

```

<210> 649

<211> 300

<212> DNA

<213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(300)
 <223> n = A,T,C or G

<400> 649
 nggtgaagat agaanaaata taagcgaaat tggataaaat agcactgaaa aaatgaggaa 60
 attattggta accaatttat tttaaaagcc catcaattta atttctgggtg gtgcagaagt 120
 tagaaggtaa agcttgagaa gatgagggtg tttacgtaga ccagaaccaa tttagaagaa 180
 tacttgaagc tagaagggga agttgggtta aaatcacatc aaaaagctac taaaaggact 240
 ggtgtaattt aaaaaaaact aaggcagaag gctttggaag agttagaaga atttgggaagg 300

<210> 650
 <211> 498
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(498)
 <223> n = A,T,C or G

<400> 650
 ngtnctgnta aacagaaggg tacaangccc ttctggcttt aagcagtcac aggaatgtga 60
 cagacattcc tcttagggag cgcctcctcc taggggttcc tcatctgtct cacactgagt 120
 ggatgtaatg ctattttaat cctgctgtgg cccccaatac tagtacttgt ccataccttc 180
 ttgcattttt agcgtctgct ctgtgggggt gttaggccct ggcaactcca ggaactagt 240
 ctaaagctgc atctntctct cccctctagg gatcgataaa gtttactgc agaaagtctc 300
 cactgcggtg tgctgacatc tgccctgaac cttcacccta cagcattaca ggctttaatc 360
 agattctgct ggaaagacac aggtgatcc acgtgacctc ttctgccttc actgggctgg 420
 ggtgatcctt ggtgcctttg tttccacaag gccttttccct gccccctgcc ttgccaaaga 480
 catttaatca gcacacag 498

<210> 651
 <211> 654
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(654)
 <223> n = A,T,C or G

<400> 651
 ctgaggggtcc ccagggtttct aaagctctca ggacgagaaa gtaggtccca agataaggag 60
 cctaaagggc ttttttcttt ctgtgtattc cttcttggcc tccaacatgg gtacagtcac 120
 aagagcatgt aacagagaag aaggactana cctaccattt tctggataaa gaattggaaa 180
 gaggatccac aggtaaccaa aaagtaccag ggaaatggca gagaaggaaa acctcaggag 240
 accaacctca taagtggat ttattagncc ctgggctcaa atccaaattg tacatgaata 300
 tgtctgggtcc tagatagggt accgaagact ttgaaagtga attttggtat atcattgccc 360
 agattccaga ctggnatttg tgtgacacaa catacaggat atatctgaat agtgctcaga 420
 agagtttgaa aatgcaaatg atattaaaat aaagatgaaa aagagaaagc tggtcagaac 480
 ttgtggacat aacccttctg gatctgtngc ctgattaaaa aatagttgat attctcgaat 540
 gaattaaaac aagatttaga gactgagcat ggtagctnat tcttgtaatc caacnctttg 600
 ggaggggcaag gcaanagaat tgcttgccgc caggagtttt gagaccagct tggg 654

211

<210> 652
 <211> 293
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(293)
 <223> n = A,T,C or G

<400> 652
 ngctctgttgc actgaggtga ctaaggatac attttgagga agtagctcca agaacatttc 60
 cattttcact gtgccttcac atacatctaa tggaaatgaa cagcaccctt catccatcca 120
 cggaagcgat taagaaaagg gtgggatgga aaaattaacc caacaatatt agatcaatac 180
 gtagtattta agngtccata atgtgccagg ctgaagatgc acgggaaaac cacactagcc 240
 ggtctgtcaa gggcttgaga ataccataaa caagaaaaca gacgaaccaa ttt 293

<210> 653
 <211> 294
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(294)
 <223> n = A,T,C or G

<400> 653
 ngtcaccac. tgcagcccta catacagttg aaaaaaaatt ccattctgtt aacatttgtt 60
 ttataagttt tcacgcaata cacaaaaaac ccctctgcac ttcttgtaaa gaacaaaaaa 120
 gatacacaac agttaagcgt aaagatcaca ggcaatagca ttcaaacatg gatgtgggta 180
 gagaaaggag tacctggcat gagtacctgc ttagtttgac tgaatccttg atttttaatt 240
 tggcttttca tgggccgctc acaacaccaa cgctgtgtga ggtatggtag tcag 294

<210> 654
 <211> 250
 <212> DNA
 <213> Homo sapien

<400> 654
 ctgtccttga acaagtatca atgtgtttat gaaaggaaga tctaaatcag acaggagtgtg 60
 gtctacatag tagtaatcca ttgttggaat ggaacccttg ctatagtagt gacaaagtga 120
 aaggaaattt aggaggcata ggccatttca ggcagcataa gtaatctcct gtcctttggc 180
 agaagctcct ttagattggg atagattcca aataaagaat ctagaaatag gagaagattt 240
 aattatgagg 250

<210> 655
 <211> 494
 <212> DNA
 <213> Homo sapien

<400> 655
 ccattataat tttataacac cattaccctt taaattctac cgattataag cagcgtaaaa 60
 gtaactatat aaagcaaaca tcgcaaagga actctgcagg agctcttaatt tcctttatgt 120

```

agctatcata aaattcactt tcctgaagac atttactctc attcacttcc aaactccaaa 180
cctttttctg gtagcaccac ttttgTTTTT aatagaaaga tgagttcata tctgtacatc 240
tctccaaagc tctaaggaat gagaaaagga tcctagtata ttgaaattac tgatgtttaa 300
tacctctgcc ttttacttaa aagccattta atatttttaa agtcaaaact tgacatacag 360
gtatttataa ggaatctcca tgactctgaa ggaatgaaat tgatgtagggt agctttggct 420
atgtaaagac atagtagagg acaattactt aaagaagagt tttcttttga ggattttag 480
atttgactaa gcag 494

```

<210> 656

<211> 477

<212> DNA

<213> Homo sapien

<400> 656

```

cgcgttactg tacatattgc tagcaggaga caactggaaa tactaaacaa atactggaat 60
tcacattaca gacagacgaa accaacaagg atgccacaca taacttcctt ttagtattca 120
cagagggcct atttgtggtt gctcagggtg ggtcatacat tgcttgaga aatggcctga 180
tcatagctct atgaaacaat gaattcggaa tgaaatctta ccatgacacc tctctgtagg 240
aaagaaatgt tgcttcacgt gtgctaagtt gagataataa tatttcacat atttatatac 300
agagaatcac tctcaaattt aaccaagat aagcaatagg atttgggggt gacttgtaga 360
catttctaac aacacttttc tttttcttag aggtcactct caaacactga tatatcata 420
tagtttgaat gtagggattc agtaatcaaa ggttggtatt gcaaaagagc caggcag 477

```

<210> 657

<211> 576

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(576)

<223> n = A,T,C or G

<400> 657

```

cctctacctg tanatcacta tttttctaaa gacaatttgg tgttttgaag ataaatgtca 60
ttagtctatg ataatagcat cataggacaa ttagccattt tagacttgac catattttct 120
cttttttagc tatagccatc ttgatattta ggtgggagac tactccaatg gagcaacagt 180
ttcattttac atgattggat ttagaaattt acaaatttta aactcataag aattctaaat 240
aatltgaaaa tggaaacatt tgaccacag tctagcagca taaatacatt tataaaatac 300
ttcattgttg atcttaggtc attgatTTAA aacagaattt ggtgactatg ggcagggtgga 360
gggggcccag gaggaaggta taaaagagaa atctttatga attgtgttca gattgatttt 420
gtataaacat aatatattca tggttgtatc tcttatttat aatacccaac taacatgaag 480
gtggtccaag ggaaggatca atatttttaa taacatattt gcttaaaata tcatacagtg 540
gctgcttcat aaaaaatctt ataaactttt attacc 576

```

<210> 658

<211> 344

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(344)

<223> n = A,T,C or G

<400> 658
cctgaaaaga aagntgctct tatggactct tgcattgttaa gactatgtct tcacatcatg 60
gtgcaaatca catgtaccca atgactccgg ctttgacaca acaccttacc atcatcatgc 120
catgatggct tccacaaagc attaaacctg gtaaccagag attactgggtg gctccagcgt 180
tgttagatgt tcatgaaatg tgaccacctc tcaatcacct ttgagggcta aagagtagca 240
catcaaaagg actccaaaat cccataccca actcttaaga gatttgtcct ggtacttcag 300
aaagaatttt catgagtgtt cttaattggc tggaaaagca ccag 344

<210> 659
<211> 230
<212> DNA
<213> Homo sapien

<400> 659
ctgctttccc tgctaaacag ttccagagca aaagcagcaa aaagaaaata tgggagggat 60
atgggcaacg tatactcgaa cgtacgcaga gaagagagta cggttagctc taatatttct 120
cattgaactt ggtggatgt gccttccctg catataaggc catagtgcct ttttgggagc 180
gctagaatat ccatccactt gacagtgacc acaaaatagg ctgtttccag 230

<210> 660
<211> 80
<212> DNA
<213> Homo sapien

<400> 660
ctggctccttg taaactcga tcaccacttt ggagagatcg actggaggct cctgggtgtt 60
ctgagggggcc tgggggacag 80

<210> 661
<211> 535
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1) ... (535)
<223> n = A,T,C or G

<400> 661
ctgaaccata tctgattaac tctttgggtct ctgttattgg aacaaaaccg acgctatgcc 60
tgcagccgcc agactgcaac caaaaacaca gtttgggggtc agaagacatt aaaaatcaca 120
ataaaaatagg atgaatgttc taagtcacgc aactgaatca aggcaccttt ttttttcaaa 180
agcaaaaagt tgtttaacaa tattccagaa tagtagatac ttcaaaaacc agattacagt 240
atataatcatt ttgctgcaca ttttagtcta ttttctgtat acatagtcac acattcttta 300
ccctctccca acttatacat gctttatccc ccagtcacat tgctatgtag gtataaaaaa 360
ataaagtgtg atctaataca gtgatttaaa aaaaaaaact aacgaatgcc ncnatnataa 420
cnctgaactt gtttccctnt tgaaggacat tggaaatgtt accgaggttn ntttacctng 480
gccgcaaccn cnctangggc naattccagc nactggggg ccgttactag gggat 535

<210> 662
<211> 257
<212> DNA
<213> Homo sapien

<400> 662

```

cctgactaaa gcacatatca cactccctac acttccatgt tttctctccc atgtggaccc    60
tctgatgcat atcaagattc aagcgccctgt tgtagccctt cccacagtcc tcacatttgt    120
atggcttttc tacactgtga actttttctt gcactttaga gaatgaattc tgtacaatgt    180
tcttcccatg ctgctcacat ttgagagggtg tttctctgct gtggcgctctc tgatgggtca    240
gacgagttga ggaccag                                     257

```

<210> 663

<211> 516

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(516)

<223> n = A,T,C or G

<400> 663

```

ccaattatag gtatttttatt ttttaaagat tagagngttc ttgaagctct ttctattttct    60
ttgtcaatga actaaacatt ggcaaatatg taggggtttcc cacataagaa cattattaac    120
atcaaaatag aaagctggtg gtagaaataa tgattgggaa cacagagtct ctactcagcg    180
ttctacttct gccataccat aactttgtga tctcacgaaa tatctctcca tgttctcatc    240
cctatgtata gttctgtcat ttttcaataa gagctttttg cttaattatg aagtactagt    300
tactataacc attattttga gttcatgta aatcaagaac acatggactc cacttgcaaa    360
acattgaaaa tgtagttagg gattgggggc aaaaagcaac attttaaaat gtgtaaagac    420
aatgagtaag caacaaagtg tccaattttt taggcgaaaag ttgcatatgt caggaaaagg    480
caggattaag taatagagaa tttgaatgat aactgg                                     516

```

<210> 664

<211> 212

<212> DNA

<213> Homo sapien

<400> 664

```

gtccgaggag gttagtgtg gcaataaaaa tgattaagga tactagtata agagatcagg    60
ttcgtccttt agtgttgtgt atggctatca tttgttttga ggtagtttg attagtcatt    120
gttgggtggt aattagtcgg ttgtgatga gatatttga ggtggggatc aatagagggg    180
gaaatagaat gatcagtact gcggcgggta gg                                     212

```

<210> 665

<211> 408

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(408)

<223> n = A,T,C or G

<400> 665

```

atccaggggt ncccggtnge tgcngggaaa cctccagcct tgttcttcaa accactcage    60
tcatgtgttt tgcgtgact agtactgaat aatacaacca ctcttattta atgttagtat    120
tatttatttg acaactcagt gtctaacagc ttgatatgca ggtccttgca tcctacattt    180
ctttaggaag ttaccatttt gtaactttta aaacaggaaa aatatcagtt ggcaaatgca    240
atcttttttt tttttaagct aaaggggggn naacngnaan naaaatnttt ntgangnngg    300
gtctataagc acccttgang ggatntgtta aaagngncat naanggggga ttctcntttt    360

```

gcaaaaaaat ntaannatca attctatanan ctttattttt nactttnt 408

<210> 666
 <211> 635
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(635)
 <223> n = A,T,C or G

<400> 666
 ctgaagnaca agggtcaggc aaaaataaga tcacaatcac caatgaccag aatcgccctga 60
 cacctgaaga aatcgaaagg atggttaatg atgctgagaa gtttgctgag gaagacaaaa 120
 agctcaagga gcgcattgat actagaaatg agttggaaag ctatgcctat tctctaaaga 180
 atcagattgg agataaagaa aagctgggag gtaaaccttc ctctgaagat aaggagacca 240
 tggaaaaagc tgtagaagaa aagattgaat ggctggaaag ccaccaagat gctgacattg 300
 aagacttcaa agctaagaag aaggaactgg aagaaattgt tcaaccaatt atcagcaaac 360
 tctatggaag tgcaggccct cccccaactg gtgaagagga tacagcagaa aaagatgagt 420
 tgtagacact gatctgctag tgctgtaata ttgtaaatac tggactcagg aacttttggt 480
 aggaaaaaat tgaaagaact tancctctga atgtcattgg aatcttcacc tcacagtggg 540
 gttgaaactg ctatagccta agcnggctgt ttactgnttt ncattagcag gtgctcacca 600
 tgtctttggg gtgggngggg ggagaaagaa agaan 635

<210> 667
 <211> 388
 <212> DNA
 <213> Homo sapien

<400> 667
 gaagggtgata taaaatgact gtcattcattt ggagtgtgca gtacagttac ttcattgttc 60
 tcagggttag aacaatttcc cctgtaagtt ctcacacaga taggcagaaa tcataactaa 120
 ttttggttaa tcaactatggc agccgttgaa gaatttaaga gaacctgcca gtaagatttg 180
 gaataagatt ctatattatt gcatccacag aaaagaatgt actgatatac tataaactct 240
 aggagaaaac ttaattgaaa tagtgttatt aagtgttgaa agtaccataa aaatataagg 300
 gaaaataagc tttcctagaa ttttctagtg ttctagtttt taaacagtga tgttttttat 360
 taacctattt catccattca aagacagg 388

<210> 668
 <211> 498
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(498)
 <223> n = A,T,C or G

<400> 668
 tgatcttaac aaaattcgta gcagtggaaac cttgaaatgc atgtggctag atttatgcta 60
 aaatgattct cagtttagcat ttagtaaca cttcaaagg ttttttttgt ttgttttcta 120
 gacttaataa aagcttagga ttaattagaa gaagcaatct agttaaat tccatttgta 180
 ttttattttc ttgaataact ttttcatagt tattcgttta aaaagattta aaaatcattg 240
 cactttgggc agaaaaataa taaatatatc ttatgaatgt ttgattccct tccttgctat 300

ttttattcag tagatttttg tttggcatca tgttgaagca ccgaaagata aatgattttt	360
aaaaggctat agagtccaaa ggaatgttct tttacaccaa ttcttccttt aaaaatntct	420
gaggaatttg ttttcgcctt actttttttt cttctgtcac aatgctaagn ggtatccgag	480
gtntttaata tgagattt	498

<210> 669

<211> 622

<212> DNA

<213> Homo sapien

<400> 669

ccttagccaa agaatgcagt ggagccttcc cccttcaact gcattgtgaa tgaataccaa	60
ttaacagcat aaaaattaat agtcccatat cagatctgga aggggtttct ggggctgtct	120
gatgtcccta tctgtttgta gtgaacacaa tagcagaaaa ttctttctgg gtccatctgc	180
tataaagtct tggtaaaaca gcattactat gaagaggatg aactcaccta ctttcagatg	240
gaggaaaagt gaaaaggact taggctttag tctccatga cttttcttaa gcactaccta	300
cctgtaataa gctgagtgc aaaggatgcc gaagaaaatc tgcacccaga agctgttaga	360
aagcactgca gagaacaggg tatgaagaaa ataaagagtt cttaataaac ccttaagatt	420
ctttgttcaa ggtaaccttg ccaaaagggc agagtaggtg gcaaagagtt gcttttaatc	480
tagctctaca ctgcatttga aaataaaatt tgcccatttt gaatatattg tttataatta	540
aatgtgcttt ttacactgca ggtcaatata aaaactgggt agtaaatttc cagcgagcat	600
ttatgttcat ttgtcacag ca	622

<210> 670

<211> 477

<212> DNA

<213> Homo sapien

<400> 670

ttgggccctc tagatgcatg ctcgagcggc cgccagtgtg atggatatct gcagaattcg	60
cccttgccgc ccgggcaggt gatggatgag gagcaaaaac tttatacgga tgatgaagat	120
gatatctaca aggctaataa cattgcctat gaagatgtgg tcgggggaga agactggaac	180
ccagtagagg agaaaataga gagtcaaacc caggaagagg tgagagacag caaagagaat	240
atagaaaaaa atgaacaaat caacgatgag atgaaacgct cagggcagct tggcatccag	300
gaagaagatc ttcggaaaga gagtaaagac caactctcag atgatgtctc caaagtaatt	360
gcctatttga aaaggttagt aaatgctgca ggaagtggga ggttacagaa tgggcaaaat	420
ggggaaaggg ccaccaggct ttttgagaaa cctcttgatt ctcagtctat ttatcag	477

<210> 671

<211> 127

<212> DNA

<213> Homo sapien

<400> 671

gtgtgtgtgt ctacttgggc gtgtttaacg tgtgcgtttg tgtctgcgtg tgcattgtgc	60
tgtgtgtgcg cgtgtatttc agtttgggtt gccggatccc atatgattgc gtgcctgtgt	120
acctgag	127

<210> 672

<211> 400

<212> DNA

<213> Homo sapien

<400> 672

gggtctgcac agctatgtta acagcatcct tataccagga gtaggaggaa agacacgact	60
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217

```

ggaaaagcaa ttcaagctgg tcacacagtg taatgcaaaa tatgtggaat gtttcagtgc 120
tcagaaagag tgtaacaaag aaaagaacag aaactcttca gttgtgccat ctgagcgtgc 180
tcgagtgggt cttgcaccat tgcctggaat gaaaggaaca gattacatta atgcttctta 240
tatcatgggc tattatagga gcaatgaatt tattataact cagcatcctc tgccacatac 300
tacgaaagat ttctggcgaa tgatttggga tcataacgca cagatcattg tcatgctgcc 360
agacaaccag agcttggcag aagatgagtt tgtgtactgg 400

```

<210> 673

<211> 600

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (600)

<223> n = A,T,C or G

<400> 673

```

ctggcggtgc tcattagtga atgtatgaca gcaggatgtg aggggatgcc caggagtacg 60
tgtagcatt gtcactgag atcactgcta ttaatatcat ccattaattt attagtgagc 120
ttcactatat gcagactggg agataaggag aaaatctgtc acattctctc tagctaatac 180
gatcagctac caattaatga gattctgaat gaaatatcaa tatgtgtttt tctaatttgg 240
acctaggaca gagctgttgc ttgtcataga gaaaaacaat aatgcttaaa catagcacat 300
tataattaaa gcaggtttct cacatacttt tcattttatc ctttggataa ttttgtgagg 360
aacgcaggac accaacttcc ctttcataga tacaatcccc atgctattga tgaaagtgtt 420
tttgaatgaa gccatacaac aaataactga tcaaagtggc attacaccaa aatttcttag 480
taggactcct gcatagaatg tttagataga cgtgaaaagt ttgttcanga ggaccagcaa 540
gagagaaact ggggttctttg ggagggtttc ggtgctacat ttataccctn catcagagtn 600

```

<210> 674

<211> 140

<212> DNA

<213> Homo sapien

<400> 674

```

ggtgggtggt gtaaagtgt gaggcaggag tccgaggagg ttagttgtgg caataaaaaat 60
gattaaggat actagtataa gagatcagggt tcgtccttta gtgttgtgta tggctatcat 120
ttgttttgag gttagtttga 140

```

<210> 675

<211> 245

<212> DNA

<213> Homo sapien

<400> 675

```

gttgggtggt tgggtgaaat gagtgaggca ggagtccgag gaggttagtt gtggcaataa 60
aaatgattaa ggatactagt ataagagatc aggttcgtcc tttagtgttg tgtatggcta 120
tcatttgttt tgaggtagt ttgattagtc attgttgggt ggtaattagt cggttgttga 180
tgagatattt ggagggtggg atcaatagag ggggaaatag aatgatcagt actgcggcgg 240
gtagg 245

```

<210> 676

<211> 621

<212> DNA

<213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(621)
 <223> n = A,T,C or G

<400> 676
 ctgtccccag ggnaaatagt ngaattcaac taagatctgt taataagatg tcagaataac 60
 taataatttt attaggaaaa aatcatgttt taaatttcaa aatgacactt atttgtcaag 120
 taatatgac ttggaaaatt ttaaagaaaa ataactctac ttataaacta cttttttata 180
 attgttttca gaaaaaaagt ttacagtctt aaggaaaata ttcagggtcta tcatatgggt 240
 tgacagattt tttaaaagt atttttggtt aggtcttctt ttagaaaaaa attaacttca 300
 aggggttttt gtaccactat aatctctaata acttactcag aattactgtg tatttactta 360
 atttcttatt atgtgcctta ttatgtgctt aagatacaat aggttagagt ttaactctaaa 420
 tatcttgaaa gctatattgt gggcttggtt agcattttgt tttttcttct tctgttttgg 480
 taaggattta aaattttttt cattgcaatt ttaagtgggt ttcaataagt aatagttttt 540
 atcaaatttt tgggtgcttg tgcagagacg gcgtggggaa ggggtgaatg ttttgggaat 600
 aattcagtgc acacctgggg g 621

<210> 677
 <211> 210
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(210)
 <223> n = A,T,C or G

<400> 677
 tttacataa atattatcag catttaccat ctcaattcta ggaatactag tatatcgctc 60
 acacctcata tcttcctac tatgcctaga aggaataata ctatcactgt tcattatagc 120
 tactctcata accctcaaca cccactccct cttagccaat attgtgccta ttgccatact 180
 agtctttgcc gcctgcgaag cagcggtagg 210

<210> 678
 <211> 383
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(383)
 <223> n = A,T,C or G

<400> 678
 gtaggagtca ggtagttagg gttaacgagg gtggtaagga tggggggaat tagggaagtc 60
 agggttaggg tgggttatagt agtgtncatg gttattagga aaatgagtag atatttgann 120
 aactgattaa tgtttgggnn tgagttnta tatcacagcc anaattntat gatgnaccat 180
 gtancgaaca atgctacagg gatgaatatt atggagaagt antctanttt gaagcttagg 240
 gagagctggg ttgtttgggt tngggctcan tgcagttcc anataataac ttcttgggtc 300
 aggcacatga atattgttgt ggggaanaga ctgataataa aggtggatgc gacaatggat 360
 tttacataat gggggtatna gtt 383

<210> 679

<211> 371
 <212> DNA
 <213> Homo sapien

<400> 679
 aaaatgaaaa tattgacaag agtttcagat agaaaaatgaa aaacaagcta agacaagtat 60
 tggagaagta tagaagatag aaaaatataa agccaaaaat tggataaaat agcactgaaa 120
 aaatgaggaa attatttgta accaatttat tttaaaagcc catcaattta atttctggtg 180
 gtgcagaagt tagaaggtaa agcttgagaa gatgaggggtg tttacgtaga ccagaaccaa 240
 tttagaagaa tacttgaagc tagaagggga agttgggttaa aaatcacatc aaaaagctac 300
 taaaaggact ggtgtaattt aaaaaaaact aaggcagaag gcttttggaa gagttagaag 360
 aatttggaag g 371

<210> 680
 <211> 176
 <212> DNA
 <213> Homo sapien

<400> 680
 cctaggattg tgggggcaat gaatgaagcg aacagatttt cgttcatttt ggttctcagg 60
 gtttggtata attttttatt tttatgggct ttggtgaggg aggtaagtgg tagtttgtgt 120
 ttaatatattt tagttgggtg atgaggaata gtgtaaggag tatgggggta attatg 176

<210> 681
 <211> 152
 <212> DNA
 <213> Homo sapien

<400> 681
 ctggagatgg atatgagact agtcaagatg tgaatgctaa ttggagagaa atataatttt 60
 aggaagatgc acattgatgt ggggttttga tgtgtctgat tttgactact caagctctgt 120
 ttacagaaga aaattgaatg gcgagggtgt gg 152

<210> 682
 <211> 141
 <212> DNA
 <213> Homo sapien

<400> 682
 ccagtgcctt cttgccgtgg tttagtattt ggggtgttaga aataaaaact caggtctatt 60
 tcttaccagt cagtaacaat ttttagagaa tgtacttggg atataatata tggacttcag 120
 gaactttgtt ggggtggggg g 141

<210> 683
 <211> 308
 <212> DNA
 <213> Homo sapien

<400> 683
 ccagcaatgg tacagagtga ggggtgttctg ctaatgactt cagagaagta ttttaagaaa 60
 acatagaaaa acgtgtgcgg agtttgccag aaatagatgg cttgagcaaa gagacagtgt 120
 tgagctcatg gatagccaaa tatgatgcca tttacagagg tgaagaggac ttgtgcaaac 180
 agccaaatag aatggcccta agtgcagtgt ctgaacttat tctgagcaag gaacaactct 240
 atgaaatgtt tcagcagatt ctgggtatca aaaaactaga acaccagctc ctttataatg 300
 catgtcag 308

<210> 684
<211> 277
<212> DNA
<213> Homo sapien

<400> 684
tggtattagg attaggatgt gtgaagtata gtacggatga gaagggtggg gaacagctaa 60
atagggttgtt gttgatttgg ttaaaaaata gtagggggat gatgctaata attaggctgt 120
gggtgggttgt gttgattcaa attatgtgtt ttttggagag tcatgtcagt ggtagtaata 180
taattgttgg gacgattagt tttagcattg gagtaggttt aggttatgta cgtagtctag 240
gccatattgt ttggagattg agactagtag ggctagg 277

<210> 685
<211> 457
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(457)
<223> n = A,T,C or G

<400> 685
ctgtggcgtn ccctacttct cccaaacctc gcaactocct cccaggacag tcagtgccaa 60
agaaacaggt cgctgaaaac taaaatgtcc acatccctaa ctggcaaccc acatcaaccc 120
caaaagggttg aagaatcatc taagatattt cagatgctct atgaagaaat tcactttaac 180
acttataact gtaagacttt gcatacatta caacagtgca ttagtgatac aagttgtaaa 240
atacgttttc attcctttgg attttgcata tgatggtttt gcatacagtc ctgcaggtag 300
attgagcaag ctttttgtgt ttgtttttt aaacatgcat tcaactagat atgattcaga 360
atagattaat actccctttt tatcactaca gttagctaaa aaattgccag gcagtccaca 420
aaacagaatt tgctttaaga ccaaccaca gagtcag 457

<210> 686
<211> 234
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(234)
<223> n = A,T,C or G

<400> 686
ntggatttat aaaatagttg caatgacaaa agaagtatgt tttgacagta aaaaaaagac 60
attatggaca aaatatgcaa aatgtgcaaa gaaaaataa atttgcatta gaaagggtggg 120
catttgatct ctgagccctg tgccatgtaa cattgccatg ttctttcact gttgtttgaa 180
tgttgtaccc cagcccttga ctctggactt aaggcaagct atgactggct ttgg 234

<210> 687
<211> 315
<212> DNA
<213> Homo sapien

<220>

221

<221> misc_feature
 <222> (1)...(315)
 <223> n = A,T,C or G

<400> 687
 nngtctgtga aaaactcttt ggatgattct gccaaaaagg tacttctgga aaaatacaaa 60
 tatgtggaga attttggctt aattgatggt cgcctcacca tctgtacaat ctctgtttc 120
 ttgccatag tggctttgat ttgggattat atgcaccctt ttccagagtc caaacccgtt 180
 ttggctttgn gtgtcatatc ctattttgtg atgatgggga ttctgaccat ttataacctca 240
 tataaggaga agagcatctt tctcgtggcc cacaggaaag atcctacagg aatggatcct 300
 gatgatattt ggcag 315

<210> 688
 <211> 522
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(522)
 <223> n = A,T,C or G

<400> 688
 ctgaattaga ggaggagaaa agaagccatt nnggagtact ttaattgttt agatgtgaga 60
 ggctgaatgt ttgggttaag atgttagttg tcagaatcat gagaaaagg ttttaagcaag 120
 gggcatttct aattctaaaa ataacaacta ctgttattta ttgagcacta tctttttgtt 180
 gggtagctgc taaagtactt gatttatttt ttaaaacctt acaaaaaact tacaaggtag 240
 gtactgaaag attcagtaat ttgttcaaag tcacacagca aataagcaac agactctgga 300
 tttgaaccag gcaatcctag agcctgtact gtttagtaatt atacttttagc acctgtcaag 360
 aattcctgtt gagtgtcaag aagcaanca caagttagga tttaaagcaa acatgattga 420
 agaatactgt ggtgtggtg acagtagtgc ctaagtctgt tttcagagtg aaaaatgaca 480
 aattagattt taagtatggt ttggagataa tatcaggaca gt 522

<210> 689
 <211> 158
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(158)
 <223> n = A,T,C or G

<400> 689
 tctcaactta ntntnatacc cacaccacc caanaacagg gtttgtagg nattgtttgc 60
 attaataaat taaagctcca tagggctctc tcgtcttgct gtgtcatgcc cgcctcttca 120
 cgggcaggtc aatttcactg gttaaaagta agagacag 158

<210> 690
 <211> 300
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature

222

<222> (1) ... (300)

<223> n = A,T,C or G

<400> 690

tagaactcgt	attttttaa	ac	ttctattctc	tanccttttc	cactacatta	tgacacaaga	60
ccctgcagaa	agtcgtctgg	aaaat	atcag	accatctctt	acttgtccca	tccaatctta	120
catcgaatta	tatgcaccct	taaaa	agtta	tttggagttt	taaaaaactc	tattagccca	180
aattacctga	aataaactcc	tggtt	gttc	ccctaagt	tataaaaaat	tgattgaaaa	240
tattcatttt	aaaaatgaag	ntctt	gaatt	tatttaaatt	actgtcttgc	agtgagttgg	300

<210> 691

<211> 305

<212> DNA

<213> Homo sapien

<400> 691

ctgttcagaa	agctcattgg	acctggtttt	gaaaataaaa	caaagttaaa	accctgggag	60
gagttattgt	gcagtgtgga	gtactcaggc	tttcttataa	agaaaaaaa	agttatctgg	120
taccaaagt	tgcaacctac	agaccctcag	gtactgccct	gtgacttctc	tgtatgacat	180
cacaaggctg	ccaagtgcct	gtttttctag	aactaggagt	tggtgaggtt	tggttagtgc	240
tgaaaccatg	cataggattg	gtttactaaa	ttaaaacctt	attacgtacg	tcctccaaaa	300
gacag						305

<210> 692

<211> 582

<212> DNA

<213> Homo sapien

<400> 692

caggaaatgg	ataaccattt	taactgtatt	ttttgcagcc	cgtaccttct	tggaataaca	60
attgtctaac	tttttatttt	tggtctggct	gttgtgggtg	gcaaaactcc	gtacattgct	120
attttgccac	actgcaacac	cttacagatg	tggaagatgt	gaaatttgct	atcaattatg	180
actaccctaa	ctcctcagag	gatttatattc	atcgaattgg	aagaactgct	cgcagtacca	240
aaacaggcac	agcatacact	ttctttacac	ctaataacat	aaagcaggtg	agcgacctta	300
tctctgtgct	tcgtgaagct	aatcaagcaa	ttaatcccaa	gttgcttcag	ttggctgaag	360
acagaggtgc	aggtaaggat	gactgatagg	aaatgttgg	agttacgagt	cacatcgttg	420
tctacaaatc	cattttaaag	gtattggagg	gtgagtaaaa	ccttgaatgt	gaaaacttaa	480
gctgaaaaat	tgtaaaaaa	tttcacgcct	accatgaata	gatctgtttc	tttctgtcca	540
caatgatattg	tgatcatagac	ataattgac	aatttgcaat	tg		582

<210> 693

<211> 275

<212> DNA

<213> Homo sapien

<400> 693

ccaattgatt	tgatggtaag	ggagggatcg	ttgacctcgt	ctgttatgta	aaggatgcgt	60
agggatggga	gggcgatgag	gactaggatg	atggcgggca	ggatagttca	gacggtttct	120
atctcctgag	cgtctgagat	gttagtatta	gttagttttg	ttgtgagtgt	taggaaaagg	180
gcatacagga	ctaggaagca	gataaggaaa	atgactatga	gggcgtgatc	atgaaagggtg	240
ataagctctt	ctatgatagg	ggaagtagcg	tcttg			275

<210> 694

<211> 397

<212> DNA

223

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (397)

<223> n = A,T,C or G

<400> 694

nggtctgcat	ttttattgcg	atctgcagat	gaactggaaa	atctcatttt	acaacagAAC	60
tgagacagac	gaccaccata	ttcactgagg	tctaaatttg	cagtttccac	taatgacatt	120
ttgattttccc	aacagagata	cttctgggtct	tactgcacag	tcttttaaga	gaaatacttc	180
cattatgcca	cattgtcctt	gatccgtaag	tgatgtgtta	aggTgcttca	aaggaaactct	240
gacctctgaa	gtacttgagc	tactttagta	tgtccagcct	attgcttttt	gttttagtgt	300
gtcaccataa	atatcagggg	cataaaaggc	tatctattct	taattcaagg	ataaaacaga	360
agaagcttgt	ggtataaaac	aatagttcaa	gatccag			397

<210> 695

<211> 609

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (609)

<223> n = A,T,C or G

<400> 695

ctgagcttcc	atttgtcagc	tagcactgng	gtagtcaacc	atgcgaatga	ggctatttttg	60
gacctcatga	ttgtccagtg	cctgggctga	taccngggga	aacgaaattt	tgtggctgcc	120
cacaaaatca	tggaaaataa	tgatttttta	gaaaacctcc	actgntttgt	tgtgcagcaa	180
taaataactg	aaacaccaat	ccaaaaaact	tataaagcta	taacaattaa	aacagnataa	240
taatagtnc	gggatacaaa	aatgggtcaa	ttgaagagga	tacaaagcct	caaagcagtc	300
ctcactcata	ananccttgt	tgtatcacta	aaanggcatt	aaaattgaga	anaaggaana	360
actagtggat	taattaataa	atgagaagta	tccataagga	aaaattaaaa	ttnnattctt	420
gcttcacatt	atgaaaaaat	acaaacaaca	gattgattaa	agacttaa	gngatcaaca	480
aaatgttaaa	actgtgataa	gaacatttaa	gaaaatagtt	ctatnaccct	gggataaaac	540
attttontcc	aaggcattaa	agtgttaaat	gaaaagactg	atncatttat	tcattagaat	600
ttaaattcn						609

<210> 696

<211> 300

<212> DNA

<213> Homo sapien

<400> 696

ctgcaaaata	agcgtgctaa	attaaattgt	cttaagggtt	ttccacttca	ttttgtgact	60
ttgtgtgggt	cgaattttct	agtattttta	ccagtgtgtt	gatgttaaag	tcaaaggctg	120
cagtatgtct	atattcttgc	tgtactcatt	ggtagtttca	gtatatgtaa	tgtgagttaa	180
aatagtga	ttgtatctca	tattaacatt	tcaaatgtct	atattgaaaa	tggaaaatag	240
taaacacggg	aattgatttt	attctgggtg	tctataatac	ttcattttta	atgtaaatgg	300

<210> 697

<211> 391

<212> DNA

<213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (391)
 <223> n = A,T,C or G

<400> 697
 nngtcatgtn tgatgnatct gancaggttg ctccacaggt agctctagga gggctggcaa 60
 cttagagggtg gggagcagag aattctctta tccaacatca acatcttggt cagatttgaa 120
 ctcttcaatc tcttgactc aaagcttggt aagatagtta agcgtgcata agttaacttc 180
 caatttacat actctgctta gaatttgggg gaaaatttag aaatataatt gacaggatta 240
 ttggaaattt gttataatga atgaaacatt ttgtcatata agattcatat ttacttctta 300
 tacatttgat aaagnaaggc atggttggtg ttaatctggt ttatttttgn tccacaagtt 360
 aaataaatca taaaacttga acaaaaaaaa a 391

<210> 698
 <211> 536
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (536)
 <223> n = A,T,C or G

<400> 698
 ctgagcatac agcaataaaa ataacataat ttttatgtgt acaatattta tggaatacgt 60
 tactggaaca gataaataat ttagttaata acatgacaaa gaacagaaat tgtatacact 120
 atacagcata gtaatagaat aatgaatgat taaagttatt aatattaggt agaaaatgaa 180
 gggatatctt gagagcagaa ctcaaggaag caagcaattt gccttatgag gaaagagtta 240
 cctgtggata aaggagaaac tgaaaaattt acaagtcaag actttttgag caaagacaaa 300
 aatatgacta tgagtcacca attcagtaca gtgaaaaaaa agttgaagag atatcttgga 360
 agtaaaccat gttgtggaag agcagggttt tgataatcat gggattattc tgaatgaatt 420
 ttaaattgca taggaatata tgagataatt tcaccagaga ataatatgat catgtttgca 480
 tttcaaaggg gtgtatctgg tgcactgngt agaataaata ggntatgtga gcaagt 536

<210> 699
 <211> 419
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (419)
 <223> n = A,T,C or G

<400> 699
 ngtcacctg agggcaggtg acaaggacct gacagagccc atgcagggct ttagatttgg 60
 acacacaaga gttgataact tcctcatgaa ctcttgccct gatctaaact catattatgg 120
 gttctgactg tttgagtaat catcttcaag gttaaaccctc ttggcagtta cctttttcac 180
 aaagtgcaca gtgggaatcg agaatcgata gggttaattt tggagcagtg gcttatacca 240
 ttcacctctg tttttttgtg attatttcac agataatgag accttaataa caaataggcg 300
 taaaaaaatt ttcacattga aatgatagaa acatttgatg taataaaact tggttggctt 360
 gatattttta ggaattgaaa cctagcaatc ttattggaga gacaagaatt ggtctccag 419

<210> 700
<211> 336
<212> DNA
<213> Homo sapien

<400> 700
ccacttattg tccttaaaaa tccatactga tacatggaca gfaagtgtgt tttcagatgg 60
agtaccagca ccgaaaatgg gttgagggag gatggggtgt atgtatgttt ctgcccacta 120
attttgagca gccatattat gaattaaatc gtcacagcca agtaataacc caagaatggt 180
atgagtttca tgtgtaatag ctcaaagga ataagcatga atgctggagt ggaccattat 240
cctcaaatat tctatgtcac ttctcattta aagactcttg ttatgaacta ttagaaactt 300
taggcaaaat caaaagtatt tgcggcaaaa taaagg 336

<210> 701
<211> 418
<212> DNA
<213> Homo sapien

<400> 701
ccatgtgatg atgttgacaa cccctgaaga gcctcagtcc attgttccac gtttaagaac 60
taggaatacc aggactgatg caattctact gggtcactat cgcttggtcac aagacacaga 120
caatcagacc aaagtatttg ctgtaataac taagaaaaaa gaagaaaaac cacttgacta 180
taaatacaga tattttcgtc gtgtccctgt acaagaagca gatcagagtt ttcattgtggg 240
gctacagcta tgttccagtg gtcaccagag gttcaacaaa ctcatctgga tacatcattc 300
ttgtcacatt acttacaat caactggtga gactgcagtc agtgcttttg agattgacaa 360
gatgtacacc cccttgttct tcgccagagt aaggagctac acagctttct cagaaagg 418

<210> 702
<211> 261
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(261)
<223> n = A,T,C or G

<400> 702
gggcctgttg tgggggtggg ggaagcaggg aggggaacag ctaaataagg tgcgttgat 60
ttggttaaaa aatagtaggg ggatgatgct aataattagg ctgnggggtg ttgtgttgat 120
tcaaattatg tgttttttgg agagtcattg cagtggtaga aatataattg ttgggacnat 180
tagntttagc attggagtag gtttaggtta tgtacgtagt ctaggccata tgtgttggan 240
attgagacta gtagggctag g 261

<210> 703
<211> 261
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(261)
<223> n = A,T,C or G

<400> 703

226

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gggcctgttg tgggggtggg ggaagcaggg aggggaacan ctaaataagg tgcgtgtgat    60
ttggttaaaa aatagtaggg ggatgatgct aataattagg ctgnggggtgg ttgtgttgat    120
tcaaattatg tgttttttgg agagtcagt cagtggtagt aatataattg ttgggacnat    180
tagnttttagc attggagtag gtttaggtta tgtacgtagn ctaggccata tgtgttggag    240
attganacta gtagggctag g                                     261

```

<210> 704

<211> 381

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(381)

<223> n = A,T,C or G

<400> 704

```

ngtntgaatt ctattaaaga taaaaagagg agctgggtacc atttcttctg aaactattac    60
aaacaactga aaaggtggaa tttctcccta attcatttta ggaggccagc attatactga    120
taccaaaacc tggcagaggt acaataataa aaggaaactt caagtcagta tcaactgatga    180
acaccaatgt gaaaatcctc aataaaaatac tggcaaaactg aattcagcag cacatcaaaa    240
agctaatacca ccacaatcaa gtcagcttca tccctgcgat gcaagtctgg ttcaacatat    300
gcaaatcaat aaatacaatt catcagataa acagagctaa agacaaaatt cacatgattt    360
tctcaataga tgcagaaaag g                                     381

```

<210> 705

<211> 477

<212> DNA

<213> Homo sapien

<400> 705

```

ctgaaccctc gtggagccat tcatacaggt ccctaattaa ggaacaagtg attatgctac    60
ctttgcacgg ttaggggtacc gcggccgcta aacatgtgtc actgggcagg cgggtgcctct    120
aataactgggt atgctagagg tgatgttttt ggtaaacagg cggggtaaga tttgccgagt    180
tcccttttact ttttttaacc tttccttatg agcatgcctg tgttgggttg acagtgaggg    240
taataatgac ttgttgggtga ttgtagatat tgggctgtta attgtcagtt cagtgtttta    300
atctgacgca ggcttatgcy gaggagaatg ttttcatgtt acctatacta acattagttc    360
ttctataggg tgatagattg gtccaattgg gtgtgaggag ttcagttata tgtttgggat    420
tttttaggta gtgggtgttg agcttgaacg ctttcttaat tgggtggctgc ttttagg    477

```

<210> 706

<211> 266

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(266)

<223> n = A,T,C or G

<400> 706

```

ccatggctag gtttatagat agttgggtgg ttggtgtaaa tgagtgaggc aggagtccga    60
ggagggttagt tgtggcaata aaaatgatta aggatactan tataagagat caggntcgtc    120
ctttaagtgt gtgtatggct atcatttgtt ttgaggntag tttgattagt cattgttggg    180
tggtaattag tcggttgttg atgagatatt tggagggtgg gatcaataga gggggaaata    240

```

gaatgatcag tactgcggcg ggtagg

266

<210> 707

<211> 358

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (358)

<223> n = A,T,C or G

<400> 707

ccatcagaga	aatgcaaadc	aaaaccacaa	tgagatacca	tctcacacca	gttagaatgg	60
caatcattaa	aaagtcagga	aacaacaggt	gctggagagg	atgtggagaa	ataggaacac	120
ttttacaccg	ntgggtggac	tgtaaaactag	ttcaaccatt	gtggaagtca	gtgtggcgat	180
tcctcaagga	tctagaacta	gaaataccat	ttgacccagc	cggccaatat	tcaacattct	240
taaaggaaag	aattttcaac	ccagaatttc	atatccagcc	aaactaagct	tcgttagtga	300
aggagaaata	aaatacttta	cagacaagca	aatactgaga	gattttgtca	ccaccagg	358

<210> 708

<211> 491

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (491)

<223> n = A,T,C or G

<400> 708

cctactatgg	gngttaaat	ttttactctc	tctacaaggt	tttttcctag	tgtccaaaga	60
gctgttcctc	tttgactaa	cagttaaatt	tacaagggga	tttagagggt	tctgtgggca	120
aatttaaagt	tgaactaaga	ttctatcttg	gacaaccagc	tatcaccagg	ctcggtagg	180
ttgtgcctc	tacctataaa	tcttccact	atcttgctac	atagacgggt	gtgctctttt	240
agctgttctt	aggtagctcg	tctggtttcg	gggtcttag	ctttggctct	ccttgcaaa	300
ttatttctag	ttaattcatt	atgcagaagg	tataggggtt	agtccttgct	atattatgct	360
tggttataat	ttttcatctt	tcccttgccg	tactatatct	attgcgccag	gtttcaattt	420
ctatcgccct	tactttattt	gggtaaatgg	tttggtctag	gttgtctggt	agtaaggng	480
gagtgggttt	g					491

<210> 709

<211> 460

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (460)

<223> n = A,T,C or G

<400> 709

nggtttttt	tgtagagcaa	ataatttatg	caaaatatgt	tacaaaatct	gggatgctaa	60
atagttgaca	caagtactgt	gtttgacatt	tagtttcatt	tgaattagta	atagaatttg	120
ctccttccaa	catttacatc	ttttttcttt	ctgactttat	atattttcaa	taaaaatttg	180

```
ctccacagtt ttttaagntca ttcttcttga atccgntttt acatttgctg ngacaaacct 240
gcataaaact agattttata gatataactt ctttggaga gataaaaatt caaaagtgtg 300
acattgcttt canttattct tttcttcatt gttttgattg gcccctgtta gattgatgta 360
ttgccaatct acttttgatg gcatgaatnt aaaatgacaa cataaaaagc ncttctagtg 420
caacagtaat tgaaacttgc agttttccat taaaaaaaaa 460
```

<210> 710

<211> 542

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(542)

<223> n = A,T,C or G

<400> 710

```
ctgttacagt gacaagagat aaaaagatag acctgcagaa aaaacaaact caaagaaatg 60
tgttcagatg taatgtaatt ggagtgaaaa actgtgggaa aagtggagt cttcaggctc 120
ttcttggaaag aaacttaatg aggcagaaga aaattcgtga agatcataga tcctactatg 180
cgattaacac tgtttatgta tatggacaag agaaataactt gttgttgcat gatatctcag 240
aatcggaatt tctaactgaa gctgaaatca tttgngatgt tgtatgcctg gtatataatg 300
tcagcaatcc caaatccttt gaatactgtg ccaggatttt taagcaacac tttatggaca 360
gcagaatacc ttgcttaatc gtagctgcaa agtcagacct gcatgaagt aaacaagaat 420
acagtatttc acctactgat ttctgcagga aacacaaaat gcctccacca caagccttca 480
cttgcaatac tgctgatgcc cccagtnagg atatctttgt taaattgaca acaatggacc 540
tg 542
```

<210> 711

<211> 394

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(394)

<223> n = A,T,C or G

<400> 711

```
caaaccctact ccaccttact accagacaac cttagccaaa ccattttacc aaataaagta 60
taggcgatag aaattgaaac ctggcgcaat agatatagta ccgcaaggga aagatgaaaa 120
attataacca agcataatat agcaaggact aaccctata ccttctgcat aatgaattaa 180
ctanaaataa ctttgcaagg agagccaaag ctaagacccc cgaaaccaga cgagctacct 240
aagaacagct aaaagagcac acccgtctat gtagcaaaat agtgggaaga tttataggna 300
gaggcgacaa acctaccgag cctggtgata gctggtgtgc caagatagaa tcttagttca 360
actttaaatt tgcccacaga accctctaaa tccc 394
```

<210> 712

<211> 552

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(552)

<223> n = A,T,C or G

<400> 712

```
gaggtctgta naatgccagg ctcaaatttg tctttataat ttaataccag aaatctttcc    60
cttgtgatgt ttctttcttt ctggattgcc tctatagcag gggatagcgg gggaggataa    120
ggcacatctt tgntgtactg agaaatttga ccacgcagga tgatgtggct gttctcattc    180
atctgcacag agaaaaataa tgataaaata tccctttcct atgtttactg attttatggc    240
tgccataatg gaagcctcct tgactattta atcctttctg tcaactaggt tcgatttttt    300
ttttaattta cctgttagag gtatttaana attttaacta gctanaaata attacattcc    360
aaaggaacac caaggcaaat aaatggttgg taatcagcaa aagaattaca ttagttgttg    420
ntgctactta ttagggggag aactgttttt ttttaaattt aaacaattta ataatctcaa    480
ctgcaaataa ttttagatgc agcaaaggac tatgtagncg ttaatacctc atgttgatat    540
tttcataata tt                                     552
```

<210> 713

<211> 518

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (518)

<223> n = A,T,C or G

<400> 713

```
ccaaaaactg gaagcagctc actaaacaaa cagtggcata cccatagaac tgcatacttc    60
tcagcagtat gaaagaatga gctacttata taagcatcat tgataaacct caaaaaaaaaa    120
atgccacatg aanaaaccca aagggganaa acataaaaac tttatatgtc agtcatataa    180
aattctanaa aatgcaaaact aatccatcnt aaaggaaaagt aaatcaacag ttgtctggag    240
gaccananag agcaggagga ganagattat taaaggggtt aaagtaaatt tgggagtgcc    300
cttccntttt taaatnctat gaaaatgaaa gttaaaggcnc atgcatgttg taaactaata    360
gtaacaaaca naatgggttg gagtggggtg ttgtctgggg acatcattac aaaatgtaag    420
ccagtttatn taaattttga aaagaccgtg gactctgata tgactgatna atgttggaag    480
agataagtgt gctgcaaatg ggggaattaa taaaacag                                     518
```

<210> 714

<211> 281

<212> DNA

<213> Homo sapien

<400> 714

```
ccaattgatt tgatggtaag ggagggatcg ttgacctcgt ctgttatgta aaggatgcgt    60
agggatggga gggcgatgag gactaggatg atggcgggca ggatagttca gacggtttct    120
atttcctgag cgtctgagat gttagtatta gttagttttg ttgtgagtgt taggaaaagg    180
gcatacagga ctaggaagca gataaggaaa atgactatga gggcgtgata atgaaagggtg    240
ataagctctt ctatgatagg ggaagtagcg tcttgtagac c                                     281
```

<210> 715

<211> 443

<212> DNA

<213> Homo sapien

<400> 715

```
cttgaaatca gcaacacact taaaaatgag aaaaatgaaa tagaagagta tataaagaaa    60
gggaaagagg attatgaaga gagtcatcag agagctgtgg ctgcagaggt atccgtactt    120
```

230

gaaaactgga	aggagagtga	agtgtataag	ctacagatca	tggagtcaca	agcagaagcc	180
tttctgaaga	agctggggct	gattagccgt	gatcctgcag	catatcccga	catggagtct	240
gatatacgtt	catgggaatt	gtttctttct	aatgttacia	aagaaattga	gaaagcaaag	300
tctcagtttg	aagaacaaat	taaggcaatt	aaaaatgggt	cccggctcag	tgaactttct	360
aaagtgcaga	tttctgagct	ttcatttcct	gcctgtaaca	cggttcaccc	cgagttactc	420
cctgagtcct	caggccacga	tgg				443

<210> 716

<211> 639

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(639)

<223> n = A,T,C or G

<400> 716

ccaaanaaaa	tgaagtacag	agtctgcata	gtaagcttac	agataccttg	gtatcaaaac	60
aacagttgga	gcaaagacta	atgcagttaa	tggaatcaga	gcagaaaagg	gtgaacaaag	120
aagagtcctc	acaaatgcag	gttcaggata	ttttggagca	gaatgaggct	ttgaaagctc	180
aaattcagca	gttccattcc	cagatagcag	cccagacctc	cgcttcagtt	ctagcagaag	240
aattacataa	agtgattgca	gaaaaggata	agcagataaa	acagactgaa	gattcttttag	300
caagtgaacg	tgatcgttta	acaagtaaag	aagaggaact	taaggatata	cagaatatga	360
atttcttatt	aaaagctgaa	gtgcagaaat	tacaggccct	ggcaaatgag	caggctgctg	420
ctgcacatga	attggagaag	atgcaacaaa	gtgtttatgt	taaagatgat	aaaataagat	480
tgctggaaga	gcaactacaa	catgaaattt	caaacnaaat	ggaagaattt	angattctaa	540
atgaccaaaa	canagcatta	aaatcagaag	ttcagaagct	gcagactcct	gtttctgcac	600
angcctaata	aggatgntgn	ggaacaaatg	gaaaaattg			639

<210> 717

<211> 473

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(473)

<223> n = A,T,C or G

<400> 717

nntgaggcta	ctgctgtttt	attacaacat	tacctcttgt	ttttataaag	tgtaccaaga	60
tttaaattga	taactttatt	ttacttgaaa	aaaaaaagtt	tnntttatca	ccagtgttac	120
agttgtcttc	tgtttctttt	tggtttgntt	tatttgnntt	ccttttttagc	caaagagtga	180
acagaanatt	ttcttatttt	ggtggctatt	cattttactt	ttaaaagtga	ttggtggatt	240
ttagactaat	tatgggggaa	tttgccacca	aaataaaaaa	tatgtaaagn	gtagtgatta	300
cagagtgggt	aaaatgtggg	ttagtactta	tttattccat	taattgatta	tttgactggt	360
tataaagaaa	gttgctttat	ttctttaaac	atcttcaaaa	gatgatcctt	tcttctcaca	420
ttatagccaa	aagaagcaga	gaacttcact	gtctgcattt	ggttcctggg	tgg	473

<210> 718

<211> 207

<212> DNA

<213> Homo sapien

<400> 718
ggtaaagct agtataatat ttaccatctc acttctagga atactagtat atcgctcaca 60
cctcatatcc tccctactat gcctagaagg aataatacta tcactgttca ttatagctac 120
tctcataacc ctcaacaccc actccctctt agccaatatt gtgcctattg ccatactagt 180
ctttgccgcc tgcgaagcag cggtagg 207

<210> 719

<211> 255

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (255)

<223> n = A,T,C or G

<400> 719
cctatattac ggatcatttc tctactcaga aacctgaaac atcggcatta tcctcctgct 60
tgcaactata gcaacagcct tcataggcta tgcctcccg tgaggccaaa tatcattctg 120
agggggccaca gtaattacaa acttactatc cgccatccca tacattggga cagacctagt 180
tcaatgaatc tgaggaggct actcagtaga cagncccacc ctcacacgat tctttacctt 240
tcacttcac tggcc 255

<210> 720

<211> 455

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (455)

<223> n = A,T,C or G

<400> 720
ccaatgtcga aacctacaag atttccttaa aatctcta atagaggcatta cttgctttca 60
attgacaaat gatgccctct gactagtaga tttctatgat ccttttttgc cattttatga 120
atatcattga ttttataatt ggtgctattt gaanaaaaaa atgtacattt attcatagat 180
agataagtat caggctctgac ccagtgga aacaaaagcca aacaaaactg aaccacaaaa 240
aaaaaggctg gtgttcacca aaaccaaact tgttcattta gataatttga aaaagctcca 300
tagaaaaggc gtgcagtact aagggaaaca tccatgtgat taatgnttnc attatgttca 360
tgtaanaagc cccttatttt tagccataat tttgcatact gaaaatccaa taatcagaaa 420
agtaattttg ccacattatt tatnaaaaat gttcc 455

<210> 721

<211> 530

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (530)

<223> n = A,T,C or G

<400> 721
ccagtgcctg ctgccgtggt ttagtgattg ggtgttagaa ataaaaactc aggtctattt 60

```

cttaccagtc agtaacaatt tttagagaat gtacttggtataataatataat ggacttcagg 120
aactttattg gggngggggg ttaattttgc cttaccctgt tcactttcag atgattaggc 180
ttttgcactt tagaatgaga aacttgtgac gttagtgtgt tcttactagc ttttaattgt 240
atgtagcaat gaattgtgaa tcttagtgca gtgggttttt ttaaaaaact caaaaagctg 300
ggaattaagt ggtttcagta ataatgctat accgaggtgc ttgcattgta tttcataatt 360
ttgttacaaa ccaaaattat ttttaatgan aacggctctg ggttcagagg tgtgatgcca 420
gaatgtattt tctactgtt aggcccttgg aacagatacc ggtgctttct tgaaagatga 480
aagaaatgca atgggtgctc ttcatgcaag gttgcaaacc taccaagaat 530

```

<210> 722

<211> 242

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (242)

<223> n = A,T,C or G

<400> 722

```

ccaagggtca tgatggcagg agtaatcana ggtgntcttg tgttggtgata agggngggaga 60
ggttaaagga gccacttatt agtaatgttg atagtagaat gatggctagg gtgacttcat 120
atgagattgt ttgggtact gctcgagtg cgccgatcag ggcgtagttt gagtttgatg 180
ctcatcctga tnagaggatt gagtaaacgg ctaggctaga ggtggctaga ataaatagga 240
gg 242

```

<210> 723

<211> 472

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (472)

<223> n = A,T,C or G

<400> 723

```

cctactatgg gtgttaaatt ttttactctc tctacaagggt tttttcctag tgtccaaaga 60
gccgttcctc ttggactaa cagttaaatt tacaagggga ttttagagggt tctgtgggca 120
aatttaaagt tgaactaaga ttctatcttg gacaaccagc tatcaccagg ctcggtagg 180
ttgtcgccctc nacctataaa tcttccact attttgctac atagacgggt gtgctctttt 240
agctgttctt aggtagctcg tctggnttcg ggggtcttag ctttggtctt ccttgcaaa 300
ttatttctag ttaattcatt atgcagaagg tataggggtt agtccttgct atattatgct 360
tggttataat ttttcatctt tcccttgccg tactatatct attgcgccag gtttcaattt 420
ctatcgcccta tactttattt gggtaaatgg tttggctaen gttgtctggt ag 472

```

<210> 724

<211> 292

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (292)

<223> n = A,T,C or G


```

<400> 724
nccaccactg cagccctaca tacagntgaa aaaaaattcc attctgttaa catttgtttt      60
ataagttttc acncaataca caaaaaaacc ctctgcactt cttgtaaaaga acaaaaaaga      120
tacacaacag ttaagcgtaa agatcacagg caatagcatt caaacatgga tgtgggnaga      180
gaaaggagta cctggcatga gtacctgtct agttnngactg aatccttgat ttttaatttg      240
gcttttcatg ggccgntcac aacaccaacg ctgngngagg tatggtagtc ag                292

```

```

<210> 725
<211> 122
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1) ... (122)
<223> n = A,T,C or G

```

```

<400> 725
atagaaaggg cataccctaaa atgttactga aaatntaata caaattccaa gattcaccaa      60
ngaagtaaca aaaacctggc ctgcangngg ncccctatcc cgtggctcca tggntgatgt      120
gg.                                122

```

```

<210> 726
<211> 477
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1) ... (477)
<223> n = A,T,C or G

```

```

<400> 726
ctgaaccctc gtggagccat tcatacaggt ccctaattaa ggaacaagtg attatgctac      60
ctttgcacgg ttaggggtacc gcggccggtta aacatgtgtc actgggcagg cggtgcctct      120
aatactgggtg atgctagagg tgatgttttt ggtaaacagg cggggtaaga ttgcccaggt      180
tccttttact ttttttaacc ttcccttatg agcatgcctg tgttgggttg acagtgaggg      240
taataatgac ttgttggtga ttgtanatat tgggctgtta attgtcagtt cagtgtttta      300
atctgacgca ggcttatgcg gaggagaatg ttttcatgtt acttatacta acattagttc      360
ttctataggg tgatagattg gtccaattgg gtgtgaggag ttcagttata tgtttgggat      420
tttttaggta gtgggtgttg agcttgaacg ctttcttaat tggcggctgc ttttagg      477

```

```

<210> 727
<211> 416
<212> DNA
<213> Homo sapien

```

```

<400> 727
cctgtctttg aatggatgaa atagggttaat aaaaaacatc actgttttaa aactagaaca      60
ctgaaaaaatt ctaggaaagc ttattttccc ttatatTTTT atgggtacttt caacacttaa      120
taacactatt tcaattaagt tttctcctag agtttatagt atatcagtac attcttttct      180
gtggatgcaa taatatagaa tcttattcca aatcttactg gcaggttctc ttaaattctt      240
caacggctgc catagtgatt aaccaaaatt agttatgatt tctgcctatc tgtgtgagaa      300
cttacagggg aaattgttct aaacctgagg aactgaagt aactgtactg cacactccaa      360

```

atgatgacag tcattttata tcaccttcaa ttacccaaca gcttttaata gtctgg 416

<210> 728

<211> 416

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (416)

<223> n = A,T,C or G

<400> 728

cctgtctttg	aatggatgaa	ataggttaat	aaaaaacatc	actgtttaaa	aactagaaca	60
ctgaaaaatt	ctaggaaagc	ttattttccc	ttatatTTTT	atggtaactt	caacacttaa	120
taacactatt	tcaattaagt	tttctcctag	agtttatagt	atatacgtac	attcttttct	180
gtggatgcaa	taatatagaa	tcttattcca	aatcttactg	gcaggttctc	ttaaattctt	240
caacggctgc	catagtgatt	aaccaaaatt	agttatgatt	tctgcctatc	tgtgtgagaa	300
cttacagggg	aaattgttct	aaacctgagg	aacatgaagt	aactgtactg	cacactccaa	360
atgatgacag	tcattttata	tcaccttcaa	ttacccaaca	gcttttaata	ntctgg	416

<210> 729

<211> 564

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (564)

<223> n = A,T,C or G

<400> 729

ctgtgagtag	aggagtcttc	ccgagagtag	cagttgttga	tccaaatgat	tgaagccttc	60
aggtaaggga	ataactgctg	caggaattct	ttcttgaaga	atttaagctg	tttggttaaga	120
attctgtaac	tacatacctt	tgaaacacta	ttcacattca	aataaacgct	tgttttctag	180
ccaggcacag	gctcaattag	tttttcaaac	tctagccaag	gcagtatttc	atttgggaaa	240
tcatgcaaca	gaactgctca	attcttaact	tctcctgctg	ttaacattta	cacttagact	300
gccagcaaca	gttaacttaa	attttggtct	caagggaaca	aaaaaaaaatt	gcattcagaa	360
tttaatatag	tattttaaaa	ctaatttttag	cctgtaagnc	attatgagca	atagtaactt	420
ttatacctcc	tcattctgnc	tgataatata	ttctatatgc	tgncaatctg	attatatagt	480
ctatatgcta	gaagttgctg	attttcattc	tgccacccaa	aaaaactgtc	cttttttttt	540
tatgggggaa	aaagggaatt	taaa				564

<210> 730

<211> 310

<212> DNA

<213> Homo sapien

<400> 730

ccatttttat	ttcttcttca	gagaagtgtt	tatttaggtc	tgttgcccat	tttacaatta	60
ggccatatgt	tttcttgctg	ttgagttgta	tgtgtgtttg	tataaatttt	gcatattaac	120
cccttatcac	acgtatgttt	tttaaaataa	attttgctta	ttaatctttt	atcagatgta	180
tggtttccaa	atatattctt	ccgatccatg	gattctcttt	tttggtatga	ttgtttcttt	240
gctcttcgga	agctttttgt	tttgttttgt	tatttgtttt	actttgatat	agtcaccttt	300
attgtttttg						310

<210> 731
 <211> 467
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1) ... (467)
 <223> n = A,T,C or G

<400> 731
 ngacaacctt agccaaacca tttacccaaa taaagtatag gcgatagaaa ttgaaacctg 60
 gcgcaataga tatagtaccg caagggaaag atgaaaaatt ataaccaagc ataataaagc 120
 aaggactaac ccctatacct tctgcataat gaattaacta gaaataactt tgcaaggaga 180
 gccaaagcta agacccccga aaccagacga gctacctaag aacagctaaa agagcacacc 240
 cgtctatgta gcaaaatagn gggaagattt ataggagag gcgacaaacc taccgagcct 300
 ggtgatagct gggtgtccaa gatagaatct tagntcaact ttaaatttgc ccacagaacc 360
 ctctaaatcc ccttgtaaat ttaactgnta gnccaaagag gaacagntct ttggacacta 420
 ggaaaaaacc ttgtagagag agtaaaaaat ttaacaccca tagtagg 467

<210> 732
 <211> 492
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1) ... (492)
 <223> n = A,T,C or G

<400> 732
 cctactatgg gtgttaaatt ttttactctc tctacaaggt tttttcctag tgtccaaaga 60
 gctgttcctc tttggactaa cagctaaatt tacaagggga ttttagagggt tctgtgggca 120
 aatttaaagt tgaactaaga ttctatcttg gacaaccagc tatcaccagg ctccggtaggt 180
 ttgtcgcttc tacctataaa tcttcccact attttgctac atagacgggt gtgctctttt 240
 agctgttctt aggtagctcg tctggnttcg ggggtcttag ctttggctct ccttgcaaag 300
 ttatttctag ttaattcatt atgcagaagg tataggggtt agnccttgct atattatgct 360
 tggntataat ttttcatctt tcccttgagg tactatatct attgcgccag gtttcaattt 420
 ctatcgctta tactttattt gggtaaatgg tttggctaag gttgtctggt agtgaggcgg 480
 agnggggttg gg 492

<210> 733
 <211> 562
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1) ... (562)
 <223> n = A,T,C or G

<400> 733
 ntgaaatggc aatagcattc actgtcgtat tttgcagtgc tcaggaagtg ggacgttaac 60
 tttgaagggtg cttgtttgta ttagctctgc taggtttacc tctacaacgt agatttcagc 120

236

```

agctatgctg actgacacta cattctagtt ctttaagattt tttttccana tcccccttc 180
cccagctaga catacgtagc atactttcat cttattcagt ctttctgtaa cctgctgctg 240
cttttagtcc tcctcacctc agatcggaat caatggagtg ggcccagagg atacatttta 300
attccagtaa tggtaggtag atttgtcctg ctttctaaaa catctcctca tttcatattt 360
ccactccata ttgattccat aagggaaaaat taatgggtgn ttcctccttt agggaggcaa 420
tgcaaagagn gtggacatct tctaattcttg aggaacagtn gttgatttcc cttgaaggag 480
cttacatatt gactgtnttt cacaataacc tgnttgcccc agntcaatcc ctcattttaa 540
tacttaatgt tggtnctggg ct 562

```

<210> 734

<211> 265

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (265)

<223> n = A,T,C or G

<400> 734

```

nggtccagaa caagagaaat aactgcagaa aacacatatg gttggaaacc atgcgcttgt 60
gactttttct gtagcctatg ggagtggaca gagtgggtaa cccaagatgt ttttaagact 120
gactggacta agaatggcgt acttatagcc aactacttcc cccctaagt gactgaaggg 180
attcataatg atcacaatta gcattacggt taagtatttt aggggtgacg tctaagctca 240
cacttgaaag gtatttatct aatgg 265

```

<210> 735

<211> 216

<212> DNA

<213> Homo sapien

<400> 735

```

atttaatacg tgctcactgc tcggcacgcg ctgaagctac agttaacaat cagtgaacac 60
atattaaatg ataaaaaat gctgatggta aacattcata acagcagagt aagatttttg 120
cagttttgtg tctcggtaac ataactgtaa ccttagatga acacctatcc cttcatgatc 180
tgactttaga ggcaaggagt ttgtaacatc taatgg 216

```

<210> 736

<211> 285

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (285)

<223> n = A,T,C or G

<400> 736

```

ctgaaaggca acntggagac tagttagtct agtccccctca tattataaat tggtagtctg 60
aggccaggca gtaaatgct atggagctct ccaatttaag gccagtttga ctccaagggt 120
agggtttcta gtaaaatttt gtgattaaat tggaaactct aatttatttt tctatgngtt 180
tttggtacct aatcctcata agcaagccat atttcaaggc tgatcaatga aaacacaaaa 240
taccaaagct tcctttccct tccaaattta ctgacccttt gtcag 285

```

<210> 737

237

<211> 509
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (509)
 <223> n = A,T,C or G

<400> 737
 agangaagaa gangaagatt aagggaaaag tacatcggtc aagaagagct caacaaaaca 60
 aagcccatct ggaccagaaa tcccgcacgat attactaatg aggagtacgg agaattctat 120
 aagagcttga ccaatgactg ggaagatcac ttggcagtga agcatttttc agttgaagga 180
 cagtttgaat tcagagccct tctatttgtc ccacgacgtg ctctttttga tctgtttgaa 240
 aacagaaaga aaaagaacaa catcaaattg tatgtacgca gagttttcat catggataac 300
 tnggaggagc taatccctga atatctgaac ttcattagag ggggtggnaga ctcgaggagat 360
 ctccctctaa acatatcccg tgagatgttg caacaaagca aaattttgaa agttatcang 420
 aagaatttgg gtcaaaaaat gcttanaact ctttactgaa ctggcggaag atnaagagaa 480
 ctncaagana ttctatgagc agntctctt 509

<210> 738
 <211> 97
 <212> DNA
 <213> Homo sapien

<400> 738
 cagtgaattg aatacgactc ctatagggcg aattggggccc tctagatgca tgctcgagcg 60
 gccgccagtg tgatggatat ctgcagaatt cgccctt 97

<210> 739
 <211> 209
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (209)
 <223> n = A,T,C or G

<400> 739
 ccgncagtgt gatggatata tgcagaattc gcccttagcg gcccgcccg gcagggtcct 60
 tatatatagt agcttagttt gaaaaaatgt gaaggacttt cgtaacggaa gtaattcaag 120
 atcaagagta attaccaact taatgttttt gcattggact ttgagttaag attatttttt 180
 aaatcctgag gactagcatt aattgacgg 209

<210> 740
 <211> 164
 <212> DNA
 <213> Homo sapien

<400> 740
 ccaagcta at gggtgacact gtgaatgcaa ctctaata gca gcctggcgta aatggtccta 60
 tgggcactaa ctttcaagtt aacacaaaca gaggaggtgg tgtgtgggaa tctggtgcag 120
 caaactccca gactacatca tggggaagtg gaaatggcgc aat 164

238

<210> 741
 <211> 514
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (514)
 <223> n = A,T,C or G

<400> 741
 ccagtcagaa ttgagatgtg ctgtgagtgc aaaatacact caaatctaag acttagtatg 60
 gaagaaaaag aagataagggt gnttcattaa taatctttta tattgattac atgttgaaat 120
 gatattttta atatactggg ttacataaac tgttattaag attaatattg cttgtttctt 180
 ttttaatatg gctactagaa aattaaaaat tatgttggtg ttcacattat atttctgttg 240
 aacaatgtgg acatagataa tctacagtca ttacattagc cttagaattt agcatcatatc 300
 ttttaagcac tctgggttac taacttgaac tcccagaaac ccataagcac actctgcata 360
 taaattattg caaaattcat tcttatctct ctgaaagata tgcatttttaa gggtaaaaag 420
 aattcacaaa atattgantc cttaacaaat gtcaattagt atatggagag agctaaagga 480
 cttcntgtag actggtncat tggggaaaaa caga 514

<210> 742
 <211> 439
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (439)
 <223> n = A,T,C or G

<400> 742
 gcaggtccta tgcatagtta ataaggnta taatctactc aacatggaaa atgggagcct 60
 atttgcaaac acacgagtaa ttaaagtacc aattctctct tagtttcttt ttttatagtt 120
 ggnttatattt gcaattataa atgntaaaca tccctagaga tgaaagttaa aatggctgat 180
 cacagatcag tagcaaaata caaattgaca attcaaaatt ataaataaaa ctctgttgag 240
 gatgttttaac tttgagctc caaatttaag agctaagctt ggaagaaaca aatttatagg 300
 ttatatattc ctcttaaat aaaaaacaaa ctctctctgg cagtagnttg tgaattcctt 360
 tcattgnaat gataccatga ttacaggatc aaaaatgctt aacttacttg ccattctgct 420
 cacatcatca cagttgttt 439

<210> 743
 <211> 275
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (275)
 <223> n = A,T,C or G

<400> 743
 cangacgcta cttcccctat catagaagag cttatcacct ttcatgatca cgccctcata 60
 gtcattttcc ttatctgctc ctagtctctg tatgcccttt tctaactact cacaacaaaa 120
 ctaactaata ctaacatctc agacgctcag gaaatagaaa ccgtctgaac tatcctgccc 180

gccatcatcc tagtccatc cgccctccca tccctacgca tcctttacat aacagacgag 240
gtcaacgatac cctcccttac catcaaatca attgg 275

<210> 744

<211> 295

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(295)

<223> n = A,T,C or G

<400> 744

ctgtncctttt aaaaaatctg gatgtttttt atttagtgat tgttcgacaa ttagctgctt 60
caaaacataa tgtgcattgc ttatgaatgc cttcatatac taatacagat actctgataa 120
tattacactc taataaggat aatgctgaat tttgaaagga cacaaaacat ctaatgccaa 180
tatatacatg attagccaac atctttgcta tcaagaccac tcgtttttta ataaagatgc 240
aagtgtcagt tgtagattat tgggatgaag ctaaattccc agaatgcagc agcag 295

<210> 745

<211> 477

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(477)

<223> n = A,T,C or G

<400> 745

cgcgttactg tacatattgc tagcaggaga caactggaaa tactaaacaa atactggaat 60
tcacattaca gacagacgaa accaaccatgg atgccacaca taacttcctt ttagtattca 120
cagagagcct atttgtggtt gctcagggtg ggtcatacat tgcttgacga aatggcctga 180
tcatagctct atgaaacaat gaattcggaa tgaaatctta ccatgacacc tctctgtagg 240
aaagaaatgt tgcttcacgt gtgctaagtt gagataataa tatttcacat atttatatac 300
agagaatcac tctcaaattt aaccacaagat aagcaatagg atttgggggt gacttgatca 360
cattttctaac aacacttttc ttttttctag aggtcactct caaacactga tatatcacta 420
tagtttgagt gtanggattc agtaatcaaa ggttggttatt gcaaaagagc caggcag 477

<210> 746

<211> 524

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(524)

<223> n = A,T,C or G

<400> 746

ctgtgaaatt ggggtgggag agccaaaata ctttacaact tcagaccgga gaaaaggcca 60
gagggtgtgaa gttagactct atgatgaaac agagtcgtct tttgcgatga catgttggga 120
taatgaatcc attctacttg cacagagctg gatgccacga gaaacagtaa tatttgcttc 180
agatgtaaga ataaattttg acaaatttcg gaactgcatg acagcaactg taatctcaaa 240

240

```

aaccattatt acaactaatc cagatatacc agaagctaac attctgctga attttatacg      300
agaaaaataaa gaaacaaatg ttctggatga tgaaattgac agttatttca aagaatccat      360
aaatttaagt acaatagttg atgtctacac agntgaacaa ttaaaggga aagctttgaa      420
gaatgaagga aaagctgatc cttcctatgg catcctttat gcctacattt ccacactcaa      480
cattgatgat gaaactcaaa agtagttcga aatagatggt ccag                          524

```

<210> 747

<211> 456

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (456)

<223> n = A,T,C or G

<400> 747

```

cctcagttct tgattgtggt tgacggggcg tcaccatgaa ggagcccatt tagtataaag      60
cttccaacct tttctcttaa tcgtttcttt aatcttttaa accatcttca agtgcatagg      120
ggagtttccg atgccagagg atgaaagcaa gtgctttctc caccctctcc tcccagagtg      180
aaaacaaatc cttttgctga tacttgtttc aaaagcatcc attgtaaagc ttctcagtga      240
cacaaaatac tgagaggtaa ctttttatca atcaaaccac atacccaat ttaacacctt      300
tcagtgtctc gaattcaact gacagactaa aggggtgttc ctgtaacagt ctgaaatatt      360
aagtgttttt tttgttttgt ttttaaatct tatttcagaa aacttcctct nggggtagga      420
aagtacacat gaagcagcaa agtaacgaag aaaaac                          456

```

<210> 748

<211> 474

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (474)

<223> n = A,T,C or G

<400> 748

```

ccanaccagg gaaccaaagc cagacagnga agttctctgc ttcttttggc tataatngna      60
caagaaaggg atcatctttt gaagatgttt aaagaaataa agcaactttc tttataaaca      120
gtcaaataat caattaatgg aataaataag tactaaccce cattttaacc actctgtaat      180
cactacactt tacatatctt ttatttnggn ggcaaaantcc ccataatta gtctaaaatc      240
caccaatcac tttttaaagt aaaatgaata gccacaaaaa taagaaaatc ttctgttcac      300
tctttggcta aaaaggaaaa caaataaaac aaaacaaaaa gaaacagaag acaactgtaa      360
cactgggtgat aaaagaaact ttttttttac aagtaaaata aagttatcaa tttaaatctt      420
ggncacttta taaaaacaag aggtaatggt gtaataaaac agcagtagcc tcag                          474

```

<210> 749

<211> 355

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (355)

<223> n = A,T,C or G

<400> 749
cctgggttnna gnggctgact gnaacctcca cttcctgttc tcaggcaatc ctccctgcctc 60
agccttcctta gtagctggga ctacaggagt gtgcaaccat gcccaactaa tttttgtatt 120
tttaatatag acagggtttc accatgttga tcaggttggt ctccaactcc tgacctcagg 180
tgatccacct gtcccagcct cccaaagtgc tgggattaca ggcatgagcc accacgcccg 240
gnccaggata aagtaaaaat ttgtaagcac acaaggccct ttgcaacctg gctcctgggt 300
actactttaa ncctcctgcc ctcccaaatag tntcactgt ttttctanac atacc 355

<210> 750

<211> 493

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(493)

<223> n = A,T,C or G

<400> 750
ccatgctggt ctggaactcc tgaactcagg tgatccaccc gcctcagtct cccaatagat 60
tacatatatt attaataaat tgcttccttt aacaccctat tcattgaatt ttccagtaaa 120
ccacaattac taattactcc tgaaatcaga aaagagggtta aaaagatttt ataacagtat 180
cctatgaaat ctactacttt caagtaatat tagttgaatt accaaaaccc gtcactcaag 240
ccaatgacta caattaagat atgagtaaca tttcctagat aaataaagtc aattaattat 300
atgtgcatct gggaaataga gaaagtacat ataagccatg attttgaagn caaaagagag 360
agantatttg ccaaggaggg gtgagttata gtatgtaatt ataacatata gaagcttttt 420
gtatgctggt aactaatttt aatttcctac attnttatgg agatttctgc tattcttgtc 480
ctattttcca cct 493

<210> 751

<211> 364

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(364)

<223> n = A,T,C or G

<400> 751
cgaggctctg naaggctcacc aagtctgccc aganagctca gaaggctaaa tgaatattat 60
ccctaataacc tgccacccca ctcttaatca gtggtggaag aacggctctca gaactgtttg 120
tttcaattgg ccatttaagt ttagtagtaa aagactggtt aatgataaca atgcatcgta 180
aaaccttcag aaggaaagga gaatgttttg nggaccactt tgggttttct ttttgctgtg 240
ggcagtttta agttattagt ttttaaaatc agtacttttt aatggaaaaca acttgaccaa 300
aaatttgta cagaattttg agaccatta aaaaagttaa atgagataaa aaaaaaaaaa 360
cntg 364

<210> 752

<211> 498

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature
<222> (1)...(498)
<223> n = A,T,C or G

<400> 752
ctggattatg ggttgggnatt ggtcatatgt tagactccat acaggcatag ctatgatgca 60
gtgaatccct tagaagttac aattctcaaa ttacatactt cctcagatgt aacattagaa 120
ctcaatattt ctaacaataa cataccagaa aaggctggac tggcactcat ctgctgacta 180
acttgtagcc tcagtaatat gacatacttg cctttaacaa attatctcaa attaactaac 240
agaccttcag aaaatggaga ttctttttga tggggacata atcaaattta agtctgagaa 300
atatgcttaa cagttggaac tcaaattaaa tgtactgatt ttaaagttaa gacattaaca 360
agtatanat tagcctcaaa aaaagacaat ttgnaagggn ttaggtcttt taatttggtg 420
cttgntcaca acttgactgg tgcttctttc cttgctgctt cacatcaagc atggggccaa 480
ttctattttc agtaaatg 498

<210> 753
<211> 467
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(467)
<223> n = A,T,C or G

<400> 753
nacaacctta gccanaacca tttacccaaa taaagggata ggcgatagaa attgaaacct 60
ggcgcaatag atatagnacc gcaagggaaa gatgaaaaat tataaccaag cataatatag 120
caaggactaa cccctatacc ttctgcataa tgaatttaact agaaataact ttgcaaggag 180
agccaaagct aagacccccg aaaccagacg agctatctaa gaacagctaa aagagcacac 240
ccgtctatgt agcaaaatag tgggaagatt tataggtaga ggcgacaaac ctaccgagcc 300
tggtgatagc tggntgncca agatagaatc ttagntcaac tttaaatttg cccacagaac 360
cctctaaatc cccttgtaaa ttttaactgtt agtccaaaga ggaacagctc ttggacacna 420
ggaaaaaacc ttgcagagag agtaaaaaat ttaacaccca tagtagg 467

<210> 754
<211> 196
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(196)
<223> n = A,T,C or G

<400> 754
gtcatgttca agtgttntaa tctgacgcag gcttatgcgg aggagaatgt tttcatgtta 60
cttatactaa cattagttct tctatagggt gatagattgg tccaattggg tgtgaggagt 120
tcagttatat gtttgggatt ttttaggcag tgggtgttga gcttgaacgc tttcttaatt 180
ggtggctgct tttagg 196

<210> 755
<211> 381
<212> DNA
<213> Homo sapien

<400> 755
ctggaaagga ttctgtacat ataagacatc aaatattgag ggatactgga actttttaa 60
taatggggcaa agaaagtcaa caaaggaagt tcatatgaaa tcaaactagt aatatgatta 120
caaaaaaaaaa gttaaaatt tttcttgcc ccagtcttat catttctgag ccaaatacaa 180
ttctatcgaa atcacctgaa actgaaatca ccattctagg ctggttttcc cataaagatg 240
gactgctcca aaaagaggaa tcaagaaaga atttggctca cagtgaatta ttcactttgt 300
cttagttaac taaaaataaa atctgactgt taactacaga aatcatttca aattctgtgg 360
tgataataaa gtaatgaccg c 381

<210> 756

<211> 341

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (341)

<223> n = A,T,C or G

<400> 756
ggntataaac ctattattta ttgcagaact aataaaaaat ccaaagcctt gtatttgtac 60
atctttatta tctctaaagc actttcctca acctaatttc agtttttaca attggtactc 120
aagaaaatag agacagaaat catttgattt tgcccagaaa ccactctgctt atatttataa 180
ggccacctaa ttgaaatca catatagacc aggcgcggtg gctcacgcct gtaattccaa 240
cactttggaa ggccaaggca ggtggatcac aaggtcaaga gattgagacc atcttggcca 300
acatggcgaa accccgtctc taccaaaaat acaaaaatca g 341

<210> 757

<211> 479

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (479)

<223> n = A,T,C or G

<400> 757
cgnttactg tacatattgc tagcaggagg acaactggaa atactaaaca aatactggaa 60
ttcacattac agacagacga aaccaacatg gatgccacac ataacttcct ttgtagtctc 120
acagagagcc tatttgtggt tgctcagggt gggtcatata ttgcttgagc aaatggcctg 180
atcatagctc tatgaaacaa tgaattcggg atgaaatctt accatgacac ctctctgtag 240
gaaagaaatg ttgcttcacg tgtgctaagt tgagataata atatttcaca tatttatata 300
cagagaatca ctctcaaatt taaccaaga taagcaatag gatttggggg tgacttgtn 360
acatttctaa caacactttt cttttttcta gaggtcactc taaaacactg atatatcact 420
atagnttgag ngtagggatt caagtaatca aaggttggtt ttgcaaaaga gccaggcag 479

<210> 758

<211> 267

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

244

<222> (1) ... (267)

<223> n = A,T,C or G

<400> 758

ccatgnctag	gtttatagat	agttgggtgg	gttggtgtaa	atgagtgagg	caggagtccg	60
aggaggttag	ttgtggcaat	aaaaatgatt	aaggatacta	gtataagaga	tcagggttcgt	120
ccttttagtgt	tgtgtatggc	tatcatttgt	tttgagggtta	gtttgactag	tcattgttgg	180
gtggtaatta	gtcggttgtt	gatgagatat	ttggagggtgg	ggatcaatag	agggggaaat	240
agaatgatca	gtactgcggc	gggtagg				267

<210> 759

<211> 449

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (449)

<223> n = A,T,C or G

<400> 759

cgagggtcttg	aaatcagcaa	cacacttaca	aatgagaaaa	tgaaaataga	agagtatata	60
aagaaagggga	aagaggatta	tgaagagagt	catcagagag	ctgtggctgc	agaggatatcc	120
gtacttgaaa	actggaagga	gagtgaagtg	tataagctac	agatcatgga	gtcacaagca	180
gaagcctttc	tgaagaagct	ggggctgatt	agccgtgatc	ctgcagcata	tcccgcacatg	240
gagtctgata	tacgttcatg	ggaattgttt	ctttctaata	ttacaaaaga	aattgagaaa	300
gcaaagtctc	agtttgaaga	acaaattaag	gcaattaaaa	atgggtcccg	gctcagtgaa	360
ctttctaaag	ngcagatttc	tgagctttca	tttcctgcct	gtaacacggg	tcaccccgag	420
ttactccctg	agtccttcagg	ccacgatgg				449

<210> 760

<211> 414

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (414)

<223> n = A,T,C or G

<400> 760

ccatnaactg	gaagcagctc	actaaacaaa	cagnggcata	cccatagaac	tgcatacttc	60
tcagcagtat	gaaagaatga	gctacttata	taagcatcat	tgataaacct	caaaaaaaaa	120
atgccacatg	aagaanccca	agggggagaa	acataaaaaac	tttatatgnc	agncatataa	180
aattctagaa	aatgcaaact	aatccatcnt	aaaggaaagt	aatcancag	ttgtctggag	240
gaccanagag	agcaggagga	gagagattnt	taanggggtt	aaagtaaatt	ngggagtgcc	300
cttccatttt	taaatnctat	gaaaatgaaa	gtaaaggccc	ntgcatgttg	taaactaata	360
gtaacaaaca	gattgggttg	gagtgggggtg	ttgtctgggg	acatcattac	aaan	414

<210> 761

<211> 428

<212> DNA

<213> Homo sapien

<400> 761

245

```

gagcctcact aaaataacag atttcagtat agccaagttc atcagaaaga ctcaaattgga      60
atgattttaca agatagaaca ctttaaacca ggtcagtcct atctttttgt agctgaaggc      120
tatcagtcac aacacaattt cgcgtacacc tctgctcatt atggaattac acttaaaacg      180
aatctcaaga ggggtgaccat tgttgtttca gataccatcc ctaaggagag tgggttaacag      240
gaagattgcc agtggttactg atggaaagaa gtgtttgttt gttttttttc ttgtcaaaga      300
cttacaccat agtttttaaa taaactgtca ggcattttct cagacagggt ttccttttca      360
atgcagtaat gaagaactaa gataaaaatc atgacttttg actgccactc aacattatta      420
catgcacc                                     428

```

<210> 762

<211> 574

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (574)

<223> n = A,T,C or G

<400> 762

```

caggctctgaa ctgataagta ttaagagacg tttgttgcta gttaagngtt ccagttgaga      60
gttcgaagtg aaaacctggg ctctttacca gtgttgagtg agaagattta tttctctttc      120
ctctgaattt accacatgta acatcacaga gacatgtaga gttccttttag gatttgcgat      180
ttgaaccagn ccagtctgat tttcaggtga attctgtgaa gagcttgatg ggggaagtct      240
gaagacagaa ggaattaggg aaaaggggtga tacttacaga gtaaaggaaa taaatgaaaa      300
gataatggta tttttggtag ccacagggaa atagcaggag gggactggag atcacacaca      360
cgcacacgca cacacacaaa cacacacaca cgctaaaact caaactaaaa acctcccaaa      420
ggagctgctt tgtttgcaga cttcaattng aagtagatac taagggaag aatagaccag      480
ttaaaattca cctgaaaatc tcttccann cttcaaatgt gctaaaatat cactgtcagc      540
ttagcatctc tncatgtatg tatatataga tgta                                     574

```

<210> 763

<211> 465

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (465)

<223> n = A,T,C or G

<400> 763

```

cctactatgg gtgttaaaat tttttactct ctctacaagg ntttttccta gtgtccaaaag      60
agctgttcct ctttgacta acagttaaat ttacaagggg atttagaggg ttctgnnggc      120
aaatttaaaag ttgaactaag attctatctt ggacaaccag ctatcaccag gctcggtagg      180
tttgctgcct ctacctataa atcttccacac tattttgcta catagacggg tgtgctcttt      240
tagctgttct taggtagctc gtctggtttc gggggctctta gctttggctc tccttgcaaa      300
gttattttcta gttaattcat tatgcagaag gtataggggt tagtccttgc tatattatgc      360
ttggatataa tttttcatct ttcccttgcg gtactatata tattgcgcca ngtttcaatt      420
tctatcgcct atactttatt tgggtaaatg gtttggtctaa gggttg                                     465

```

<210> 764

<211> 151

<212> DNA

<213> Homo sapien

<400> 764
ctgtcaatta atgctagtc tcaggattta aaaaataatc ttaactcaaa gtccaatgca 60
aaaacattaa gttggaatt actcttgatc ttgaattact tccgttacga aagtccttca 120
catttttcaa actaagctac tatatttaag g 151

<210> 765
<211> 251
<212> DNA
<213> Homo sapien

<400> 765
gaagagctta tcacctttca tgatcacgcc ctcatagtc ttttccttat ctgcttccta 60
gtcctgtatg ccccttttct aacactcaca acaaaactaa ctaatactaa catctcagac 120
gctcaggaaa tagtaaccgt ctgaactatc ctgcccgcga tcctcctagt cctcatcgcc 180
ctcccatccc tacgcctcct ttacataaca gacgagggtca acgatccctc ccttaccatc 240
aatcaattg g 251

<210> 766
<211> 375
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1) ... (375)
<223> n = A,T,C or G

<400> 766
cgaggctctg cctcctggtt cttcatccat tattaacaga agagcatact ggtttcggtc 60
cataaaatct ttgggaaggg acaactgtaa aggaagttca tagtcgtcaa tatgaaggat 120
tttaatttct ggctttccta tcttcttctt caggatagct tccttcagca tagaattggt 180
ttccaatata aaatattttg ctgggttggtc cgtactatgt aggctgacca ctgggaccct 240
tggaccttca cagaataata agaaatgttg attcatggga ctaaaactgg catcaaaata 300
tgtacattgt tctttcatga aattacatga aatgcattgg cgattcaata atccttcagt 360
agaagcactg tacag 375

<210> 767
<211> 485
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1) ... (485)
<223> n = A,T,C or G

<400> 767
cgaggctctga accctcgtag agccattcat acagggtccct aattaaggaa caagtgatta 60
tgctaccttn gcacggttag ggtaccgcgg cccgttaaac atgtgtcact gggcaggcgg 120
tgctctaat actggtgatg ctagagggtga tgtttttggn aaacaggcgg ggtaagattt 180
gccgagttcc ttttactttt tttaaccttt ccttatgagc atgcctgtgt tgggttgaca 240
gtgagggtaa taatgacttg ttggtgattg tagatattgg gctgttaatt gtcagttcag 300
tgttttaatc tgacgcaggc ttatgcccag gagaatgttt tcatgttact tatactaaca 360
ttagttcttc tatagggtga tagatnggtc caattgggtg tgaggagntc acttatatgt 420

247

ttggggatttt ttaggtaagn ggggtgttgag cttgaacgct ttcttaattg ggggctgctt 480
ttang 485

<210> 768

<211> 379

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(379)

<223> n = A,T,C or G

<400> 768

ctgatattct attaaagata caaagaggag ctggnaccat ttcttctgaa actattacaa 60
acaactgaaa aggtggaatt tctccctaatt tcatttttagg aggccagcat tatactgata 120
ccaaaacctg gcagaggtag aataataaaa ggaaacttca agtcagtagc actgatgaac 180
accaatgtga aaatcctcaa taaaatactg gcaaactgaa ttcagcagca catcaaaaag 240
ctaaccacc acaatcaagt cagcttcac cctgcgatgc aagtcgtggt caacatagc 300
aaatcaataa atacaattca tcagataaac agagctaaag acaaaattca catgattttc 360
tcaatagatg cagaaaagg 379

<210> 769

<211> 518

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(518)

<223> n = A,T,C or G

<400> 769

cgagggtccat atgatgatca gtctatatag ttttaaggcgc agatacacaa attttcaaaa 60
atatgggtag aatatagtagc atatgaatgg aatagacaat gctttgaaaa tcaactggagg 120
gaggctttat tggttgtaga aacatgttgt catcactttt tgctttaagc ccttggtggt 180
gaaataactc aaaccattct tccttatgct gaagatcgag aacccaagt atcacatcta 240
ccatcccact catcaatgtg attggtagc ctttgctgag gncctgcata gccagtttta 300
aagttagagt tcttgcatat acatatgaaa aggcattgta ctttgctgtt caaagagctt 360
tttgcttggt gtaaaaagaa aactcaaatt acagtgtgat gtggaatata atgggtgtag 420
tttcatcgag atgatgggaa agaattgata agataaagcn gaaagatgag cagaattttc 480
agattgggtt tggaagagc acttaagaaa gaggggtg 518

<210> 770

<211> 378

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(378)

<223> n = A,T,C or G

<400> 770

tatgggtcct gagtgtggaa tataagataa caagacaatt cccttgcttt caagggaaat 60

248

```

cacactttat aaaactttga attcttgaaa tgggtttcag aggttccaag gtcaaattca 120
agaataagag ttaagaagaa aaagactatg agaaaggaag tgntgacccc atttgcatTT 180
aaatggcagg aatagtctca atctactcat tggggaaaaa tgtatgttgc atatttttga 240
gatattgcaa cttgctctct ctctttgcca cccacccctt tgnatgctc tgtttttggg 300
ctgaattggc aagaaaaatg gctggagggc tggaagaagn tggacccttc ttccttcttc 360
cttcttcttc ctttctcc 378

```

```

<210> 771
<211> 207
<212> DNA
<213> Homo sapien

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<400> 771
cataaatatt atactagcat ttaccatctc acttctagga atactagtat atcgctcaca 60
cctcatatcc tccctactat gcctagaagg aataatacta tcactgttca ttatagctac 120
tctcataacc ctcaacaccc actccctctt agccaatatt gtgcctattg ccatactagt 180
ctttgccgcc tgcgaagcag cggtagg 207

```

```

<210> 772
<211> 384
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1) ... (384)
<223> n = A,T,C or G

```

```

<400> 772
cctactatgg gtgttaaatt ttttactctc tctacaaggt tttttcctag tgtccaaaga 60
gctgttcttc tttggactaa cagttaaatt tacaagggga ttttagagggt tctgngggca 120
aatttaaagt tgaactaaga ttctatcttg gacaaccagc tatcaccagg ctcggtagggt 180
ttgtgcctc tacctataaa tcttccact attttgctac atagacgggt gtgctctttt 240
agctgttctt aggtagctcg tctggtttcg ggggtcttag ctttggctct ccttgcaaa 300
ttatttctag ttaattcatt atgcagaagg tataggggtt agtccttgct atattatgct 360
tggttataat ttttcatctt tccc 384

```

```

<210> 773
<211> 182
<212> DNA
<213> Homo sapien

```

```

<400> 773
cccttttctt aacactcaca acaaaactaa ctaatactaa catctcagac gctcagggaa 60
atagaaaccg tctgaactat cctgcccgcc atcatcctag tctcatcgc cctcccatcc 120
ctacgcatcc ttacataac agacgaggtc aacgatccct cccttaccat caaatcaatt 180
gg 182

```

```

<210> 774
<211> 191
<212> DNA
<213> Homo sapien

```

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<400> 774
ccatggctag gtttatagat agttgggtgg ttgggtgtaa atgagtgagg caggagtccg 60

```


aggaggttag ttgtggcaat aaaaatgatt aaggatacta gtataagaga tcaggttcgt 120
ccttttagtgt tgtgtatggc tatcatttgt tttagaggta gtttgattag tcattgttgg 180
gtggttaatta g 191

<210> 775

<211> 192

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(192)

<223> n = A,T,C or G

<400> 775

ccatggctaa gntatataga tagctgggtg gctggagtaa atgantgagg nacgagtcgg 60
angagggttag ttgaggcaat aaaaatgatn aaggatacta gtataagaga tcangttcgt 120
cctttacatg ttgngtatgg ctatcatttg ttttgaggct agnttgatta gtcattgttg 180
ggtggttaatt aa 192

<210> 776

<211> 144

<212> DNA

<213> Homo sapien

<400> 776

ctgacccctt agaaccctgg ctctgccatt agctaggacc taagactctg cccacatttt 60
ggtctgttct ctcccattac acataggttt gtctcagcat gcaagagttt ttcctttaa 120
aaaaaaaaa aaaaaaaaaa aaaa 144

<210> 777

<211> 483

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(483)

<223> n = A,T,C or G

<400> 777

cctactatgg gtgntaaatt ttttactctc tctacaagggt tttttcctag tgtccaaaga 60
gctgttcctc tttaggactaa cagttaagtt tacaagggga ttttagagggt tctgtgggca 120
aatttaaagt tgaactaaga ttctatcttg gacaaccagc tatcaccagg ctcggtagggt 180
ttgtcgcctc tacctataaa tcttcccact attttgctac atagacgggt gtgctctttt 240
agctgttctt aggtagctcg tctggtttcg ggggtccttag ctttggtctt ccttgcaaaag 300
ttatttctag ttaattcatt atgcagaagg tataggggnt aagtccttgc tatattatgc 360
ttggatataa tttttcatct ttcccttgcg gtactatata tattgcgcca ggtttcaatt 420
tctgccgcct atactttatt tgggtaaatg gtttggctaa ngttgctgggt agaaggtgga 480
gtg 483

<210> 778

<211> 393

<212> DNA

<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(393)
<223> n = A,T,C or G

<400> 778
ctgcattttt attgcatct gcagatgaac tgggaaaac tcattttaca acagaactga 60
gacagacgac caccatattc actgaggtct aaatttgcag ttccactaa tgacattttg 120
atttcccaac agagatactt ctggtcttac tgcacagtct ttaagagaa atacttccat 180
tatgccacat tgccttgat ccgtaagtga tgtgttaagg tgcttcaaag gaactctgac 240
ctctgaagta cttgagctac tttagtatgt ccagcctatt gctttttgtt ttagngngtc 300
accataaata tcaggggcat aaaaggctat ctattcttaa ttcaaggata aaacagaaga 360
agcttggtgn ataaaacaat agtcaagatc cag 393

<210> 779
<211> 277
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(277)
<223> n = A,T,C or G

<400> 779
cctnttgatt tgatgggtaa ggggagggat cgttgacctc gtctgttatg taaaggatgc 60
gtaggggatgg gagggcgatg aggactagga tgatggcggg caggatagtt cagacggttt 120
ctatttcttg agcgtctgag atgttagtat tagttagttt tgttgtagt gttaggaaaa 180
gggcatacag gactaggaag cagataagga aaatgactat gagggcgtga tcatgaaagg 240
tgataagctc ttctatgata ggggaagtag cgtcttg 277

<210> 780
<211> 328
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(328)
<223> n = A,T,C or G

<400> 780
catgntatgg ataaccatnt taactgtatt ttntgcance cgtaccttct tgggaataca 60
attgtctaac tttttatttt tggncgtggt gttgtggtgt gcaaaactcc gtacattgct 120
atlttgccac actgcaacac cttacagatg tggaagatgt gaaatttgct atcaattatg 180
actaccctaa ctctcagag gattatattc atcgaattgg aagaactgct cgcagtacca 240
aaacaggcac agcatacact ttctttacac ctaataacat aaagcagggg agcgacctta 300
tctctgtgct tcgggaagct aancaaac 328

<210> 781
<211> 305
<212> DNA
<213> Homo sapien

251

<220>
 <221> misc_feature
 <222> (1) ... (305)
 <223> n = A,T,C or G

<400> 781
 ctgttcagaa agctcattgg acctgggttt gaaaataaaa caaagttaaa accctgggag 60
 gagttattgt gcagngtggg gtactcaggc tttcttataa agaaaaaaaa agttatctgg 120
 taccaaagtg tgcaacctac agaccctcag gtactgccct gtgacttctc tgtatgacat 180
 cacaaggctg ccaagtgcct gtttttctag aactaggagt tggtgagggt tggctantgc 240
 tgaaccatg cataggattg gtttactaaa ttaaacctt attacgtacg tcctccaaaa 300
 gacag 305

<210> 782
 <211> 497
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (497)
 <223> n = A,T,C or G

<400> 782
 cgagggtggct ttaattgatg ttaatgcctt atgtcaaatg taaagttaga atttgctagg 60
 gctgggtagat ggagtgatat ttctaggact tagacattga aaactaatc agcctgtagt 120
 aacctggatg gttttcaatg gcatggtag tcaaattcat ggttttaaac ttagaagcag 180
 ctttcggggg agagggtagg ttggagcatt tattacatat ttactgttt aatgtcttaa 240
 ccgtgggcct tttaatttgt aaacactgaa atgattgttg ggctgtggaa aacatttacc 300
 tatttacctt ggaagtttta aaagacagtc cacttttttag catgtgtgtt gcgtccagcc 360
 tgtggtcgtc ttaactaata aatgngattt ttctctcaaa aaaaaaacct ccccgggcgg 420
 ccgctcaagg gcnaattccn cacactggcg gccgttacta ggggatccga nctcgggtcca 480
 agcttggcgt aatcatg 497

<210> 783
 <211> 364
 <212> PRT
 <213> Homo sapien

<400> 783
 Met Trp Gln Pro Leu Phe Phe Lys Trp Leu Leu Ser Cys Cys Pro Gly
 1 5 10 15
 Ser Ser Gln Ile Ala Ala Ala Ala Ser Thr Gln Pro Glu Asp Asp Ile
 20 25 30
 Asn Thr Gln Arg Lys Lys Ser Gln Glu Lys Met Arg Glu Val Thr Asp
 35 40 45
 Ser Pro Gly Arg Pro Arg Glu Leu Thr Ile Pro Gln Thr Ser Ser His
 50 55 60
 Gly Ala Asn Arg Phe Val Pro Lys Ser Lys Ala Leu Glu Ala Val Lys
 65 70 75 80
 Leu Ala Ile Glu Ala Gly Phe His His Ile Asp Ser Ala His Val Tyr
 85 90 95
 Asn Asn Glu Glu Gln Val Gly Leu Ala Ile Arg Ser Lys Ile Ala Asp
 100 105 110
 Gly Ser Val Lys Arg Glu Asp Ile Phe Tyr Thr Ser Lys Leu Trp Ser

115	120	125
Asn Ser His Arg Pro Glu Leu Val Arg Pro Ala Leu Glu Arg Ser Leu		
130	135	140
Lys Asn Leu Gln Leu Asp Tyr Val Asp Leu Tyr Leu Ile His Phe Pro		
145	150	155
Val Ser Val Lys Pro Gly Glu Glu Val Ile Pro Lys Asp Glu Asn Gly		
165	170	175
Lys Ile Leu Phe Asp Thr Val Asp Leu Cys Ala Thr Trp Glu Ala Met		
180	185	190
Glu Lys Cys Lys Asp Ala Gly Leu Ala Lys Ser Ile Gly Val Ser Asn		
195	200	205
Phe Asn His Arg Leu Leu Glu Met Ile Leu Asn Lys Pro Gly Leu Lys		
210	215	220
Tyr Lys Pro Val Cys Asn Gln Val Glu Cys His Pro Tyr Phe Asn Gln		
225	230	235
Arg Lys Leu Leu Asp Phe Cys Lys Ser Lys Asp Ile Val Leu Val Ala		
245	250	255
Tyr Ser Ala Leu Gly Ser His Arg Glu Glu Pro Trp Val Asp Pro Asn		
260	265	270
Ser Pro Val Leu Leu Glu Asp Pro Val Leu Cys Ala Leu Ala Lys Lys		
275	280	285
His Lys Arg Thr Pro Ala Leu Ile Ala Leu Arg Tyr Gln Leu Gln Arg		
290	295	300
Gly Val Val Val Leu Ala Lys Ser Tyr Asn Glu Gln Arg Ile Arg Gln		
305	310	315
Asn Val Gln Val Phe Glu Phe Gln Leu Thr Ser Glu Glu Met Lys Ala		
325	330	335
Ile Asp Gly Leu Asn Arg Asn Val Arg Tyr Leu Thr Leu Asp Ile Phe		
340	345	350
Ala Gly Pro Pro Asn Tyr Pro Phe Ser Asp Glu Tyr		
355	360	

<210> 784
 <211> 6353
 <212> DNA
 <213> Homo sapien

<400> 784

tggcgaatgg gacgcgccct gtagcggcgc attaagcgcg gcgggtgtgg tggttacgcg	60
cagcgtgacc gctacacttg ccagcgcctt agcgcgccgt cctttcgctt tcttcccttc	120
ctttctcgcc acgttcgccg gctttccccc tcaagctcta aatcgggggc tccctttagg	180
gttccgattt agtgctttac ggcacctcga ccccaaaaaa cttgattagg gtgatggttc	240
acgtagtggg ccatcgccct gatagacggt ttttcgccct ttgacgttgg agtccacgtt	300
ctttaatatg ggactcttgt tccaaactgg aacaacactc aaccctatct cggctctattc	360
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 Lys Ala Asp Lys Val Arg Tyr Asp Arg Glu Met Lys Asp Tyr Gly Pro
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 Ala Lys Gly Gly Lys Lys Lys Lys Asp Pro Asn Ala Pro Lys Arg Pro
 85 90 95
 Pro Ser Gly Phe Phe Leu Phe Cys Ser Glu Phe Arg Pro Lys Ile Lys
 100 105 110
 Ser Thr Asn Pro Gly Ile Ser Ile Gly Asp Val Ala Lys Lys Leu Gly
 115 120 125
 Glu Met Trp Asn Asn Leu Asn Asp Ser Glu Lys Gln Pro Tyr Ile Thr
 130 135 140
 Lys Ala Ala Lys Leu Lys Glu Lys Tyr Glu Lys Asp Val Ala Asp Tyr
 145 150 155 160
 Lys Ser Lys Gly Lys Phe Asp Gly Ala Lys Gly Pro Ala Lys Val Ala
 165 170 175
 Arg Lys Lys Val Glu Glu Glu Asp Glu Glu Glu Glu Glu Glu
 180 185 190
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 195 200

<210> 790
 <211> 457
 <212> DNA
 <213> Homo sapiens

<400> 790
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 tcccaggagc ccagtaatgg agagcccaa aaagaagaac cagcagctga aagtcgggat 180
 cctacacctg ggcagcagac agaagaagat caggatacag ctgagatccc agtgcgcgac 240
 atggaagggtg atctgcaaga gctgcatcag tcaaaccaccg gggataaatc tggatttggg 300
 ttccggcgctc aaggtgaaga taatacctaa agaggaacac tgtaaaatgc cagaagcagg 360
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 tagatatttg acttaaacta tctcaataaa gttttgc 457

<210> 791
 <211> 126
 <212> PRT
 <213> Homo sapiens

259

<400> 791

Ser Pro Val Leu Gly Thr Arg Arg Ser Cys Glu Pro Ala Thr Arg Val
 5 10 15

Pro Glu Val Trp Ile Leu Ser Pro Leu Leu Arg His Gly Gly His Thr
 20 25 30

Gln Thr Gln Asn His Thr Ala Ser Pro Arg Ser Pro Val Met Glu Ser
 35 40 45

Pro Lys Lys Lys Asn Gln Gln Leu Lys Val Gly Ile Leu His Leu Gly
 50 55 60

Ser Arg Gln Lys Lys Ile Arg Ile Gln Leu Arg Ser Gln Cys Ala Thr
 65 70 75 80

Trp Lys Val Ile Cys Lys Ser Cys Ile Ser Gln Thr Pro Gly Ile Asn
 85 90 95

Leu Asp Leu Gly Ser Gly Val Lys Val Lys Ile Ile Pro Lys Glu Glu
 100 105 110

His Cys Lys Met Pro Glu Ala Gly Glu Glu Gln Pro Gln Val
 115 120 125

<210> 792

<211> 461

<212> DNA

<213> Homo sapiens

<400> 792

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 gagagcccca aaaagaagaa ccagcagctg aaagtcggga tcctacacct ggcgcagcaga 180
 cagaagaaga tcaggatata gctgagatcc caggtgctgg gaagggaaat gcgcgacatg 240
 gaaggtgatc tgcaagagct gcatcagtca aacaccgggg ataatcttgg atttgggttc 300
 cggcgtcaag gtgaagataa tacctaaaga ggaacactgt aaaatgccag aagcaggtga 360
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 atatttgact taaactatct caataaagtt ttgcagcttt c 461

<210> 793

<211> 108

<212> PRT

<213> Homo sapiens

<400> 793

Arg Arg Ser Cys Glu Pro Ala Thr Arg Val Pro Glu Val Trp Ile Leu
 5 10 15

Ser Pro Leu Leu Arg His Gly Gly His Thr Gln Thr Gln Asn His Thr
 20 25 30

Ala Ser Pro Arg Ser Pro Val Met Glu Ser Pro Lys Lys Lys Asn Gln

260

35	40	45
Gln Leu Lys Val Gly Ile Leu His Leu Gly Ser Arg Gln Lys Lys Ile		
50	55	60
Arg Ile Gln Leu Arg Ser Gln Val Leu Gly Arg Glu Met Arg Asp Met		
65	70	75
		80
Glu Gly Asp Leu Gln Glu Leu His Gln Ser Asn Thr Gly Asp Lys Ser		
	85	90
		95
Gly Phe Gly Phe Arg Arg Gln Gly Glu Asp Asn Thr		
100	105	

<210> 794

<211> 970

<212> DNA

<213> Homo sapiens

<400> 794

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<210> 795

<211> 152

<212> PRT

<213> Homo sapiens

<400> 795

Arg Pro Lys Glu Glu Val Pro Arg Ser Lys Ala Leu Glu Val Thr Lys
5 10 15
Leu Ala Ile Glu Ala Gly Phe Arg His Ile Asp Ser Ala His Leu Tyr
20 25 30
Asn Asn Glu Glu Gln Val Gly Leu Ala Ile Arg Ser Lys Ile Ala Asp
35 40 45

261

Gly Ser Val Lys Arg Glu Asp Ile Phe Tyr Thr Ser Lys Leu Trp Ser
50 55 60

Thr Phe His Arg Pro Glu Leu Val Arg Pro Ala Leu Glu Asn Ser Leu
65 70 75 80

Lys Lys Ala Gln Leu Asp Tyr Val Asp Leu Tyr Leu Ile His Ser Pro
85 90 95

Met Ser Leu Lys Pro Gly Glu Glu Leu Ser Pro Thr Asp Glu Asn Gly
100 105 110

Lys Val Ile Phe Asp Ile Val Asp Leu Cys Thr Thr Trp Glu Ala Met
115 120 125

Glu Lys Cys Lys Asp Ala Gly Leu Ala Lys Ser Ile Gly Val Ser Asn
130 135 140

Phe Asn Pro Gln Ala Ala Gly Asp
145 150

<210> 796

<211> 2435

<212> DNA

<213> Homo sapiens

<400> 796

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262

```

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taatttaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2435

```

<210> 797

<211> 120

<212> PRT

<213> Homo sapiens

<400> 797

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Thr Thr Arg Pro Arg Thr Arg Gly Gln Arg Glu Ser Trp Arg His Leu
          5                      10                      15

```

```

Ala Ser Gly Ala Gly Val Gly Leu Gly Thr Ala Gly Ser Arg Pro Asp
          20                      25                      30

```

```

Arg Gly Gly Val Gly Gly Glu Thr Arg Ala Ala Leu Ala Arg Ala Pro
          35                      40                      45

```

```

Pro Pro Gly Arg Ala Glu Trp Tyr Gly Pro Ala Gly Val Lys Ala Gly
          50                      55                      60

```

```

Gly Arg Arg Arg Val Pro Arg Arg Arg Arg Arg Trp Gly Cys Val Gln
          65                      70                      75                      80

```

```

Glu Glu Arg Trp Ala Gly Pro Ala Arg Val Gly Gly Arg Pro Arg Gly
          85                      90                      95

```

```

Pro Gly Arg Ala Ala Ala Arg Arg Ala Ala Ala Ser Thr Arg Ala Ala
          100                      105                      110

```

```

Ser Pro Arg Cys Thr Thr Cys Arg
          115                      120

```

<210> 798

<211> 164

<212> PRT

<213> Homo sapiens

<400> 798

```

Pro Arg Val Arg Gly Arg Val Gly Ser Ala Ser His Gly Gly Thr Trp

```

263

	5	10	15
Arg Ala Glu Pro Glu Ser Gly Trp Gly Pro Arg Gly Arg Gly Arg Thr	20	25	30
Ala Ala Gly Ser Gly Glu Lys Arg Ala Leu Pro Trp His Gly Pro Pro	35	40	45
Pro Pro Ala Ala Arg Asn Gly Met Ala Arg Pro Glu Leu Arg Pro Gly	50	55	60
Gly Gly Gly Glu Ser Arg Gly Gly Gly Asp Asp Gly Ala Ala Cys Arg	65	70	75
Arg Asn Ala Gly Gln Gly Arg Arg Gly Ser Gly Gly Ala Arg Gly Ala	85	90	95
Arg Ala Glu Arg Arg Arg Ala Gly Arg Gln His Pro Leu Gly Pro His	100	105	110
Arg Arg Gly Ala Gln Arg Ala Ala Glu Arg Ala His Pro Ala Ala Ala	115	120	125
Val Arg Val Gly Pro Arg Gln Gly Ala Glu Pro Arg Gly His Asp Pro	130	135	140
Gly Gly Pro Arg Gln Arg Ala Pro His Arg Cys Pro Leu Asp Gln Arg	145	150	155
Gly Pro Gly Arg			160

<210> 799

<211> 60

<212> PRT

<213> Homo sapiens

<400> 799

His Ala Ser Ala Asp Ala Trp Ala Ala Arg Val Met Ala Ala Pro Gly	5	10	15
---	---	----	----

Glu Arg Ser Arg Ser Arg Ala Gly Asp Arg Gly Val Glu Ala Gly Pro	20	25	30
---	----	----	----

Arg Arg Gly Arg Gly Arg Asn Ala Arg Cys Pro Gly Thr Gly Pro Pro	35	40	45
---	----	----	----

Pro Arg Pro Arg Gly Met Val Trp Pro Gly Arg Ser	50	55	60
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<210> 800

<211> 2477

<212> DNA

<213> Homo sapien

<400> 800

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gtgtttgaat  tccagttgac  ttcagaggag  atgaaagcca  tagatggcct  aaacagaaat  180
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<210> 801

<211> 1619

<212> DNA

<213> Homo sapien

<400> 801

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<210> 802

<211> 3115

<212> DNA

<213> Homo sapien

<400> 802

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<400> 806

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Cys Leu Leu Lys Gly Gly Tyr Glu Arg Phe Ser Ser Glu Tyr Pro Glu
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ttataacttt ataaagtttt tcatcatcac cacagcaatc acaaagagaa taattatgaa 3780
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```

<210> 808

<211> 781

<212> DNA

<213> Homo sapiens

<400> 808

```

gcggcggagc tgtgagccgg cgactcgggt ccctgaggtc tggattcttt ctccgctact 60
gagacacggc gggtaggtcc acaggcagat ccaactggga gttgaagtgt gaggtagagt 120
gaagaggaac cagcaggctt ccggagggtt gtgtgggtcag tgactcagag tgagaaggcc 180
ctcgaagtcg tcgtccctct catgcggtgc cagcccatg gaccttcttg tctcgtcacg 240
gccataacta gggaggaagg agggccgagg agtggagggg ctcaggcgaa gctggggtgc 300
tgttgggggt atccgagtc cagaagcacc tggaaacctg acagaagatt ctggactccc 360
cagacgggac caggagagg acggcatgag cgacacacac aaacacagaa ccacacagcc 420
agtcccagga gccagtaat ggagagcccc aaaaagaaga accagcagct gaaagtcggg 480
atcctacacc tgggcagcag acagaagaag atcaggatac agctgagatc ccagtgcgcg 540
acatggaagg tgatctgcaa gagctgcac agtcaaacac cggggataaa tctggatttg 600
ggttccggcg tcaaggtgaa gataaatcct aaagaggaac actgtaaaat gccagaagca 660
ggtgaagagc aaccacaagt ttaaatgaag acaagctgaa acaacgcaag ctggttttat 720
attagatatt tgacttaaac tatctcaata aagttttgca gctttcacca aaaaaaaaaa 780
a

```

781

<210> 809

<211> 160

273

<212> PRT

<213> Homo sapiens

<400> 809

Met Arg Cys His Ala His Gly Pro Ser Cys Leu Val Thr Ala Ile Thr
 5 10 15

Arg Glu Glu Gly Gly Pro Arg Ser Gly Gly Ala Gln Ala Lys Leu Gly
 20 25 30

Cys Cys Trp Gly Tyr Pro Ser Pro Arg Ser Thr Trp Asn Pro Asp Arg
 35 40 45

Arg Phe Trp Thr Pro Gln Thr Gly Pro Gly Glu Gly Arg His Glu Arg
 50 55 60

His Thr Gln Thr Gln Asn His Thr Ala Ser Pro Arg Ser Pro Val Met
 65 70 75 80

Glu Ser Pro Lys Lys Lys Asn Gln Gln Leu Lys Val Gly Ile Leu His
 85 90 95

Leu Gly Ser Arg Gln Lys Lys Ile Arg Ile Gln Leu Arg Ser Gln Cys
 100 105 110

Ala Thr Trp Lys Val Ile Cys Lys Ser Cys Ile Ser Gln Thr Pro Gly
 115 120 125

Ile Asn Leu Asp Leu Gly Ser Gly Val Lys Val Lys Ile Ile Pro Lys
 130 135 140

Glu Glu His Cys Lys Met Pro Glu Ala Gly Glu Glu Gln Pro Gln Val
 145 150 155 160

<210> 810

<211> 624

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(624)

<223> n=A,T,C or G

<400> 810

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 agccctcat gatnggcacc gggacagtca cgaggaaggg ctccaccttc cggcccatgg 120
 acacggatgc cgaggaggca ggggtgagca ccgatgccgg cggccactat gactgcccgc 180
 agcggggccgg ccgccacgag tacgcgctgc ccctggcgcc cccggagccc gagtacgcca 240
 cggccatcgt ggagcggcac gtgctgcgcg cccacacgtt ctctgcgcag agcggctacc 300
 gcgtcccagg gccccagccc ggccacaaac actccctctc ctcgggcggc ttctcccccg 360
 tagcgggtgt gggcgcccag gacggagact atcaaaggcc acacagcgca cagcctgcgg 420
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```

actctcagaa gcccccaacg catccccgga caagtgcag ctattctgcc cccagagact 540
gcctcacacc cctcaaccag acggccatga ctgccctttt gtgaacacaa tgtgaaagaa 600
gcctgctgtg gtactgagcg tcgg                                     624

```

```

<210> 811
<211> 572
<212> DNA
<213> Homo sapiens

```

```

<400> 811
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acggcctgga gcaggcgctg cggaggcgcg agagcgagca cgagaggagag gtgcgcgctc 180
tgtacgagga gacggagcag cttcgggagc agagccggcg cccgccgagt cagaacttcg 240
cccgcgggga gcggagaagc cgtctggagc tggagctgca gatccgcgag caggacctgg 300
aacgcgcggg cctgcggcag cgggagttag agcagcagct gcacgcccag gctgcggagc 360
acctggaggc acaggcccag aactcccagc tgtggcgggc gcacgaggcg ctgcgaacgc 420
agctggaggg ggcgcaggag cagatccgca ggctggagag cgaagcacga ggccgccagg 480
agcaaaccga acgagacgtg gtcgccgtct ccaggaacat gcagaaagag aaagtcagcc 540
tgctacggca actggagctg ctcaggagc tg                                     572

```

```

<210> 812
<211> 594
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(594)
<223> n=A,T,C or G

```

```

<400> 812
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gctgccgagg gccgcgcggt gtacgtggtg gacgacgcag ctgtcctggg cgcagaggac 180
ccagcgggtgt acggcgattc tgcccgtgag aaggcattgc gtggagctct gcgagcctcc 240
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ggtttccgtt acgagctcta ctgcctggca cgggcggcgc gcaccccgcg ctgcctggtc 360
tactgcgtac ggcccggcgg cccgatcgcg ggacctcagg tggcggggcg gaacgagaa 420
cctggccgga acgtcagtggt gagttggcgg ccacgcgctg aggaggacgg gagagcccag 480
gcggcgggca gcagcgtcct cagggaactg catactgcgg actctgtagt aaatggaagt 540
gcccaggccg acgtacccaa ggaactggag cgagaagaat ccggggctgc ggag 594

```

```

<210> 813
<211> 561
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(561)

```

<223> n=A,T,C or G

<400> 813

```
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tagatgaagc caaacattgt tggaggtagt gaaatcttag actccaccat gtgtccagga 120
nccccattgac gtccctctct ctgaaaactc cgtgtggccc tcgctctgca ctgtcatgag 180
gcggtgatgg agctagatac ccaccacgga caatgatcat cagtttgggg ttctctgggt 240
ctcacaggga cgcacattct aggggtagca cgacactccc cctgtagttg ctccacacaa 300
acgggatctc tcatccaggc gatacgtctg gtccctgtggc atgtgggtct cnacgaaaca 360
ccagggangc attatgttgg ggacttcttg gggctctgct ggtctctgct ccagacacga 420
ttaatccgaa atgtgttaan tcgancacat ggggccacgt ccaggacagc tcccatcgaa 480
ctctcnaggc tctctanctc agggatgaag gaggtnaagt gatcgatnct cacaagcgan 540
agctctcgcn cnatatctgc g                                     561
```

<210> 814

<211> 307

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(307)

<223> n=A,T,C or G

<400> 814

```
cntcgnngng ttggttgtgt gggntnttct cgggtgattg ggtgnnatta ctggacccaa 60
ccnncgtgga aanggctggg nncgcggccg ntctngcaga agtatccga tttttttttt 120
tttttttttt tttttggngg agggaaantt ncagacatag ctttattgct gactccctgc 180
cccttcnag ccctagtcac aggcnnacag gntgtttgt aanttaaant ttcnggaaaa 240
tngngtntt tntgcatnca anagaagggg tgccaaangn ggggtattgc ttctgggtgg 300
nttacc                                     307
```

<210> 815

<211> 784

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(784)

<223> n=A,T,C or G

<400> 815

```
ggcacgagat ataatcagac tcttactcct gtacttctag aaatgatgca aacacttcaa 60
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gttggattaa gctgcttatg agctctttga cagtgttgat tttgatcagt ggtttaaaaa 180
ccagcttctt ccagaattac aagtcattca caataggtat aagccattgc gacgcagggt 240
gatttggctc atcggtcagt ggatttctgt gaaattcaag tctgacttaa gacctatgct 300
ttatgaagca atctgtaact tgcttcaaga tcaagattta gtggccgtat tgaaacagct 360
acaactttga agttaactgt tgatgatttt gaatttagaa cagatcagtt tctaccgtat 420
ttggaaacca tgttcacact actttttcag ttactgcagc aagttacaga atgtgacaca 480
aagatgcatg ttttgcatgt cctttcttgt gtgatcgaaa gagtcaacat gcagatacga 540
ccatatgtgg gatgttggg acaatatattg cccctccttt ggaagcagaa gtgaanaaca 600
caatatgttg agatgtgcta ttttgaccac acttattcat cttggtcagg gattangagc 660
agacagcaag acctgtccct ttctgtctcc agttattcac tgagtaccag atgtttcaca 720
```

276

gccttcncat gtttattttt ctggaaaatg ggtaaaaaat atnggtanga acctttggga 780
aaac 784

<210> 816
<211> 813
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(813)
<223> n=A,T,C or G

<400> 816
ggcacgagca ggctgggaag aagtccttgc ttctcaaggc cacgtaccgg ccgcgtcctt 60
ccacccttgc cctttaaacc acagatgcca aatgatacgc caacagacac tacattcccc 120
agcagctgct gccagagccc tcttgtagct tctttatttt ctgtttcttt ccagctttcc 180
taccctccta tcccccttg tgtttgggcc acaattttga aataattttt attataggta 240
tgtgtgcca aagccagatt ttataaagg aaataaatt aagaatttaa acagtaaaag 300
ccagtgtctc aaaatgtcag cattaaaatg tgaaggggac agcaggggtg gaaccggaaa 360
cacacattgc caaacagttg ccaactgaac tgctgcttct catgggccgt tcttttcttt 420
gcccttaagg tcaatgccag tgtccagacg agcagtgtag aaaagctccc tgtgtgggtt 480
gtcgtgaggt ctgcttgat ctcttcactg gcgttagttt cattagctct ttattctcct 540
tacgttcgag tgaatctgcc aagaacactg gtggatagta ttatcctaac acttttggtt 600
tggtggcggtg gaagggggcag ggaatagtga gctggcttta ccaccttcag gatctcgaat 660
tggtgcgctt aacctaaaga agattgtgga cttatcaaaa gtcaccgctc agtggtcgtc 720
aagcatgtat ttatgtgacn atcatactag ggaggggatg gttgggaatt cttccatgtg 780
caaatttngn ccgcaanaa gcaaaactgg ngt 813

<210> 817
<211> 229
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(229)
<223> n=A,T,C or G

<400> 817
gaaactttta cattaatgat ttattaaaaa aaacaactcc ttgtccact ccactgngct 60
gcttgtaatc tccatacatg gcctccattt tcaactgttt tnttggtcac anagctccaa 120
acanacacat ttttttttcc aggtaaaagc tgtttttagt ttgtagtaca aatgtgactg 180
catccaatac tgacacattg ttcctttggc ccacagtccc antcaccac 229

<210> 818
<211> 781
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(781)
<223> n=A,T,C or G

<400> 818
ggcacgaggt gtgtgtgtgt gtgtgtgtgt aacacatggg cattggctct tccaggacaa 60
cttggtagg gctccagggt ggccctctcag gcaggaacag gcttttttcc tcctgtcttt 120
tcctcacatc acgtcctgcc ccaggctact gcataaataa gtgctttgga aagtattcat 180
ctagaaagta acataaatac tgtacataga aaagggttgc cgccccttag ccttcgcact 240
gccccagaga gctctccaca tattgcacac ggccctccca gccctgtggg gtccaggcct 300
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tgctccaaa ggggagctct agggtagtca gtgggtacca gaagccttgc tcggcctcgc 420
tggtggcctt ctaccangga tgctttcaca aggatgagac agaatcccaa tggtaggcc 480
ctgcttgga actctgtca aggtctgcat gtggcctggg aggagacagg caggctgang 540
gcaggtggac aggtgantcc tggccacana aggcaggctc acacccttca cangaatagg 600
tggtttngc tgcatctcg gccacggtc tctnntgcg ccaccccccc ttntgaatc 660
gnaantctc aaanccctta ccaccactt atgaccnanc atttttangg cctggcttga 720
aggngggggc cttnggcccc ccnaagggg aaatncccc ggnngaattc ccaangggga 780
a 781

<210> 819
<211> 199
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(199)
<223> n=A,T,C or G

<400> 819
cnnngtgga anggctgggn nngcgccgt tttcgnngta gtatcgcn tttttttttt 60
ttttgtggg aggtntgcn gtntttgntt gctctctcaa attccaggaa ttgacttatt 120
taattaatgc ctgcaacctg tgctagcaaa tatttgnaca aaacnanttg tgttgngat 180
gttcttttgg gtcgggcag 199

<210> 820
<211> 211
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(211)
<223> n=A,T,C or G

<400> 820
nnnggcacga ggagagagag agagagagag agagagagag agagagagag agagagagag 60
agagagagag agagagagag agagagagag agagagagag agagagagag agagagagag 120
agacagtact ntgtgtgtct ctctgtctcn aagtaacnnc tgaggatct gntntctgt 180
tntngtaca cngtatctct cntggncata t 211

<210> 821
<211> 952
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

<222> (1)...(952)

<223> n=A,T,C or G

<400> 821

```
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cagcaccaag acgaaatggg aaactacatg tccccagggt cgaggctgca ggggcagact 180
ctggtgtgaa caggggggat gtgaccacct aaggaaaagg tcacacctgt ctggtatca 240
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caactccagg gtcatgaggt cagagtaaag tgcagaggtt tttaaacata accaaaattt 360
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cctcatcttt agcaacacat ttgcttttca aggtgttcct tgtggaaaca cacatacaca 480
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ggcccaatgt aaatacttcc gcagagatgg agggcattca aaacagggtt tgaaaggatc 660
cagcctatct tggactttgt tctggaancc anggattcag cnttggccac ctgtgccagg 720
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tttgngtggg ccaacgtttg gcctnaacaa atctngcggg ttgggatntt cttnntttcn 840
cncccagggg accnaaaacc ccctacntg naataacctt ttttttttnn aaccttttan 900
ccantgggnt tncnaaaaa acttgncccc ttttttttnc caanggnaaa at 952
```

<210> 822

<211> 587

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(587)

<223> n=A,T,C or G

<400> 822

```
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ttttagggaa gacacgcagt ttcacaagaa acaatgatth ttctcaaaca atagaaaaaa 120
aggtcttttt gaaaaatcca ctgtcttaga tgaaaagtct acccagcaag cactggggca 180
gttctgagag tagaaaccag tgtggtggaa gttacttata ggaagtccag tgcagaggtc 240
tccacaagtc ctgattagtt ctgnaaggct ccattggggc agctcagggt aacagtggga 300
atgagctcac agacaaaggc aggcaccagt tcctntgccc gggatgcagg ctggctcact 360
ccccangcgg ntgcattctg cttcagactc atcaaactgc tgctgtccan ctncgncatg 420
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ttctgcttag ccttctncac tntgaaggnt gggctctttaa ctttttgatt tttttttccn 540
ggcaggggga accatgaatg gggtacatac ccacncnggg ntltggc 587
```

<210> 823

<211> 264

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(264)

<223> n=A,T,C or G

<400> 823

```
ntcnatnct actangncaa actgactccg ccctnagnca cctngtggtc canggctgcg 60
```

```

gagctgcgat acagccttcc gcgggtctgn tggaaacccg acctntcntg gtgtntntcc 120
ntcccncc ccaacccgcc aagggcctgc ctttctnct gggcctttgc cagcgtntng 180
ccanaccggg gccaaaccgg nccccgggca cattttaacc nagggcncnc ttntagaana 240
aaaccccggn tgatgttata aagg                                     264

```

<210> 824

<211> 520

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(520)

<223> n=A,T,C or G

<400> 824

```

tcaagcngcc cccantntga tggatatctg caaaattcnc cctttcaccc gccgcccgc 60
gcatgtctta ttatacaaca natccaactt ccctaagngg ntcacacatn ntaaggtatt 120
gttaacaaaa taggaaantc tattngaact aacaatcatc tctttgaatc tcntatccc 180
attaaaagca ttttctcaa tattctcat atcggttatg gncaatggat acccatctga 240
gctgggtgan ccctttaaat tnattatact taactttttg aaggctgtta taccgaagg 300
acaaacctaa ncaaccanca gatatacttg anggtntctc ctgtnatctc tcagattcca 360
atataccatt ttgccttnac acctacagcc cttaggggca tctctnttcc ncanaacaaa 420
ncatntcac taagacagnc tggggtnntn caccaatggc taccaaacct ctgnccgcna 480
cccaccgcnt aaanggcnga aattncnan ccacacgggt 520

```

<210> 825

<211> 2064

<212> DNA

<213> Homo sapiens

<400> 825

```

cggctgcgctg agcgcgggag gagcgtaggc agggcagcgc tggcgccagt ggcgacagga 60
gccgcgcgac cggaacaaat acacgggagg cgtcgccga aaagagtcgg cggtcctctc 120
tcgtaaacac actctcctcc accgggcctt cccctcgcg tctgcgcgac gcccggtcgg 180
gcgcccaggc ccgctccgac tgctatgtga ccgcgaggct gcgggaggaa ggggacaggg 240
aagaagaggg tctcccgcgg gagccctga ggaccaagt tgcggccact tctgcaggcg 300
tccctcttta gctctcgccc ccccttctt cagacctagg cggcccgggt tctcttctct 360
tctcgcgcg cccagccgcc tcggttcccc gcgacctagg tgacgatgga ggagctgcgg 420
gagatggact gcagtgtgct caaaaggctg atgaaccggg acgagaatgg cggcggcgcg 480
ggcggcagcg gcagccacgg caccctgggg ctgccgagcg gcggcaagt cctgctgctg 540
gactgcagac cgttcctggc gcacagcgcg ggctacatcc taggttcggg caacgtgcgc 600
tgtaacacca tcgtgcggcg gcgggctaag ggctccgtga gcctggagca gacccgcc 660
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caggcgtgc gccgcaacgc cgagcgacc gacatctgcc tgctcaaagg cggtatgag 840
aggtttctct ccgagtacct agaattctgt tctaaaacca aggccctggc agccatcca 900
cccccggttc ccccgagtgc cacagagccc ttggacctgg gctgcagctc ctgtgggacc 960
ccactacag accagggggg tctgtggag atccttccct tctctacct cggcagtgcc 1020
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tctcggact gcccaaacca ctttgaagga cactatcagt acaagtgcac cccagtggaa 1140
gataaccaca aggccgacat cagctcctgg ttcattggaag ccatagagta catcgatgcc 1200
gtgaaggact gccgtgggcg cgtgctggg cactgccagg cgggcacctc gcggtcggcc 1260
accatctgcc tggcctacct gatgatgaag aaacgggtga ggctggagga ggccttcgag 1320
ttcgtaagc agcgcgcgag catcatctcg cccaacttca gcttcatggg gcagctgctg 1380

```

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Val Asn Val Arg Cys Asn Thr Ile Val Arg Arg Arg Ala Lys Gly Ser
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Val Ser Leu Glu Gln Ile Leu Pro Ala Glu Glu Glu Val Arg Ala Arg
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Leu Arg Ser Gly Leu Tyr Ser Ala Val Ile Val Tyr Asp Glu Arg Ser
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Gly Gly Tyr Glu Arg Phe Ser Ser Glu Tyr Pro Glu Phe Cys Ser Lys
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Thr Lys Ala Leu Ala Ala Ile Pro Pro Pro Val Pro Pro Ser Ala Thr
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Gln Gly Gly Pro Val Glu Ile Leu Pro Phe Leu Tyr Leu Gly Ser Ala
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Leu Leu Asn Val Ser Ser Asp Cys Pro Asn His Phe Glu Gly His Tyr
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282

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290 295 300

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Arg Gly Lys Thr Pro Ala Thr Pro Thr Ser Gln Phe Val Phe Ser Phe
355 360 365

Pro Val Ser Val Gly Val His Ser Ala Pro Ser Ser Leu Pro Tyr Leu
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His Ser Pro Ile Thr Thr Ser Pro Ser Cys
385 390

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09/560,406	27 April 2000 (27.04.2000)	US
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(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:

— with international search report

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2 August 2001

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.



WO 01/00828 A3

(54) Title: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF LUNG CANCER

(57) Abstract: Compositions and methods for the therapy and diagnosis of cancer, such as lung cancer, are disclosed. Compositions may comprise one or more lung tumor proteins, immunogenic portions thereof, or polynucleotides that encode such portions. Alternatively, a therapeutic composition may comprise an antigen presenting cell that expresses a lung tumor protein, or a T cell that is specific for cells expressing such a protein. Such compositions may be used, for example, for the prevention and treatment of diseases such as lung cancer. Diagnostic methods based on detecting a lung tumor protein, or mRNA encoding such a protein, in a sample are also provided.

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 00/18061

A. CLASSIFICATION OF SUBJECT MATTER IPC 7 C12N15/12 C07K14/47 C07K14/705 C07K16/18 C12N15/62 A61K38/17 C12Q1/68 G01N33/577 C07K17/00		
According to International Patent Classification (IPC) or to both national classification and IPC		
B. FIELDS SEARCHED Minimum documentation searched (classification system followed by classification symbols) IPC 7 C12N C07K A61K C12Q		
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched		
Electronic data base consulted during the international search (name of data base and, where practical, search terms used) EPO-Internal, BIOSIS, MEDLINE		
C. DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 97 33993 A (SAGAMI CHEMICAL RESEARCH CENTER ;KATO S ET AL.) 18 September 1997 (1997-09-18) whole document especially SEQ ID NO:2 ---	1,2,4-60
X	WO 98 31799 A (HUMAN GENOME SCIENCES INC ; NI J ET AL.) 23 July 1998 (1998-07-23) whole document especially pages 16, 42 and 43 --- <div style="text-align: center;">-/--</div>	1,2,4-60
<div style="display: flex; justify-content: space-between;"> <input checked="" type="checkbox"/> Further documents are listed in the continuation of box C. <input checked="" type="checkbox"/> Patent family members are listed in annex. </div>		
<div style="display: flex;"> <div style="flex: 1;"> <p>* Special categories of cited documents :</p> <p>"A" document defining the general state of the art which is not considered to be of particular relevance</p> <p>"E" earlier document but published on or after the international filing date</p> <p>"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)</p> <p>"C" document referring to an oral disclosure, use, exhibition or other means</p> <p>"P" document published prior to the international filing date but later than the priority date claimed</p> </div> <div style="flex: 1;"> <p>"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention</p> <p>"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone</p> <p>"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.</p> <p>"&" document member of the same patent family</p> </div> </div>		
Date of the actual completion of the international search <div style="text-align: center; font-weight: bold;">2 February 2001</div>		Date of mailing of the international search report <div style="text-align: center; font-weight: bold;">16.02.01</div>
Name and mailing address of the ISA European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016		Authorized officer <div style="text-align: center; font-weight: bold;">Cupido, M</div>

INTERNATIONAL SEARCH REPORT

In. .ational Application No
PCT/US 00/18061

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>WU Y ET AL: "Activation of globin gene expression by cDNAs from induced K562 cells"</p> <p>JOURNAL OF BIOLOGICAL CHEMISTRY,US,AMERICAN SOCIETY OF BIOLOGICAL CHEMISTS, BALTIMORE, MD, vol. 266, no. 26, 15 September 1991 (1991-09-15), pages 17566-17572, XP002037858 ISSN: 0021-9258 figure 8</p> <p style="text-align: center;">---</p>	1,2,4-17
X	<p>DATABASE EMBL/GENESEQ [Online] EBI; XP002153175 AC NO X21973 18 May 1999;Human HP00966 coding sequence, having 100% sequence identity in a 400 bp overlap with SEQ ID NO:1</p> <p style="text-align: center;">---</p>	1,2,4-17
A	<p>GÜRE ET AL: "Human lung cancer antigens recognized by autologous antibodies: definition of a novel cDNA derived from the tumor suppressor gene locus on chromosome 3p21.3"</p> <p>CANCER RESEARCH,AMERICAN ASSOCIATION FOR CANCER RESEARCH, BALTIMORE, MD,US, vol. 58, 1 March 1998 (1998-03-01), pages 1034-1041, XP002103188 ISSN: 0008-5472 page 1038</p> <p style="text-align: center;">---</p>	1-60
A	<p>CHEN S-L ET AL: "Isolation and characterizaton of a novel gene expressed in multiple cancers"</p> <p>ONCOGENE,GB,BASINGSTOKE, HANTS, vol. 12, no. 4, 15 February 1996 (1996-02-15), pages 741-751, XP002106655 ISSN: 0950-9232 the whole document</p> <p style="text-align: center;">---</p>	1-60
A	<p>US 5 589 579 A (BOLLON ARTHUR P ET AL) 31 December 1996 (1996-12-31) the whole document</p> <p style="text-align: center;">---</p>	1-60
X	<p>DATABASE EMBL/GENESEQ [Online] EBI; XP002159111 AC NO AA948244 5 May 1998; Human cDNA clone IMAGE:1588176 3', nt 1-379 are 100% identical to nt 770-392 in SEQ ID NO:808</p> <p style="text-align: center;">---</p> <p style="text-align: center;">-/--</p>	5-8,58, 59

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 00/18061

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>DATABASE EMBL/GENESEQ [Online] EBI; XP002159112 AC NO AA620697 16 October 1997; Human cDNA clone IMAGE:1049185 3', nt 1-378 are 100% identical to nt 769-392 in SEQ ID NO:808 -----</p>	<p>5-8,58, 59</p>

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 00/18061

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

Although claims 21, 22, 29-31, 34, 35 (insofar as an in vivo method is envisaged) and 37-39 are directed to a method of treatment of the human body, the search has been carried out and based on the alleged effects of the compositions.
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

1-60 (all partly)
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☒ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International Application No. PCT/US 00/18061

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1,2 and 4-60 (all partly and as far as applicable)

Invention 1:

Polypeptide encoded by a polynucleotide sequence recited in SEQ ID NO:1 or polypeptide encoded by sequences that hybridize to a sequence recited in SEQ ID NO:1. Fusion protein comprising said polypeptide. Polynucleotide encoding said fusion protein. Pharmaceutical composition or vaccine comprising said polypeptide, and method for inhibiting the development of a (lung) cancer in a patient, isolated polynucleotide; method for removing tumour cells from a biological sample; method for stimulating and/or expanding T cells specific for a lung tumour protein; isolated T cell population; method for determining or monitoring a cancer in a patient; diagnostic kit; oligonucleotide.

2. Claims: 1-60 (all partly and as far as applicable)

Inventions 2-652:

As invention 1, the subject-matter of said inventions is limited to SEQ ID NOs:

11-13,15,20,23-27,29,30,33,34,39,41,43-46,51,52,57,58,60,62,65-67,69-71,74,76,79,80,84,86,89-92,95,97,98,101,110,111,113-119,121-128,130-134,136,138,139,141,143,146-151,153,154,157-160,162-164,167-178,180,181,183,186-190,192,193,195-220,224,226-231,234,236,237,240,241,244-246,248,254,255,261,262,266,270,275,280,282,283,288,289,290,292,295,301,303,304,309,311,341-782,784-787,790-800,802,804,806-809 and 811-827.

wherein

invention 2 is limited to SEQ ID NO 11
invention 3 is limited to SEQ ID NO 12, etc...
invention 652 is limited to SEQ ID NO 827

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 00/18061

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			CA 2248355 A	18-09-1997
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